

STIC-Biotech/ChemLib

176081

From: Seharaseyon, Jegatheesan  
 Sent: Tuesday, January 10, 2006 9:20 AM  
 To: STIC-Biotech/ChemLib  
 Subject: Re: 10/007270

CFF

Importance: High

Hi,  
 Please search in the commercial and interference databases for  
 1. Nucleotides encoding SEQ ID NO: 2.  
 2. Nucleotides of SEQ ID NO: 1 and a word search of atleast 12 nucleotides.

Thanks.

J. Seharaseyon  
 Art Unit 1647  
 Remsen 4C61  
 Mailbox 4C70  
 Phone: (571)-272-0892  
 Fax: (571)-273-0892

1-3330 NA  
 2-797 aa  
 LB

\*\*\*\*\*  
 Searcher: \_\_\_\_\_  
 Searcher Phone: \_\_\_\_\_  
 Date Searcher Picked up: \_\_\_\_\_  
 Date completed: \_\_\_\_\_  
 Searcher Prep Time: \_\_\_\_\_  
 Online Time: \_\_\_\_\_

\*\*\*\*\*  
 Type of Search  
 NA# \_\_\_\_\_ AA# \_\_\_\_\_  
 S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
 Encode/Transl: \_\_\_\_\_  
 Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
 Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
 Vendors and cost where applicable  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 QUESTEL/ORBIT: \_\_\_\_\_  
 LEXIS/NEXIS: \_\_\_\_\_  
 SEQUENCE SYSTEM: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (Specify): \_\_\_\_\_

Searcher	STIC	IC
Searcher Phone	CM-1	STN
Date Searcher Picked up	Pre-S	Dialog
Date completed	Type of Search	APS
Searcher Prep Time	N.A. Sequence	Geninfo
Online Time	A.A. Sequence	SDC
	Structure	DARC/Questel
	Bibliographic	Other CGN

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2006, 04:51:25 ; Search time 1895 Seconds  
(without alignments)  
11711.571 Million cell updates/sec

Title: US-10-007-270-1  
Perfect score: 3330  
Sequence: 1 taacacgaagaggtatctc.....tactatagacataatcaat 3330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: geneeqn1980s:\*  
2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2004as:\*  
12: geneeqn2004bs:\*  
13: geneeqn2004bs:\*  
14: geneeqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3330	100.0	3330	9	ACCS7946 Human int
2	3330	100.0	3330	10	ADA14840 Human int
3	3125.6	93.9	3263	3	AAA46205 enco
4	3124.6	93.8	3261	9	ACCS7960 Human int
5	3124.6	93.8	3261	10	ADA14866 Human int
6	2765.8	83.1	2887	9	ACCS7947 Human int
7	2765.8	83.1	2887	10	ADA14842 Human int
8	2724.6	81.8	2966	3	AAA46328 enco
9	2184.2	65.6	2244	9	AAA46329 Interphot
10	2184.2	65.6	2244	9	ACCS7948 Human int
11	2184.2	65.6	2244	10	ADA14844 Human int
12	1375.6	41.3	3668	10	ACCS7950 Human int
13	1375.6	41.3	3668	10	ADA14847 Human int
14	1127.2	33.8	3206	3	AAA46309 enco
15	534	16.0	1726	10	ACCS7951 Mouse int
16	534	16.0	1726	10	ADA14849 Mouse int
17	491.6	14.8	1321	9	ACCS7952 Mouse int
18	491.6	14.8	1321	10	ADA14851 Mouse int
19	439	13.2	555	3	AAA46204 enco

20	439	13.2	555	9	ACCS7953	ACCS7953 Monkey in
21	439	13.2	555	10	ADA14853	ADA14853 Monkey in
22	204.6	6.1	1858	3	AAA46327	AAA46327 Exon 1 an
23	204.6	6.1	1858	9	ACCS7949	ACCS7949 Human int
24	204.6	6.1	1858	10	ADA14846	ADA14846 Human int
25	203.4	6.1	1465	3	AAA46206	AAA46206 enco
26	203.4	6.1	1465	13	ADA46596	ADA46596 Cancer-as
27	203.4	6.1	1466	9	ACCS7954	ACCS7954 Human int
28	203.4	6.1	1466	10	ADA14855	ADA14855 Human int
29	197.8	5.9	4204	9	AAA46310	AAA46310 enco
30	197.8	5.9	4204	9	ACCS7958	ACCS7958 Mouse int
31	197.8	5.9	4204	10	ADA14862	ADA14862 Mouse int
32	184.8	5.5	2964	9	ACCS7955	ACCS7955 Human int
33	184.8	5.5	2964	10	ADA14857	ADA14857 Human int
34	103	3.1	1094	3	AAA46321	AAA46321 Exon 13 o
35	61.8	1.9	1088	3	AAA46312	AAA46312 Exon 3 of
36	61	1.8	113515	6	AB134174	AB134174 Human imm
37	60	1.8	113515	6	ABN43651	ABN43651 Human spl
38	57.6	1.7	1817	3	AAA46320	AAA46320 Exon 12 o
39	56.4	1.7	434	5	ABV58531	ABV58531 Human pro
40	54.8	1.6	2000	11	ACL37108	ACL37108 Rice stre
41	54.6	1.6	3683	8	ABE210199	ABE210199 Haemato
42	54	1.6	16633	6	ABN79984	ABN79984 Human che
43	53.4	1.6	2000	11	ACL35887	ACL35887 Rice stre
44	53.2	1.6	6255	6	AB132960	AB132960 Human imm
45	52.6	1.6	516	8	ABX40620	ABX40620 Bovine ES

## ALIGNMENTS

RESULT 1	ACCS7946	standard; cDNA; 3330 BP.
ID	ACCS7946	
XX	ACCS7946	
XX	ACCS7946	
DT	11-AUG-2003	(first entry)
XX	ACCS7946	
DE	Human interphotoreceptor matrix IPM 150, isoform A, cDNA.	
KW	Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;	
KW	receptor; ophthalmological; gene therapy; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	131..2586
FT		/*tag= a
FT		/product= "IPM 150"
FT		/transl_except= (pos:668..756,aa:Thr-Asp)
FT	sig_peptide	131..190
FT		/*tag= b
XX		
PN	W02003039346-A2.	
XX		
XX	15-MAY-2003.	
PD		
XX		
PF	08-NOV-2002; 2002MO-US036090.	
XX		
PR	08-NOV-2001; 2001US-00077270.	
XX		
XX	(IOWA) UNIV IOWA RES FOUND.	
PA		
XX		
PI	Hageman GS, Kuehn MH;	
XX		
DR	WPI; 2003-441440/41.	
XX		
XX	P-PSDB; ABR42342.	
PT		
PT	New interphotoreceptor matrix proteins and polynucleotides, useful for	
PT	treating or preventing photoreceptor death or retinal detachment, or for	
PT	treating ocular disorders.	
XX		

PS Claim 1; Page 77; 105bp; English.

XX The present sequence is that of cDNA encoding isoform A of novel human  
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or IPM2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polypeptides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression

Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;

Query Match 100.0%; Score 3330; DB 9; Length 3330;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TAACCAAGAGGATTCCTCATCATCTGATCATATATATATATTTTACATTTTC	60
DB	1	TAAACCAAGAGGATTCCTCATCATCTGATCATATATATATATTTTACATTTTC	60
QY	61	TGTATCTTTTATAGATTTGAAGGTTGTTCTGTGATTTGTAACAAATTCAAATGAC	120
DB	61	TGTATCTTTTATAGATTTGAAGGTTGTTCTGTGATTTGTAACAAATTCAAATGAC	120
QY	121	AAAAGCAGAAATGTATTTGAAAAGTAAAGAGCTATTTTGTGATTTTCTCA	180
DB	121	AAAAGCAGAAATGTATTTGAAAAGTAAAGAGCTATTTTGTGATTTTCTCA	180
QY	181	AGTTCAAGGAACCAAGATATCTCCATTAATATATATATATATTTTCAAGATAGA	240
DB	181	AGTTCAAGGAACCAAGATATCTCCATTAATATATATATATATTTTCAAGATAGA	240
QY	241	CAATCCCAAGAAATGAAACAACTGAAAGTAAGTAAATGTACAAATGTCAATAT	300
DB	241	CAATCCCAAGAAATGAAACAACTGAAAGTAAGTAAATGTACAAATGTCAATAT	300
QY	301	GAGAGCAATATTCGATTTGGCAAGATGGAACAAAGATTCGATTTTCCCAACGGG	360
DB	301	GAGAGCAATATTCGATTTGGCAAGATGGAACAAAGATTCGATTTTCCCAACGGG	360
QY	361	GGTTAAAGCTGTCCACAGGAATCCATGAACAGATTTTGAAGCTTCGAGCTTATTA	420
DB	361	GGTTAAAGCTGTCCACAGGAATCCATGAACAGATTTTGAAGCTTCGAGCTTATTA	420
QY	421	TGATTTGAGAGTGTCTCAGGAAGCAGATATGGAAGATATCGGATCTTTCTGATCGAT	480
DB	421	TGATTTGAGAGTGTCTCAGGAAGCAGATATGGAAGATATCGGATCTTTCTGATCGAT	480
QY	481	CCCTGACACAGGGGAATATCAGAGCTGGGTCAAGCATCTCCAGCAGGAACCTTCTGCT	540
DB	481	CCCTGACACAGGGGAATATCAGAGCTGGGTCAAGCATCTCCAGCAGGAACCTTCTGCT	540
QY	541	CTTTGACATTTGAAAAAATCTGACAAATCCAGGAGACCTGGATCTTCCAGCAGAG	600
DB	541	CTTTGACATTTGAAAAAATCTGACAAATCCAGGAGACCTGGATCTTCCAGCAGAG	600
QY	601	AATTAACACAGAAAGTTTCTCTGACAGAAAGATGAATATCTGACAGAAAGCATTGGG	660
DB	601	AATTAACACAGAAAGTTTCTCTGACAGAAAGATGAATATCTGACAGAAAGCATTGGG	660
QY	661	AGAGCTGTGGAACCATTTGTCAATTTCAACAGCAATCTATCTTCAAGACTTTGGGAGT	720
DB	661	AGAGCTGTGGAACCATTTGTCAATTTCAACAGCAATCTATCTTCAAGACTTTGGGAGT	720

QY	721	ATTCAGAAAAACCTCAGAGAACAAATTCAGATGTGGCAACGTCTCACTTGGGCT	780
DB	721	ATTCAGAAAAACCTCAGAGAACAAATTCAGATGTGGCAACGTCTCACTTGGGCT	780
QY	781	TTCCCTGTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATATATCTCAAGAC	840
DB	781	TTCCCTGTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATATATCTCAAGAC	840
QY	841	ACCAAGATGCTTACACAGAAAGAGAAACAGATTTGCTGTGTGGAGACAGAGGTG	900
DB	841	ACCAAGATGCTTACACAGAAAGAGAAACAGATTTGCTGTGTGGAGACAGAGGTG	900
QY	901	GAGCTCAGCGTCTCTGTGTAAACAGAAAGTTTCAAGGACAGCTCGTCACTCCAGTCC	960
DB	901	GAGCTCAGCGTCTCTGTGTAAACAGAAAGTTTCAAGGACAGCTCGTCACTCCAGTCC	960
QY	961	CCATATTTACAGAGAGCTAGCAGAAAGTCCCACTTCAGATGCAAAAGATTTTAAGAA	1020
DB	961	CCATATTTACAGAGAGCTAGCAGAAAGTCCCACTTCAGATGCAAAAGATTTTAAGAA	1020
QY	1021	CTTCAGAGATTCAAAAAATCCATGTGTAGATTTTGAACCAAGAAAGAAAGATGGC	1080
DB	1021	CTTCAGAGATTCAAAAAATCCATGTGTAGATTTTGAACCAAGAAAGAAAGATGGC	1080
QY	1081	TCAAGCTCAGAGAGATGCACTTACGAGCATCTTTAAGAGACACAGTGCAGAAACAAA	1140
DB	1081	TCAAGCTCAGAGAGATGCACTTACGAGCATCTTTAAGAGACACAGTGCAGAAACAAA	1140
QY	1141	AGCCTGCAAGTACCTCTGTCTTTTGTATTCACAAATAATGAAAGTGAAGATCTAT	1200
DB	1141	AGCCTGCAAGTACCTCTGTCTTTTGTATTCACAAATAATGAAAGTGAAGATCTAT	1200
QY	1201	CATGGAACCATGAGAGAGAGCAAGCAACCAAGATCTATCTCAGAGCTACAGACTCAA	1260
DB	1201	CATGGAACCATGAGAGAGAGCAAGCAACCAAGATCTATCTCAGAGCTACAGACTCAA	1260
QY	1261	AGGCTGATCAGCAAGACCTAGAGAGAAACATCTTTGATGTGGGACAAATTCAGTTC	1320
DB	1261	AGGCTGATCAGCAAGACCTAGAGAGAAACATCTTTGATGTGGGACAAATTCAGTTC	1320
QY	1321	ACTGATGAATTTGCTGTGATCACTGCAAGCTTTGTCTGACACCCATTCAGAGTGGCC	1380
DB	1321	ACTGATGAATTTGCTGTGATCACTGCAAGCTTTGTCTGACACCCATTCAGAGTGGCC	1380
QY	1381	ACATCTTTTGTGTTATTAACAGAGAGTCTTCTTGAATCCAGAACTTCTCTGTGAA	1440
DB	1381	ACATCTTTTGTGTTATTAACAGAGAGTCTTCTTGAATCCAGAACTTCTCTGTGAA	1440
QY	1441	CCCAAGCTTGAGACAGTGAAGAGAGCAGAGATGTTACTGACACTTCTTGTGTTCCA	1500
DB	1441	CCCAAGCTTGAGACAGTGAAGAGAGCAGAGATGTTACTGACACTTCTTGTGTTCCA	1500
QY	1501	CTGTATAGGCTCTTACCTCTCTGTGAGAGCTTCACTTTCTTTATAGCATTAAGCATC	1560
DB	1501	CTGTATAGGCTCTTACCTCTCTGTGAGAGCTTCACTTTCTTTATAGCATTAAGCATC	1560
QY	1561	TTCTCTGATGATCAAGGACCAACAGATTAAGTGCATGACACAGAAATGCTATTA	1620
DB	1561	TTCTCTGATGATCAAGGACCAACAGATTAAGTGCATGACACAGAAATGCTATTA	1620
QY	1621	CCAGGCTCAGCAATCCCAACAGATTAATCTGCAATCAGCCAACTGGCTTGGGAAT	1680
DB	1621	CCAGGCTCAGCAATCCCAACAGATTAATCTGCAATCAGCCAACTGGCTTGGGAAT	1680
QY	1681	TCACATTCACCTGCATCTTCAAGATGACAGCGATCAAGTGCAGGAGGAGATATGCTC	1740
DB	1681	TCACATTCACCTGCATCTTCAAGATGACAGCGATCAAGTGCAGGAGGAGATATGCTC	1740
QY	1741	AGACCTTAAGTGAATGATCTGTCTGACACTCTGCGCCATCTGAGGTACCAAGATGC	1800
DB	1741	AGACCTTAAGTGAATGATCTGTCTGACACTCTGCGCCATCTGAGGTACCAAGATGC	1800
QY	1801	AGCGAATATGTTTGTCTCCAGATCATTTCTTGAGAGATACCACTCTGTCTCAGCTTAA	1860

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Db 1801 AGCGAATATGTTCTGCTCCAGATCATTTCTTGGAGGAAACACACTCTGTCAGCTTTA 1860
Qy 1861 CAGTATATACACACTAAGTCTTATGACCAATGCCCCCAAGGCGGAGCTGGTAGTTC 1920
Db 1861 CAGTATATACACACTAAGTCTTATGACCAATGCCCCCAAGGCGGAGCTGGTAGTTC 1920
Qy 1921 TTCAAGTCGCGGTGGTCTTAACTAGCGCTTCTCAACGACCTGTTCAGCAAGAGCTCTCG 1980
Db 1921 TTCAAGTCGCGGTGGTCTTAACTAGCGCTTCTCAACGACCTGTTCAGCAAGAGCTCTCG 1980
Qy 1981 GAGTACCGAGCTCTGGAGCAAAATTCACAGAGCTGCTGATTCATATCTAAGATCAAT 2040
Db 1981 GAGTACCGAGCTCTGGAGCAAAATTCACAGAGCTGCTGATTCATATCTAAGATCAAT 2040
Qy 2041 CTTAAGAGATTTAAGCACTTGAATACTTAACTTCAGAAACGGAGTGTGAATTTGAAT 2100
Db 2041 CTTAAGAGATTTAAGCACTTGAATACTTAACTTCAGAAACGGAGTGTGAATTTGAAT 2100
Qy 2101 AGCAAAATGAAGTTTGTCTAAGTCTGTGCGGTATTAACCTACCAAGGCTGTGACGGGTC 2160
Db 2101 AGCAAAATGAAGTTTGTCTAAGTCTGTGCGGTATTAACCTACCAAGGCTGTGACGGGTC 2160
Qy 2161 TTGAGAGATTTTCTGCTCTGAGGCGCAACATCTCAGAAATGAGACGTAATCTT 2220
Db 2161 TTGAGAGATTTTCTGCTCTGAGGCGCAACATCTCAGAAATGAGACGTAATCTT 2220
Qy 2221 CTCAACATTTGAACAGCTGATCAAGAGATCCCTGCAAGTTCTCGGCTCGCGGCAATTT 2280
Db 2221 CTCAACATTTGAACAGCTGATCAAGAGATCCCTGCAAGTTCTCGGCTCGCGGCAATTT 2280
Qy 2281 GCGCAATGTCTAAACGAACGAACGAGCTGAGAGCGGAGTGTCTGCAACACAGATAT 2340
Db 2281 GCGCAATGTCTAAACGAACGAACGAGCTGAGAGCGGAGTGTCTGCAACACAGATAT 2340
Qy 2341 GACACCGAGGAGGAGCTTGAACGAGCTGAGAGCGGAGTGTCTGCAACACAGATAT 2400
Db 2341 GACACCGAGGAGGAGCTTGAACGAGCTGAGAGCGGAGTGTCTGCAACACAGATAT 2400
Qy 2401 TCGAGAGTCTCTCAAGGAAAGGAGCTCCAGTCAAGGATCACTCTGAAATCA 2460
Db 2401 TCGAGAGTCTCTCAAGGAAAGGAGCTCCAGTCAAGGATCACTCTGAAATCA 2460
Qy 2461 GATACCAAACTAAGTCTTAAAGTTCCAAATTCACAAATTAACAGATATCACTAA 2520
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Qy 2521 AGAAATTTCTGAATTAAGTCAAGGATTAAGAAATTAACATCAAGATTTGGAGGA 2580
Db 2521 AGAAATTTCTGAATTAAGTCAAGGATTAAGAAATTAACATCAAGATTTGGAGGA 2580
Qy 2581 AATTAATACTGAATTAAGTCAAGGATTAAGAAATTAACATCAAGATTTGGAGGA 2640
Db 2581 AATTAATACTGAATTAAGTCAAGGATTAAGAAATTAACATCAAGATTTGGAGGA 2640
Qy 2641 TCTCAAGGAAATGAGAGAGGCAATTTCAATGAGTCAATCAAGATCAAGTCA 2700
Db 2641 TCTCAAGGAAATGAGAGAGGCAATTTCAATGAGTCAATCAAGATCAAGTCA 2700
Qy 2701 CACTGAGATGAGAGAGGCAATTTCAATGAGTCAATCAAGATCAAGTCA 2760
Db 2701 CACTGAGATGAGAGAGGCAATTTCAATGAGTCAATCAAGATCAAGTCA 2760
Qy 2761 TAAATTTCTGAATTAAGTCAAGGATTAAGAAATTAACATCAAGATTTGGAGGA 2820
Db 2761 TAAATTTCTGAATTAAGTCAAGGATTAAGAAATTAACATCAAGATTTGGAGGA 2820
Qy 2821 AATTTTCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
Db 2821 AATTTTCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
Qy 2881 TCCCTGAAATTTTCTGAGATCAATTTGCAACAGATCAATTTGTTAGG 2940
Db 2881 TCCCTGAAATTTTCTGAGATCAATTTGCAACAGATCAATTTGTTAGG 2940
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Db 2881 TCCCTGAAATTTTCTGAGATCAATTTGCAACAGATCAATTTGTTAGG 2940
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Db 2941 ACTGAACAAATTTATGGAGAGCAAACTTTATATGCTAGAAAGTACATTTAAAGATGA 3000
Qy 3001 CTACTTACGAGGAGGAGTACAGGCTCTCTTAAAGCATGAATGTATGATGTAGGCA 3060
Db 3001 CTACTTACGAGGAGGAGTACAGGCTCTCTTAAAGCATGAATGTATGATGTAGGCA 3060
Qy 3061 CTGTAGTGTATATATATGCTCCACACTAGTCTGATTAACACAAACCTCAGATTTGAG 3120
Db 3061 CTGTAGTGTATATATATGCTCCACACTAGTCTGATTAACACAAACCTCAGATTTGAG 3120
Qy 3121 TTATTTAGGACACTAGTTTATACGCACTACGCTTACATGATGATGATGATGATGATG 3180
Db 3121 TTATTTAGGACACTAGTTTATACGCACTACGCTTACATGATGATGATGATGATGATG 3180
Qy 3181 AATTAATCTTTGAATTTGCTTTTAAAGAACTGAGGTTCAAGTACATACATGAGAAA 3240
Db 3181 AATTAATCTTTGAATTTGCTTTTAAAGAACTGAGGTTCAAGTACATACATGAGAAA 3240
Qy 3241 ATCTTACTTTCTTGTACTACACAAAGCTATTTTAAAGAAAGTCTATGTTGGAGAG 3300
Db 3241 ATCTTACTTTCTTGTACTACACAAAGCTATTTTAAAGAAAGTCTATGTTGGAGAG 3300
Qy 3301 GCGGAAGTTGTACTATATGACATATCAAT 3330
Db 3301 GCGGAAGTTGTACTATATGACATATCAAT 3330

RESULT 2
ADAL4840
ID ADAL4840 standard; cDNA; 3330 BP.
XX
XX ADAL4840;
AC 06-NOV-2003 (first entry)
XX
DT Human Interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX
DB Human Interphotoreceptor matrix component; IPMC, 150 isoform A cDNA.
XX
XX ss: gene; human; IPMC 150 isoform A; gene therapy;
XX interphotoreceptor matrix component; IPMC; ocular disorder;
XX macular degeneration; photoreceptor death; retinal detachment.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /product= "IPMC 150 isoform A"
FT /transl_except= (pos:689..756,aa:Thr-Asp)
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FT /*tag= a
FT /label= Signal_sequence
FT mat_peptide 191..2583
FT /*tag= c
FT /label= Mature_IPMC_150_isoform_A
FT misc_feature 692..753
FT /*tag= d
FT /note= "This region could represent intronic sequence not removed from the cDNA sequence"
FT
PN US2002160954-A1.
XX
PD 31-OCT-2002.
XX
XX 08-NOV-2001; 2001US-00007270.
XX
XX 29-OCT-1998; 98US-00183972.
XX
XX 29-OCT-1999; 99US-00430195.
XX
XX (IOWA ) UNIV IOWA RES FOUNO.
```



QY	1741	GAGACCTTAGATGAAATGGATCTGTCTGACACCTCTGGCCCATCTGAGGTACAGAGCTC	1800
Db	1741	AGACACCTTAGATGAAATGGATCTGTCTGACACCTCTGGCCCATCTGAGGTACAGAGCTC	1800
QY	1801	AGCGAATATGTTCTGTCTCCAGATCATTTCTTGAGAGTATCAACTCCCTGCTCAGCTTAA	1860
Db	1801	AGCGAATATGTTCTGTCTCCAGATCATTTCTTGAGAGTATCAACTCCCTGCTCAGCTTAA	1860
QY	1861	CAGTATATCACCACTAGTTCTATGACCATTTGCCCCCAAGGGCCGAGCTGTAGTCTTC	1920
Db	1861	CAGTATATCACCACTAGTTCTATGACCATTTGCCCCCAAGGGCCGAGCTGTAGTCTTC	1920
QY	1921	TTCACTCTGCGGTGTGCTTAACAATGGCCCTCTCCACGACCTGTTCACACAAAGCTCTCTG	1980
Db	1921	TTCACTCTGCGGTGTGCTTAACAATGGCCCTCTCCACGACCTGTTCACACAAAGCTCTCTG	1980
QY	1981	GAGTACCGAGCTCTGAGCAACAATTCAACAGCTGCTGTTCATATCTACATCCAAAT	2040
Db	1981	GAGTACCGAGCTCTGAGCAACAATTCAACAGCTGCTGTTCATATCTACATCCAAAT	2040
QY	2041	CTTACAGATTTTAAGCAACTTGAAATCTTAACTTCAGAAAAGGAGTGTATGTGAT	2100
Db	2041	CTTACAGATTTTAAGCAACTTGAAATCTTAACTTCAGAAAAGGAGTGTATGTGAT	2100
QY	2101	AGCAAAATGAAGTTTGTCTTAAGTCTGTGCCGTATTACTCTACAAAGCTGTGCAAGGGCTC	2160
Db	2101	AGCAAAATGAAGTTTGTCTTAAGTCTGTGCCGTATTACTCTACAAAGGCTGTGCAAGGGCTC	2160
QY	2161	TTGAGAGATTTTTCGTTCTGCTGACGCCCAACAACCTCCATCTGGAATATGACAGCTACTCT	2220
Db	2161	TTGAGAGATTTTTCGTTCTGCTGACGCCCAACAACCTCCATCTGGAATATGACAGCTACTCT	2220
QY	2221	CTCAACATTTGACACAGCTGATCAAGCAGATCCCTGCAAGTTCCTGCGCTGCGGCAAAATTT	2280
Db	2221	CTCAACATTTGACACAGCTGATCAAGCAGATCCCTGCAAGTTCCTGCGCTGCGGCAAAATTT	2280
QY	2281	GCCCAATGTGTAAAGACGAACGACCTGAGAAAGGAGTGTCCGTGCAAACCAAGATAT	2340
Db	2281	GCCCAATGTGTAAAGACGAACGACCTGAGAAAGGAGTGTCCGTGCAAACCAAGATAT	2340
QY	2341	GACAGCCAGGGGAGCTCTGAGCGGTCTGGAACAAGGCCCTGTGGCCCTGCGACAAAGAA	2400
Db	2341	GACAGCCAGGGGAGCTCTGAGCGGTCTGGAACAAGGCCCTGTGGCCCTGCGACAAAGAA	2400
QY	2401	TGCGAGTCTCTCAAGGAAAGGAGCTCATGACAGTTGCGAGATCACTCTGAATAATCAA	2460
Db	2401	TGCGAGTCTCTCAAGGAAAGGAGCTCATGACAGTTGCGAGATCACTCTGAATAATCAA	2460
QY	2461	GCATACAAAACTAAGTTTAAAAAGTTCAAAATCACAAAATTAACAAGTATCAGTAAA	2520
Db	2461	GCATACAAAACTAAGTTTAAAAAGTTCAAAATCACAAAATTAACAAGTATCAGTAAA	2520
QY	2521	AGAAATTTCTGAATTACTGACCGGTAGAAATATGAAGATTTTAAACATCAAGATTTGGAAAGGA	2580
Db	2521	AGAAATTTCTGAATTACTGACCGGTAGAAATATGAAGATTTTAAACATCAAGATTTGGAAAGGA	2580
QY	2581	AATTAAAACTGAAAAATGTACAAATTAATCACTTAAGGCTATCTCAAGAGAGATGATTTGCT	2640
Db	2581	AATTAAAACTGAAAAATGTACAAATTAATCACTTAAGGCTATCTCAAGAGAGATGATTTGCT	2640
QY	2641	TCTCAAGAAAAATGAGACAGGCAATTCATGGGTCAATCAAAATCCAGACATACATGTCAA	2700
Db	2641	TCTCAAGAAAAATGAGACAGGCAATTCATGGGTCAATCAAAATCCAGACATACATGTCAA	2700
QY	2701	CACGTAGAAATCAGCACACCATATTTCAAAATATAGAGAGTCAATGATCTTGGCAACAG	2760
Db	2701	CACGTAGAAATCAGCACACCATATTTCAAAATATAGAGAGTCAATGATCTTGGCAACAG	2760
QY	2761	TAAATTTCTGAAAAAAAAGACCTTACTTAATTAATTAACCCCAATGCAATCAGCGAAAC	2820
Db	2761	TAAATTTCTGAAAAAAAAGACCTTACTTAATTAATTAACCCCAATGCAATCAGCGAAAC	2820
QY	2821	ATATTTTACTATTTCTTGAGATAGTCAAAATGATCATTAAGCCAGGTTTGCTTCCACT	2880

Db	2821	ATATTTTACATTTCTGGATGATGATGATCAAAATATATATAGCCAGGTTGGCTTCCACT	2880
Qy	2881	TCCTGAAAAATTTTACTCACAGATCATTTTGCACAACATATAGCTTACTTATTTGTTAGGG	2940
Db	2881	TCCTGAAAAATTTTACTCACAGATCATTTTGCACAACATATAGCTTACTTATTTGTTAGGG	2940
Qy	2941	ACTGAACAATTTATTTGGGAAGCAAACTCTTTATATGTCTAGAAAGTACATTTTAAAGATGA	3000
Db	2941	ACTGAACAATTTATTTGGGAAGCAAACTCTTTATATGTCTAGAAAGTACATTTTAAAGATGA	3000
Qy	3001	CTACTTTCGCGGGAGATGACAGTCTCTCTTAAAGCATGTGAATGTATGTAGTGTAGGCA	3060
Db	3001	CTACTTTCGCGGGAGATGACAGTCTCTCTTAAAGCATGTGAATGTATGTAGTGTAGGCA	3060
Qy	3061	CTGTAGTAGAGTATATATATGTCTCCACACTACGTCTGATTTAAACAAACCTCAGATTTCAG	3120
Db	3061	CTGTAGTAGAGTATATATATGTCTCCACACTACGTCTGATTTAAACAAACCTCAGATTTCAG	3120
Qy	3121	TTATTTAGGACACACTAGTTTATATAGCAACTACGTCTTACATATAGTACGTGTTTGTGCC	3180
Db	3121	TTATTTAGGACACACTAGTTTATATAGCAACTACGTCTTACATATAGTACGTGTTTGTGCC	3180
Qy	3181	AATATATCTTTGAATGTGTTCTTTAAAGAACTGAGGTTCCAGATACATACCATATGAAAA	3240
Db	3181	AATATATCTTTGAATGTGTTCTTTAAAGAACTGAGGTTCCAGATACATACCATATGAAAA	3240
Qy	3241	ATCTTACTCTTCTCTGTTACTACACAAAGCTATTTTAAAGAAAGTATGTTGGGAGAG	3300
Db	3241	ATCTTACTCTTCTCTGTTACTACACAAAGCTATTTTAAAGAAAGTATGTTGGGAGAG	3300
Qy	3301	GGCGAAGTTGACTATATATGACATATATCAAT	3330
Db	3301	GGCGAAGTTGACTATATATGACATATATCAAT	3330
RESULT 3			
ID	AAAA6205		
AC	AAAA6205	standard; cDNA; 3263 BP.	
XX	AAAA6205;		
AC	AAAA6205;		
DT	04-SEP-2000	(first entry)	
XX			
DE	cDNA encoding an Interphotoreceptor matrix proteoglycan (IPM150).		
XX			
KM	Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;		
KM	chromosome 6p13-q15; ocular disease; retinal detachment;		
KM	chorioretinal degeneration; retinal degeneration; cone degeneration;		
KM	age related macular degeneration; photoreceptor degeneration;		
KM	retinal pigment epithelium degeneration; mucopolysaccharidosis;		
KM	rod-cone dystrophy; cone-rod dystrophy; SB.		
XX			
DS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
XX	FT	128..2444	
FT	CDS	/*tag= a	
FT		/transl_except= (pos: 2411..2414, aa: Lys)	
FT		/product= "interphotoreceptor matrix proteoglycan IPM150"	
XX			
PN	W0200026367-A2.		
XX			
PD	11-MAY-2000.		
XX			
PF	29-OCT-1999;	99WC-US025440.	
XX			
PR	29-OCT-1998;	98US-00183972.	
XX			
PA	(IOWA ) UNIV IOWA RES FOUND.		
XX			
P1	Hageman GS, Kuehn MH,		
XX			

DR WPI; 2000-365616/31.  
DR P-PSDB; AAY93336.

XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
PT preventing, diagnosing and treating ocular disorders such as retinal  
PT detachment and choriorretinal degeneration.

PS Claim 2, Fig 3; 183pp; English.

XX The present sequence encodes an interphotoreceptor matrix (IPM)  
CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).  
CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
CC is located on chromosome 6q13-q15, between markers CHC.GAT11F10 and  
CC D6S284. The IPM proteins may be used to supplement a patient's own  
CC production of the protein or to rectify alterations in their nucleic  
CC acids that result in expression of an inactive protein. The IPM nucleic  
CC acids may be used in this way to treat ocular diseases such as retinal  
CC detachment, choriorretinal degeneration, retinal degeneration, age related  
CC macular degeneration, photoreceptor degeneration, RPB (retinal pigment  
CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
CC also be used to assay for other modulators of IPM proteoglycan expression  
CC and activity that may be used to treat ocular diseases. The nucleic acids  
CC and proteins may also be used as diagnostic reagents to detect the  
CC presence of IPM nucleic acids and their products in samples from patients  
CC according to standard methodologies

XX Sequence 3263 BP; 1040 A; 721 C; 663 G; 838 T; 0 U; 1 Other;

Query Match 93.9%; Score 3125.6; DB 3; Length 3263;

Best Local Similarity 97.8%; Pred. No. 0;  
Matches 3257; Conservative 0; Mismatches 5; Indels 69; Gaps 6;

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QY 1 TAAACCAAGAAGTTTCTCTCAATCATCTGATTCATATATATATATTTTTCACATTTC 60
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DB 1 TAAACCAAGAAGTTTCTCTCAATCATCTGATTCATATATATATATATTTTTCACATTTC 58
   |||||
QY 61 TGTACTTTTATGAGATTGAGTTGTTCTGTGATTTGTATACGAATTACCAATGAC 120
   |||||
DB 59 TGTACTTTTATGAGATTGAGTTGTTCTGTGATTTGTATACGAATTACCAATGAC 117
   |||||
QY 121 AAAAGCAGAAATGATTTGAAAATGAAAGCTATTTTGTGATTTTCTGCA 180
   |||||
DB 118 AAAAGCAGAAATGATTTGAAAATGAAAGCTATTTTGTGATTTTCTGCA 177
   |||||
QY 181 AGTTCAAGGAACCAAGATATCTCCATTACATATACCTTGAAACTTAAAGACATGA 240
   |||||
DB 178 AGTTCAAGGAACCAAGATATCTCCATTACATATACCTTGAAACTTAAAGACATGA 237
   |||||
QY 241 CAATCCCCCAAGAAATGAACAACACTGAAGTACTGAAAAAATGTCAAAAATGCAACTAT 300
   |||||
DB 238 CAATCCCCCAAGAAATGAACAACACTGAAGTACTGAAAAAATGTCAAAAATGCAACTAT 297
   |||||
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   |||||
DB 298 GAGAGCAATATTGATTTGGCAAAAGCATGAAACAAAAGATCCGATTTTCCCAACGGG 357
   |||||
QY 361 GGTTAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGAGTCTTCAAGCTTATTA 420
   |||||
DB 358 GGTTAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGAGTCTTCAAGCTTATTA 417
   |||||
QY 421 TAGATTGAGAGTGTGTGAGAGAGCAGTATGGGAAGCATATCGGATCTTCTGGATGGCAT 480
   |||||
DB 418 TAGATTGAGAGTGTGTGAGAGAGCAGTATGGGAAGCATATCGGATCTTCTGGATGGCAT 477
   |||||
QY 481 CCCTGACACAGGGGAATATCAGGACTGGGTCAAGCATCTGCCAGCAGAGACCTTCTGCTT 540
   |||||
DB 478 CCCTGACACAGGGGAATATCAGGACTGGGTCAAGCATCTGCCAGCAGAGACCTTCTGCTT 537
   |||||
QY 541 CTTTGAATTGAAAAAATTCCAGCAATTTCCAGAGACCTGGATCTTCTCCAGCAGAG 600
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DB 538 CTTTGAATTGAAAAAATTCCAGCAATTTCCAGAGACCTGGATCTTCTCCAGCAGAG 597

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   |||||
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   |||||
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   |||||
DB 658 AGAGCTGTGAAAACCATTTGTCAATTTCAACAGCAATCTACATTTCAAAAGACTTGGGCACT 687
   |||||
QY 721 ATTCTAAGAAAAACCTCAGAAAGACCAATTCAAGATGTTGGCAACGTCTCACTTGGGCT 780
   |||||
DB 688 -----AGATGTTGCCAAGTCTCACTTGGGCT 715
   |||||
QY 781 TTCCCTCTCACTCTGATGACACCCCTCTCAATGAATTTCTGATTAATACATCAACGAC 840
   |||||
DB 716 TTCCCTCTCACTCTGATGACACCCCTCTCAATGAATTTCTGATTAATACATCAACGAC 775
   |||||
QY 841 ACCAAGATCCTTACACAGAAAAGAAAAGAAATTCGCTGTGTGTGAGAGACAGAGGTG 900
   |||||
DB 776 ACCAAGATCCTTACACAGAAAAGAAAAGAAATTCGCTGTGTGTGAGAGACAGAGGTG 835
   |||||
QY 901 GAGCTCAGCGTCTCTGTGTAAACCAAGATTTCAAGGACGCTGCTGACTCCCACTCC 960
   |||||
DB 836 GAGCTCAGCGTCTCTGTGTAAACCAAGATTTCAAGGACGCTGCTGACTCCCACTCC 895
   |||||
QY 961 CCATATTACAGAGACTAGCAGAAAAGTCCCAACTTCAGATGACAAAAGATATTTAAGAA 1020
   |||||
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   |||||
DB 1196 AGGCTGATCAGCAAAAGCACTAGAGAAAGAAACAATTTTGAATGTGGGGAACAATTCAGTTC 1255
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QY 1321 ACTGATGAATTTGCTGATCACTGCAAGCTTTGGTCTGACACCAATCAGAGCTGGCC 1380
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DB 1256 ACTGATGAATTTGCTGATCACTGCAAGCTTTGGTCTGACACCAATCAGAGCTGGCC 1315
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DB 1316 ACATCTTTTGTGTTTATTAACAGAGATGCTACTTTGAGTCCAGAACTTCTCTGTTGAA 1375
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QY 1441 CCCGAGCTTGAACAGTGAAGAGAGAGAGAGATGTCTACTGACACTTCTTGGTCTCCA 1500
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Db 1726 AGCGAATATGTTCTGTCTCCAGATCATTTCTTGAGAGATACCACTCTGTCTCAGCTTTA 1795  
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Db 1796 CAGTATATCAACAATGATTCTATGACCATTTGCCCAAGGGGCGAGAGCTGTAGTGTTC 1855  
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Db 1856 TTCAATGCGCGTGTCTTAACATGAGCTTCTGCAACGACCTGTCAACAAGAGCTCTCG 1915  
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Db 2156 CTCAACATTTGAACAGCTGATCAAGCAAGATCCCTCAAGTTCTGTGCGCGCAATTT 2215  
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QY 3301 GCGGAAGTTGATCATATGACATATCAAT 3330  
Db 3232 GCGGAAGTTGATCATATGACATATCAAT 3261

RESULT 5  
ADA14866  
ID ADA14866 standard; cDNA; 3261 BP.  
XX  
XX ADA14866;  
AC  
XX 06-NOV-2003 (first entry)  
DT  
XX  
XX Human cDNA encoding variant IPWC 150 isoform A.  
DE  
XX  
XX ss; gene; human; IPWC 150 isoform A; gene therapy;  
KW Interphotoreceptor matrix component; IPWC; ocular disorder;  
KW macular degeneration; photoreceptor death; retinal detachment.  
OS  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
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FT /\*tag= a  
FT /product= "Variant IPWC 150 isoform A"  
US2002160954-A1.  
PD 31-OCT-2002.  
PF 08-NOV-2001; 2001US-00007270.  
PR 29-OCT-1998; 98US-00183972.  
PR 29-OCT-1999; 99US-00430195.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Hageman GS, Kuehn MH;  
PI  
XX WPI; 2003-238235/23.  
DR P-PDB; ADA14867.

XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.

XX Claim 3, Page 63-66; 76pp; English.

XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding  
CC variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
XX

Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;

Query Match 93.8%; Score 3124.6; DB 10; Length 3261;

Beet Local Similarity 97.8%; Pred. No. 0;

Matches 3256; Conservative 0; Mismatches 5; Indels 69; Gaps 6;

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QY 121 AAAACCCGAATGTATTTTGAAACCTAGAAAGCTATTTTGTTTTGTGATTTTCTCA 180
DB 118 AAAACCCGAATGTATTTTGAAACCTAGAAAGCTATTTTGTTTTGTGATTTTCTCA 177
QY 181 AGTTCAAGGAACCAAGATATCTCCATTACATATACCATTTCTGAAACCTAAAGACATGA 240
DB 178 AGTTCAAGGAACCTAAAGATATCTCCATTACATATACCATTTCTGAAACCTAAAGACATGA 237
QY 241 CAATCCCCCAAGAAATGAAACCACTGAAAGTACTGAAATAATGTAACAAATGTCACTAT 300
DB 238 CAATCCCCCAAGAAATGAAACCACTGAAAGTACTGAAATAATGTAACAAATGTCACTAT 297
QY 301 GAGAGGAATATTCGATTTGGGCAAGCATGCAACAAAGATCCGATTTTCCCAACGGG 360
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QY 361 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGCTTTTCAAGCTTATTA 420
DB 358 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTGAAGCTTTTCAAGCTTATTA 417
QY 421 TAGATTGAGAGTGTGTCAAGAGCAGTATGGAGACATATCGATCTTTCTGGATCGAT 480
DB 418 TAGATTGAGAGTGTGTCAAGAGCAGTATGGAGACATATCGATCTTTCTGGATCGAT 477
QY 481 CCCTGACACAGGGGAATATCAGGACTGGGTCAAGCTTGGCCAGCAGAGACCTTCTGCT 540
DB 478 CCCTGACACAGGGGAATATCAGGACTGGGTCAAGCTTGGCCAGCAGAGACCTTCTGCT 537
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DB 538 CTTTGACATTTGGAAAAAATTCCAGCAATCCAGAGAGACCTGATCTTCTCCAGACAG 597
QY 601 AATAAACAAGAGATTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGGG 660
DB 598 AATAAACAAGAGATTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGGG 657
QY 661 AGAGCTGTGTGAACCATTTGTCAATTTCAAGACAAATCTACATTTCAAAAGACTTGGGACGT 720
DB 658 AGAGCTGTGTGAACCATTTGTCAATTTCAAGACAAATCTACATTTCAAAAGACTTGGGACGT 687
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QY 781 TTCCCTCTCACTCTGTGATGACACCTCTCTCAATGAAATTTCTGATTAATACCTCAACGAC 840
DB 716 TTCCCTCTCACTCTGTGATGACACCTCTCTCAATGAAATTTCTGATTAATACCTCAACGAC 775
QY 841 ACCAAGATGCTTAACAAGAAAGAAACGAATTCCTGTGTGGAGAGACAGAGGTTG 900
DB 776 ACCAAGATGCTTAACAAGAAAGAAACGAATTCCTGTGTGGAGAGACAGAGGTTG 835
QY 901 GAGCTCAGCGTCTCTGTGTAAACCAAGATTTCAAGCAGAGCTCGCTGATCTCCAGTCC 960
DB 836 GAGCTCAGCGTCTCTGTGTAAACCAAGATTTCAAGCAGAGCTCGCTGATCTCCAGTCC 895
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DB 896 CCATATTACAGAGAGCTAGCAGAAAGTCCCACTTCAGATGACAAAGATATTTAAGAA 955
QY 1021 CTTCCAGATTTCAAAAAATTCATGTGTAGATTTAGACCAAGAAAGAAAGATGTC 1080
DB 956 CTTCCAGATTTCAAAAAATTCATGTGTAGATTTAGACCAAGAAAGAAAGATGTC 1015
QY 1081 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAACAAA 1140
DB 1016 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAACAAA 1075
QY 1141 AGCCCTGCAAGTGAACCTCTGTCTTTTGTATTCACAAATAATTTGAAGAGAAAGTCTAT 1200
DB 1076 AGCCCTGCAAGTGAACCTCTGTCTTTTGTATTCACAAATAATTTGAAGAGAAAGTCTAT 1135
QY 1201 CATGGAACCATGGAGAGAGAGAAACCAACCAAGAAATCTATCTCAAGCTACAGACTGAAA 1260
DB 1136 CATGGAACCATGGAGAGAGAGAAACCAACCAAGAAATCTATCTCAAGCTACAGACTGAAA 1195
QY 1261 AGGCTGATCAGCAAGACACTAGAGAAAGAAACAATCTTGTGATGTGGGACAAATTCAGTTC 1320
DB 1196 AGGCTGATCAGCAAGACACTAGAGAAAGAAACAATCTTGTGATGTGGGACAAATTCAGTTC 1255
QY 1321 ACTGATGAATTTGTGTATCACTGCCAGCTTTTGTGTGACACCCCAATCAGAGCTGCC 1380
DB 1256 ACTGATGAATTTGTGTATCACTGCCAGCTTTTGTGTGACACCCCAATCAGAGCTGCC 1315
QY 1381 ACATCTTTTGTGTATTAACAAGAGATCTATTTGATCCAGAACTTCTCTGTGTAA 1440
DB 1316 ACATCTTTTGTGTATTAACAAGAGATCTATTTGATCCAGAACTTCTCTGTGTAA 1375
QY 1441 CCCCACTTGGAGACAGTGAACGAGACAGAGATGGTCACTGACATCTTCTTGGTCTCA 1500
DB 1376 CCCCACTTGGAGACAGTGAACGAGACAGAGATGGTCACTGACATCTTCTTGGTCTCA 1435
QY 1501 CTTGCTATGGCTTACCTCTCTGTCAAGAGCTTCACTTTCTTTATGGATCAAGATC 1560
DB 1436 CTTGCTATGGCTTACCTCTCTGTCAAGAGCTTCACTTTCTTTATGGATCAAGATC 1495
QY 1561 TTTCTCTGATGATCAAGGACCAACAGATCAATTTGCACTGACACAGATCTAGTA 1620
DB 1496 TTTCTCTGATGATCAAGGACCAACAGATCAATTTGCACTGACACAGATCTAGTA 1555
QY 1621 CCAGGAGCTCAGCATCCCAACAGATGATTAATCTGCAATCAGCCAACTGGCTCTGGGAAT 1680
DB 1556 CCAGGAGCTCAGCATCCCAACAGATGATTAATCTGCAATCAGCCAACTGGCTCTGGGAAT 1615
QY 1681 TCAGATCCACCTGATCTTCAATGACAGCCGATCAAGTGAAGTGGGGAAGATATGCTC 1740
DB 1616 TCAGATCCACCTGATCTTCAATGACAGCCGATCAAGTGAAGTGGGGAAGATATGCTC 1675
QY 1741 AGACACTGATGAAATGATATCTGTGACACTCTGCCCCATCTGAGGTACAGAGCTC 1800
DB 1676 AGACACTGATGAAATGATATCTGTGACACTCTGCCCCATCTGAGGTACAGAGCTC 1735
QY 1801 AGCGAATATGTGTGTCCAGATCATTTCTTGGAGATACCACTCTGTCTCAGCTTTA 1860
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Db 1726 AGCGAATATGTTCTGTCCAGATCATTTCTTGAGGATACACCTCTGTCTCAGCTTTA 1795
Qy 1861 CAGTATATCACCACTAGTTCTATGACCATTTGCCCAAGGCGGAGCTGTAGTGTTC 1920
Db 1796 CAGTATATCACCACTAGTTCTATGACCATTTGCCCAAGGCGGAGCTGTAGTGTTC 1855
Qy 1921 TTCACTGTGCGGTGTCTAACAATGAGCTTCTCAACGACTGTCAACAGAGCTCTCTG 1980
Db 1856 TTCACTGTGCGGTGTCTAACAATGAGCTTCTCAACGACTGTCAACAGAGCTCTCTG 1915
Qy 1981 GAGTACCGAGCTCTGAGCAACAATTCAACAGCTGTGTCTCATATCTAGATCCAA 2040
Db 1916 GAGTACCGAGCTCTGAGCAACAATTCAACAGCTGTGTCTCATATCTAGATCCAA 1975
Qy 2041 CTTACAGATTTTAAAGCACTTGAATTAATTCAAGAAAGGAGTGTATGTGAT 2100
Db 1976 CTTACAGATTTTAAAGCACTTGAATTAATTCAAGAAAGGAGTGTATGTGAT 2035
Qy 2101 AGCAAAATGAAGTTGCTAAGTCTGTGCGGTAACTTCAACAGGCTGTGACGGGGTC 2160
Db 2036 AGCAAAATGAAGTTGCTAAGTCTGTGCGGTAACTTCAACAGGCTGTGACGGGGTC 2095
Qy 2161 TTGAGAGATTTTCTGTCTGTGAGCCCAACAATCTGGAATAGACAGTACTCT 2220
Db 2096 TTGAGAGATTTTCTGTCTGTGAGCCCAACAATCTGGAATAGACAGTACTCT 2155
Qy 2221 CTCAACATTGAACAGCTGATCAGACAGATCCCTGCAAGTTCTGCGCTGCGGCAATTT 2280
Db 2156 CTCAACATTGAACAGCTGATCAGACAGATCCCTGCAAGTTCTGCGCTGCGGCAATTT 2215
Qy 2281 GCCCAATGTGTAAGAAAGAAAGGAGCTGAGAAAGGAGTGTCTGTCAACAGAGATTT 2340
Db 2216 GCCCAATGTGTAAGAAAGAAAGGAGCTGAGAAAGGAGTGTCTGTCAACAGAGATTT 2275
Qy 2341 GACAGCCAGGGAGGCTGTGAGCGGTCTGGAACAGGAGCTGTGAGGCTGTGCAAAAGAA 2400
Db 2276 GACAGCCAGGGAGGCTGTGAGCGGTCTGGAACAGGAGCTGTGAGGCTGTGCAAAAGAA 2334
Qy 2401 TGGCAGGCTCTTCAGAGGAAAGGAGCTCATGCAAGTGTGCAATCACTCTGAAATCA 2460
Db 2335 TGGCAGGCTCTTCAGAGGAAAGGAGCTCATGCG--GGTTCCAGATCACTCTGAAATCA 2392
Qy 2461 GCATTCAAAACCTAGTGTAAAAAGTTCCAAAATCACAAAATTAACAAGTATCTGTAA 2520
Db 2393 GCATTCAAAACCTAGTGT--AAAAGTTCCAAAATCACAAAATTAACAAGTATCTGTAA 2451
Qy 2521 AGAAATTCGAATTACTGACCGTAGAATATGAAGAAATTTAACCAATCAAGATTGGAGGA 2580
Db 2452 AGAAATTCGAATTACTGACCGTAGAATATGAAGAAATTTAACCAATCAAGATTGGAGGA 2511
Qy 2581 AATTAAAACTGAAATGTATCAATTATGACTTGGCTATCTCAAGAGATGATTTGGCT 2640
Db 2512 AATTAAAACTGAAATGTATCAATTATGACTTGGCTATCTCAAGAGATGATTTGGCT 2571
Qy 2641 TCTCAAGGAAATGAGACAGGCAATTCATGGGTCAATCAAAATCCAGACATACGTCA 2700
Db 2572 TCTCAAGGAAATGAGACAGGCAATTCATGGGTCAATCAAAATCCAGACATACGTCA 2631
Qy 2701 CACTAGATCAGACACACCACTTTTCAAAATATGAAGAGTATCTTGGGCAACAG 2760
Db 2632 CACTAGATCAGACACCACTTTTCAAAATATGAAGAGTATCTTGGGCAACAG 2691
Qy 2761 TAAATTCGAAAAAAAGACCTTACTTATTTAAACCCCAATGCAATCAGGAAAC 2820
Db 2692 TAAATTCGAAAAAAAGACCTTACTTATTTAAACCCCAATGCAATCAGGAAAC 2751
Qy 2821 ATATTTTAACTATTTTGGATATATGTCAAAATGATCATAAGCCAGTTTGTCTTCACT 2880
Db 2752 ATATTTTAACTATTTTGGATATATGTCAAAATGATCATAAGCCAGTTTGTCTTCACT 2811
Qy 2881 TCCCTGAATTTTACTCAGACATGATTTGCAACAGGATAGCTTACTTATGTTTAGG 2940
```

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Db 2812 TCCCTGAATTTTACTCAGACATCATTTGCAACAAGCATAGCTACTTATGTTTAGG 2871
Qy 2941 ACTGAACAATTTATTTGGAGAACAACTTTTATATGCTAGAAAGTACTTTTAAAGATGA 3000
Db 2872 ACTGAACAATTTATTTGGAGAACAACTTTTATATGCTAGAAAGTACTTTTAAAGATGA 2931
Qy 3001 CTACTTACGAGGAGATGAGTGTCTCTTAAAGCATGAATGTAATGATGTGAGGCA 3060
Db 2932 CTACTTACGAGGAGATGAGTGTCTCTTAAAGCATGAATGTAATGATGTGAGGCA 2991
Qy 3061 CTGTAGTAGTATATATATGCTCCACACTAGCTGTATTAACAAACCTCAGATTGAG 3120
Db 2992 CTGTAGTAGTATATATATGCTCCACACTAGCTGTATTAACAAACCTCAGATTGAG 3051
Qy 3121 TTATTTAGCACATAGTTTATATACGCACTACTGCTTACATATGACTGTGTTGTC 3180
Db 3052 TTATTTAGCACATAGTTTATATACGCACTACTGCTTACATATGACTGTGTTGTC 3111
Qy 3181 AATATCTTTGAATTTGTTCTTTAAAGAAAGTGAAGTTCAGATACATACGAGAA 3240
Db 3112 AATATCTTTGAATTTGTTCTTTAAAGAAAGTGAAGTTCAGATACATACGAGAA 3171
Qy 3241 ATCTTACTTTCTTGTACTATACAAAGCTATTTTAAAGAAAGTGTATGTTGGAGAG 3300
Db 3172 ATCTTACTTTCTTGTACTATACAAAGCTATTTTAAAGAAAGTGTATGTTGGAGAG 3231
Qy 3301 GCGGAAGTTGTACTATATGACATATCAAT 3330
Db 3232 GCGGAAGTTGTACTATATGACATATCAAT 3261

RESULT 6
ACCS7947
ID ACCS7947 standard; cDNA; 2887 BP.
XX
AC CCS7947;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human Interphotoreceptor matrix IPM 150, isoform B, cDNA.
XX
KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW receptor; ophthalmological; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..2143
FT /tag= a
FT /product= "IPM 150"
FT /partial
FT /note= "No start codon"
XX
PN WO2003039346-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036090.
XX
PR 08-NOV-2001; 2001US-0007270.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI, 2003-441440/41.
XX
PT New interphotoreceptor matrix proteins and polynucleotides, useful for
PT treating or preventing photoreceptor death or retinal detachment, or for
PT treating ocular disorders.
XX
PS Claim 1; Page 78-79; 105pp; English.
XX
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CC The present sequence is that of cDNA encoding isoform B of novel human  
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polypeptides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression  
XX  
SQ Sequence 2887 BP, 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;

Query Match 83.1%; Score 2765.8; DB 9; Length 2887;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 2851; Conservative 0; Mismatches 22; Indels 62; Gaps 1;

QY 396 TTTTGAACAGCTTCAAGCTTATATATGAGTGTGTCAGAGAGCAGTATGGAG 455  
DB 15 TTTTGGATTTTCTCCAAAGTTCAAGAACCAAGTGTCTAGAGACAGTATGGAG 74  
QY 456 CATATCGATCTTTCTGATGTCATCCCTGACACAGGGGAAATATGAGATCGGTCACA 515  
DB 75 CATATCGATCTTTCTGATGTCATCCCTGACACAGGGGAAATATGAGATCGGTCACA 134  
QY 516 TCTGACACAGAGAGACTTCTGCTCTTGTGACATTTGAAAAAATTCCAGCAATCCCAAG 575  
DB 135 TCTGACACAGAGAGACTTCTGCTCTTGTGACATTTGAAAAAATTCCAGCAATCCCAAG 194  
QY 576 AGCACCTGATCTTCTCCAGACAGAGATTAACAGAGAAATTTCCCTGACAGAAAAAGATG 635  
DB 195 AGCACCTGATCTTCTCCAGACAGAGATTAACAGAGAAATTTCCCTGACAGAAAAAGATG 254  
QY 636 AAATTCGACAGAGAGACATTTGGAGAGAGCTGTGAAAAACCTTGTCAATTTCAACAGCA 695  
DB 255 AAATTCGACAGAGAGACATTTGGAGAGAGCTGTGAAAAACCTTGTCAATTTCAAC- 309  
QY 696 TCTACATTTCAAGAAGCTTGGCAGATTTCTAAGAAAAACCTCAGAGAGCAATTCAGAG 755  
DB 310 -----AGA 312  
QY 756 TGTTCGCAACGTCATCTTGGGCTTTTCCCTCTCACTCTGTATGACACCTTCCTCAATGA 815  
DB 313 TGTTCGCAACGTCATCTTGGGCTTTTCCCTCTCACTCTGTATGACACCTTCCTCAATGA 372  
QY 816 AATTTCGATTAATACATCAACAGACCAAGATGCTCTACACAGAAAGAAACAGATTT 875  
DB 373 AATTTCGATTAATACATCAACAGACCAAGATGCTCTACACAGAAAGAAACAGATTT 432  
QY 876 CGCTGTGTGAGAGAGAGAGGTGAGTCAAGCTCTCTGTGTAAACAGAAATTTCAA 935  
DB 433 CGCTGTGTGAGAGAGAGAGGTGAGTCAAGCTCTCTGTGTAAACAGAAATTTCAA 492  
QY 936 GGCAGAGCTCGCTGACTCCCAAGTCCCATATTTACAGAGAGCTAGCAGAGAAATGCCAAT 995  
DB 493 GGCAGAGCTCGCTGACTCCCAAGTCCCATATTTACAGAGAGCTAGCAGAGAAATGCCAAT 552  
QY 996 TCAGATGCAAAAGATATTTAAGAACTTCCAGAGATTTCAAAAAAATTCATGTGTATGATTT 1055  
DB 553 TCAGATGCAAAAGATATTTAAGAACTTCCAGAGATTTCAAAAAAATTCATGTGTATGATTT 612  
QY 1056 TAGACCAAGAGAGAGAGAGATGCTCAAGCTCCACAGAGATGCAACTTAGCGCATCTT 1115  
DB 613 TAGACCAAGAGAGAGAGATGCTCAAGCTCCACAGAGATGCAACTTAGCGCATCTT 672  
QY 1116 TAGAGACACAGTGCAG 1175

DB 673 TAAGAGACACAGTGCAG 732  
QY 1176 CAAATTTGAAGTGAAGAGAGAGTCTATCTATGAAACCATGAGAGAGAGAGAGAGAGAGAGAT 1235  
DB 733 CAAATTTGAAGTGAAGAGAGAGTCTATCTATGAAACCATGAGAGAGAGAGAGAGAGAGAGAT 792  
QY 1236 CTATCTCAGAGCTACAGAGCTCAAAAAGCTGATGACAGCAACAGCATAGAGAGAGAGAGATC 1295  
DB 793 CTATCTCAGAGCTACAGAGCTCAAAAAGCTGATGACAGCAACAGCATAGAGAGAGAGAGATC 852  
QY 1296 TTTGATGTGGGAGCAATTTCACTGATGAAATTTGCTGATCATCTGCCAGCTTTGG 1355  
DB 853 TTTGATGTGGGAGCAATTTCACTGATGAAATTTGCTGATCATCTGCCAGCTTTGG 912  
QY 1356 TCTGACACCCCAATCAGAGCTGCCCACTCTTTGCTGTTTAAACAGAGAGATGCTACTTT 1415  
DB 913 TCTGACACCCCAATCAGAGCTGCCCACTCTTTGCTGTTTAAACAGAGAGATGCTACTTT 972  
QY 1416 GAGTCCAGAACTTCTCTGTTGAAACCCAGAGCTTGAGACAGTGCAGAGAGAGATG 1475  
DB 973 GAGTCCAGAACTTCTCTGTTGAAACCCAGAGCTTGAGACAGTGCAGAGAGAGATG 1032  
QY 1476 TCTACCTGACACTTCTGTTGTTCCACTGCTATGAGCTCTACCTGCTGTCAGAAAGCTCC 1535  
DB 1033 TCTACCTGACACTTCTGTTGTTCCACTGCTATGAGCTCTACCTGCTGTCAGAAAGCTCC 1092  
QY 1536 ACCTTTCTTTATGACATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1595  
DB 1093 ACCTTTCTTTATGACATCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1152  
QY 1596 GGCACATGACACAGACAAATGTAGTACAGAGGCTGACATCCCAAGATGATTTCTGTC 1655  
DB 1153 GGCACATGACACAGACAAATGTAGTACAGAGGCTGACATCCCAAGATGATTTCTGTC 1212  
QY 1656 AATCAGCCACTGCTCTGAGAAATTTCACTCACTGATCTTCAAGTATGACAGCGATC 1715  
DB 1213 AATCAGCCACTGCTCTGAGAAATTTCACTCACTGATCTTCAAGTATGACAGCGATC 1272  
QY 1716 AAGTGCAGTGGCGAAGATATGTCAGACACTGATGAAATGATGATGATGATGATGATGAT 1775  
DB 1273 AAGTGCAGTGGCGAAGATATGTCAGACACTGATGAAATGATGATGATGATGATGATGAT 1332  
QY 1776 TGCCCCATCTGAGGTACAGAGCTCAGGCAATATGTTCTGTCCAGATCAATTTCTTGA 1835  
DB 1333 TGCCCCATCTGAGGTACAGAGCTCAGGCAATATGTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GATACCACTCTGCTCTGAGCTTTAAGTATATACCACTAGTTCTATGACCATTTGCC 1895  
DB 1393 GATACCACTCTGCTCTGAGCTTTAAGTATATACCACTAGTTCTATGACCATTTGCC 1452  
QY 1896 CAAGGCGGAGAGAGCTGATGATGTTCTTCAATCTGCTGTTGCTTAAATGAGGCTTCCAA 1955  
DB 1453 CAAGGCGGAGAGAGCTGATGATGTTCTTCAATCTGCTGTTGCTTAAATGAGGCTTCCAA 1512  
QY 1956 CGACTGTTCAACAAGAGCTCTGAGATACAGAGCTCTGAGCAACAATTCACAGAGCT 2015  
DB 1513 CGACTGTTCAACAAGAGCTCTGAGATACAGAGCTCTGAGCAACAATTCACAGAGCT 1572  
QY 2016 GCTGTTCAATATCTAGATCAATCTTACAGATTTAAGCACTTGAATATCTTAATCTT 2075  
DB 1573 GCTGTTCAATATCTAGATCAATCTTACAGATTTAAGCACTTGAATATCTTAATCTT 1632  
QY 2076 CAGAAACGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2135  
DB 1633 CAGAAACGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692  
QY 2136 CCTCACAAGGCTGTGACAGGGGCTTGTGAGAGATTTTGTCTGTGACGCCCAACT 2195  
DB 1693 CCTCACAAGGCTGTGACAGGGGCTTGTGAGAGATTTTGTCTGTGACGCCCAACT 1752  
QY 2196 CCATCTGGAATTAAGACAGCTACTCTTCAACATTTGAACACAGCTGATCAAGAGATCCCTG 2255  
DB 1753 CCATCTGGAATTAAGACAGCTACTCTTCAACATTTGAACACAGCTGATCAAGAGATCCCTG 1812

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QY 2256 CAAGTTCCTGGGCTGGGCGAAATTTGCCAATGTGTAAAGACGAACTGAGGAAC 2315
DB 1813 CAAGTTCCTGGGCTGGGCGAAATTTGCCAATGTGTAAAGACGAACTGAGGAAC 1872
QY 2316 GAGAGTGCCTGCGCAAAACAGATATATGACGAGGAGGAGCTGAGCGGTCTGAAACGAG 2375
DB 1873 GAGAGTGCCTGCGCAAAACAGATATATGACGAGGAGGAGCTGAGCGGTCTGAAACGAG 1932
QY 2316 CCTGTGTGGCCCTGGCGCAAAAGAAATGCGAGGTCTTCAAGGAAAGGAGCTTCATGCG 2435
DB 1933 CCTGTGTGGCCCTGGCGCAAAAGAAATGCGAGGTCTTCAAGGAAAGGAGCTTCATGCG 1992
QY 2436 GTTGGCAAGTCACTCTGAAAAATCAAGCATACAAAATCTACTGTAAAAAGTTCCAAAATCA 2495
DB 1993 GTTGGCAAGTCACTCTGAAAAATCAAGCATACAAAATCTACTGTAAAAAGTTCCAAAATCA 2052
QY 2496 ACAAAATACAAAGTAAATCATGTAATAAGAAATCTGAATTAAGACCGTGAATATGAGA 2555
DB 2053 ACAAAATACAAAGTAAATCATGTAATAAGAAATCTGAATTAAGACCGTGAATATGAGA 2112
QY 2556 ATTTAACATCAAGATTGGGAAAGAAATTTAAAACTGAAATGTACAATTAATCACTTAG 2615
DB 2113 ATTTAACATCAAGATTGGGAAAGAAATTTAAAACTGAAATGTACAATTAATCACTTAG 2172
QY 2616 CTATCTCAAGAGATGATTTGCTTCTCAAGAAAAATGAGACAGGCATATTCATGGGT 2675
DB 2173 CTATCTCAAGAGATGATTTGCTTCTCAAGAAAAATGAGACAGGCATATTCATGGGT 2232
QY 2676 CATCAAAATCCAGACATACAGTCAACATGAGAAATGAGACACCATTTTCAATATA 2735
DB 2233 CATCAAAATCCAGACATACAGTCAACATGAGAAATGAGACACCATTTTCAATATA 2292
QY 2736 GAAAGTCAATGATCTTGGCAACAGTAATTTCTGAAAAAAAAGACACTTACTTATATTA 2795
DB 2293 GAAAGTCAATGATCTTGGCAACAGTAATTTCTGAAAAAAAAGACACTTACTTATATTA 2352
QY 2796 AAACCCCAATGCATCAGCGAAACATATTTTACTTCTTGATGATATGCAAAATGA 2855
DB 2353 AAACCCCAATGCATCAGCGAAACATATTTTACTTCTTGATGATATGCAAAATGA 2412
QY 2856 TCATTAAGCAGGTTGCTTCCACTTCCCTGAAAAATTTACTCAGCATATTTGCAAGA 2915
DB 2413 TCATTAAGCAGGTTGCTTCCACTTCCCTGAAAAATTTACTCAGCATATTTGCAAGA 2472
QY 2916 AGCATAGCTTACTTATTTGTTAGGAGCTGAAACAATTTATGGGAAACAACTCTTATAT 2975
DB 2473 AGCATAGCTTACTTATTTGTTAGGAGCTGAAACAATTTATGGGAAACAACTCTTATAT 2532
QY 2976 GCTAAGAAATACATTTAAAAAGATGACTTATCGCAGGAGATGCAAGTCTCTTAACG 3035
DB 2533 GCTAAGAAATACATTTAAAAAGATGACTTATCGCAGGAGATGCAAGTCTCTTAACG 2592
QY 3036 CATGAATGATATGATGCTAGGCTAGCACTGATGAGATGATATATGCTCAACTAGCT 3095
DB 2593 CATGAATGATATGATGCTAGGCTAGCACTGATGAGATGATATATGCTCAACTAGCT 2652
QY 3096 GATTAACACAACTCAGTATTCAGTTATTAAGGACACATGATTTTATACGCAACTAGTC 3155
DB 2653 GATTAACACAACTCAGTATTCAGTTATTAAGGACACATGATTTTATACGCAACTAGTC 2712
QY 3156 TTACATAGTAGACTGTTTGTGTCACAAATCTTTGAATGTTCTTTAAAAAACTGAG 3215
DB 2713 TTACATAGTAGACTGTTTGTGTCACAAATCTTTGAATGTTCTTTAAAAAACTGAG 2772
QY 3216 GTTTCAGATACATATCCATGAAAAATCTTACTTTCTGTATACATCAAAAGCTATTTT 3275
DB 2773 GTTTCAGATACATATCCATGAAAAATCTTACTTTCTGTATACATCAAAAGCTATTTT 2832
QY 3276 AAAAGAGATGCTATGTTGGGAGAGGCGAAGTTGATATATGACATATCAAT 3310
DB 2833 AAAAGAGATGCTATGTTGGGAGAGGCGAAGTTGATATATGACATATCAAT 2887

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RESULT 7
ADAI4842
ID ADAI4842 standard; cDNA; 2887 BP.
XX
XX ADAI4842;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.
DE
XX
XX ss; gene: human; IPMC 150 isoform B; gene therapy;
KW interphotoreceptor matrix component; IPMC; ocular disorder;
KW macular degeneration; photoreceptor death; retinal detachment.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 5..2143
FT CDS
FT
FT /tag=a
FT /partial
FT /product= "IPMC 150 isoform B"
FT /note= "No start codon given. Encodes residues 8-719 of
FT {seqid:4}"
XX
XX US2002160954-A1.
XX
XX 31-OCT-2002.
XX
XX 08-NOV-2001; 2001US-00007270.
XX
XX 29-OCT-1998; 98US-00183972.
XX 29-OCT-1999; 99US-00430195.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX WPI; 2003-238235/23.
XX DR P-PSDB; ADAI4843.
XX
XX New isolated or recombinant interphotoreceptor matrix component
PT polynucleotide and polypeptide, useful for diagnosing, preventing,
PT treating or prognosticating ocular disorders, e.g. macular degeneration
PT or retinal detachment.
XX
XX PS
XX
XX Claim 3; Page 33-34; 76pp; English.
XX
XX The invention relates to an isolated or recombinant interphotoreceptor
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC gene operatively linked to the IPMC polynucleotide. The IPMC
CC polynucleotide, polypeptides and antibodies are useful for diagnosing,
CC preventing, treating or prognosticating ocular disorders, e.g. macular
CC degeneration, photoreceptor death or retinal detachment. They are also
CC useful for identifying a compound capable of modulating IPMC gene
CC expression in a cell. The present sequence represents cDNA encoding human
CC interphotoreceptor matrix component, IPMC, 150 isoform B.
XX
XX
SQ Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;
Query Match 83.1%; Score 2765.8; DB 10; Length 2887;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2851; Conservative 0; Mismatches 22; Indels 62; Gaps 1;
QY 336 TTTTGAAGATCTTCAAGCTTATATAGATGAGAGTGTGACGAACAGATAGGGAAG 455
DB 15 TTTTGAATTTTCTCAAGTTCAAGAACCAAGTGTGCAAGAGAGATAGGAAG 74
QY 456 CATATCGATCTTTCTGATGCAATCCCTGACACAGGGAATATCAGGATGGTCAACA 515
DB 75 CATATCGATCTTTCTGATGCAATCCCTGACACAGGGAATATCAGGATGGTCAACA 134

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QY 516 TCTGCCAGCAGAGACCTTCTGCTCTTGTGACATTTGAAAACTTCAGCAATTCACAG 575  
Db 135 TCTGCCAGCAGAGACCTTCTGCTCTTGTGACATTTGAAAACTTCAGCAATTCACAG 194  
QY 576 AGCAGCTGGATCTTCTCCAGCAGAAATTAACAGAAAGTTTCCCTGACGAAAAAGT 635  
Db 195 AGCAGCTGGATCTTCTCCAGCAGAAATTAACAGAAAGTTTCCCTGACGAAAAAGT 254  
QY 636 AAATATCTGACAGAGACATTTGGAGAGCCTGTGAAACCATTTGCAATTTCAACAGAA 695  
Db 255 AAATATCTGACAGAGAGACATTTGGAGAGCCTGTGAAACCATTTGCAATTTCAAC 309  
QY 696 TCTACATTTCAAAAGACTTGGGCAATATTCTAAGAAAAACCTCGAAGAGCAATTCAGA 755  
Db 310 -----AGA 312  
QY 756 TGTTCGCAACGTCTCACTTTGGGCTTTTCCCTCTCACTCTGTGATGACCCCTCTCAATGA 815  
Db 313 TGTTCGCAACGTCTCACTTTGGGCTTTTCCCTCTCACTCTGTGATGACCCCTCTCAATGA 372  
QY 816 AATTCTGATATATACCTCAACGACACCAAGATGCTCAACAGAAAGAGAAACGAATT 875  
Db 373 AATTCTGATATATACCTCAACGACACCAAGATGCTCAACAGAAAGAGAAACGAATT 432  
QY 876 CGCTGTGTTGAGAGCAGAGAGGTGAGCTCAGCGTCTCTGTGTTAAACAGAAAGTTCAA 935  
Db 433 CGCTGTGTTGAGAGCAGAGAGGTGAGCTCAGCGTCTCTGTGTTAAACAGAAAGTTCAA 492  
QY 936 GGCAGAGCTCGCTGACTCCCACTCCCATATTACAGAGAGCTAGACAGAAAGTCCCAACT 995  
Db 493 GGCAGAGCTCGCTGACTCCCACTCCCATATTACAGAGAGCTAGACAGAAAGTCCCAACT 552  
QY 996 TCAGATGCAAAAGATATTTAAGAACTTCAGAGATTCAAAAAATCCATGTGTAGAGATT 1055  
Db 553 TCAGATGCAAAAGATATTTAAGAACTTCAGAGATTCAAAAAATCCATGTGTAGAGATT 612  
QY 1056 TAGACCAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCAATTCAGCGCATCTT 1115  
Db 613 TAGACCAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCAATTCAGCGCATCTT 672  
QY 1116 TAAAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTGAAGCTCTGTGTTGATTCGA 1175  
Db 673 TAAAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTGAAGCTCTGTGTTGATTCGA 732  
QY 1176 CAAAATTGAGAAAGTGAAGAGTCTATCATGGAACCAATGAGAGAGCAAGCAACGAAT 1235  
Db 733 CAAAATTGAGAAAGTGAAGAGTCTATCATGGAACCAATGAGAGAGCAAGCAACGAAT 792  
QY 1236 CTATCTCAGAGTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGAGAAACAATC 1295  
Db 793 CTATCTCAGAGTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGAGAAACAATC 852  
QY 1296 TTTGATGTTGGGAGCAATTCAGTTCACTGATGAAATTTGCTGGATCACTGCCAGCTTTGG 1355  
Db 853 TTTGATGTTGGGAGCAATTCAGTTCACTGATGAAATTTGCTGGATCACTGCCAGCTTTGG 912  
QY 1356 TCCCTGACCCCAATCAGAGCTGCGCACATCTTTGCTGTTATTAAGAGAGAGTCACTTT 1415  
Db 913 TCCCTGACCCCAATCAGAGCTGCGCACATCTTTGCTGTTATTAAGAGAGAGTCACTTT 972  
QY 1416 GAGTCAGAAATCTCTCTGTTGAAACCCAGCTTGAGACAGTGAACGAGCAGACATAG 1475  
Db 973 GAGTCAGAAATCTCTCTGTTGAAACCCAGCTTGAGACAGTGAACGAGCAGACATAG 1032  
QY 1476 TCTACCTGACATTTCTTGGTCTTCACCTGCTATGAGCTCTACCTCTCTGCAAGAGCTCC 1535  
Db 1033 TCTACCTGACATTTCTTGGTCTTCACCTGCTATGAGCTCTACCTCTCTGCAAGAGCTCC 1092  
QY 1536 ACCTTTCTTATGGAGTCAAGAGATCTTCTCTGACTGATCAAGGACCAAGATCAAT 1595  
Db 1093 ACCTTTCTTATGGAGTCAAGAGATCTTCTCTGACTGATCAAGGACCAAGATCAAT 1152  
QY 1596 GGCACATGACAGACATCTAGTACCAAGGCTCAACATCCACAGTGAATTAATCTGAC 1655

Db 1153 GGCACATGACAGACATCTAGTACCAAGGCTCAACATCCCAACAGTGAATTAATCTGAC 1212  
QY 1656 AATGAGCCAACTGGCTCTGGAAATTTTCAATCCACCTGCAATCTCAAGTGAACAGCGATC 1715  
Db 1213 AATGAGCCAACTGGCTCTGGAAATTTTCAATCCACCTGCAATCTCAAGTGAACAGCGATC 1272  
QY 1716 AAGTGAAGTGGCAAGATATGATCAGACACCTAGATGAATGGAATCTGTCTGACACTCC 1775  
Db 1273 AAGTGAAGTGGCAAGATATGATCAGACACCTAGATGAATGGAATCTGTCTGACACTCC 1332  
QY 1776 TGCCCATCTGAGGTACAGAGCTCAAGCAATATGTTTCTGTCCAGATCAATTTCTTGA 1835  
Db 1333 TGCCCATCTGAGGTACAGAGCTCAAGCAATATGTTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GGAATACCACTCTCTCTCAGCTTTACAGATATATCAACCACTAGTTCTATGACATTTGCCCC 1895  
Db 1393 GGAATACCACTCTCTCTCAGCTTTACAGATATATCAACCACTAGTTCTATGACATTTGCCCC 1452  
QY 1896 CAAGGGCCGAGAGCTGGTATGTTCTTCAAGCTGAGGTTGCTAACAATGAGCTTCTCGAA 1955  
Db 1453 CAAGGGCCGAGAGCTGGTATGTTCTTCAAGCTGAGGTTGCTAACAATGAGCTTCTCGAA 1512  
QY 1956 CGACCTGTTCAACAAGACTCTCTGAGTACCGAGCTCTGAGCAACAATTCACAGACT 2015  
Db 1513 CGACCTGTTCAACAAGACTCTCTGAGTACCGAGCTCTGAGCAACAATTCACAGACT 1572  
QY 2016 GCTGGTTCATATCTAGATCCAACTTTACAGAGATTTAAGCACTTGAAATATCTTAATT 2075  
Db 1573 GCTGGTTCATATCTAGATCCAACTTTACAGAGATTTAAGCACTTGAAATATCTTAATT 1632  
QY 2076 CAGAAACGGAGTGTGATTTGAAATAGCAAAATGAATTTCTAAGTGTGCGGTATTA 2135  
Db 1633 CAGAAACGGAGTGTGATTTGAAATAGCAAAATGAATTTCTAAGTGTGCGGTATTA 1692  
QY 2136 CCTCACCAGGCTGTGACCGGGGCTTTGGAGAAATTTTCTGTCTGACGCCCAACAAT 2195  
Db 1693 CCTCACCAGGCTGTGACCGGGGCTTTGGAGAAATTTTCTGTCTGACGCCCAACAAT 1752  
QY 2196 CCATCTGGAATATACAGACTCTCTCTCAATTTGAACACCACTGATCAAGAGATCCCTG 2255  
Db 1753 CCATCTGGAATATACAGACTCTCTCTCAATTTGAACACCACTGATCAAGAGATCCCTG 1812  
QY 2256 CAAGTCTCTGCGCGCGCAATTTGCCAATGTGTAAAGAACGAAACGGACTGAGGAAGC 2315  
Db 1813 CAAGTCTCTGCGCGCGCAATTTGCCAATGTGTAAAGAACGAAACGGACTGAGGAAGC 1872  
QY 2316 GGAAGTGTGCTGCAACCAAGATATGACAGCCAGGGAGCTGGAACGCTGGAACCAAG 2375  
Db 1873 GGAAGTGTGCTGCAACCAAGATATGACAGCCAGGGAGCTGGAACGCTGGAACCAAG 1932  
QY 2376 CCTCTGTGGCCCTGCGACAAAGAAATGCGAGTCTCTCAGGAAAGGAGCTCCATGAG 2435  
Db 1933 CCTCTGTGGCCCTGCGACAAAGAAATGCGAGTCTCTCAGGAAAGGAGCTCCATGAG 1992  
QY 2436 GTTGCCAGATCACTCTGAAAAATCAAGCATACAAAATCTAGTGTAAAGATTCCAAAATCA 2495  
Db 1993 GTTGCCAGATCACTCTGAAAAATCAAGCATACAAAATCTAGTGTAAAGATTCCAAAATCA 2052  
QY 2496 ACAAAATTAACAAGTAAATCAATAAAAGAAATTCGAATTAAGTGAATATGAAGA 2555  
Db 2053 ACAAAATTAACAAGTAAATCAATAAAAGAAATTCGAATTAAGTGAATATGAAGA 2112  
QY 2556 ATTTAAACATCAAGATTTGGAGAGAAATTAATAAACTGAAAAATGTAATTAATCACTTAG 2615  
Db 2113 ATTTAAACATCAAGATTTGGAGAGAAATTAATAAACTGAAAAATGTAATTAATCACTTAG 2172  
QY 2616 CTATCTCAAGAGAGTGAATTTGCTTCTCAAGGAAATGAGACAGGCAATTTCAATGAG 2675  
Db 2173 CTATCTCAAGAGAGTGAATTTGCTTCTCAAGGAAATGAGACAGGCAATTTCAATGAG 2232  
QY 2676 CATCAAAATCCAGACATCACTGATCAACATGGAATCAGACACACATATTTCAATATA 2735

Db 2233 CATCAAAATCCAGACATATACATCACTGAGATCAGACACACATATTTCAATATTA 2292  
 Qy 2736 GAAGAGTCATGTACTGGGACACAGTAATCTCGAAAAAAGACCTTACTTATTTA 2795  
 Db 2293 GAAGAGTCATGTACTGGGACACAGTAATCTCGAAAAAAGACCTTACTTATTTA 2352  
 Qy 2796 AAACCCCAATGCAATCAGCGAAACATATTTTACTATTCTTGAGATAGTCAAAATGA 2855  
 Db 2353 AAACCCCAATGCAATCAGCGAAACATATTTTACTATTCTTGAGATAGTCAAAATGA 2412  
 Qy 2856 TCATTAAGCCAGGTTTCTTCCACTTCCCTGAAATTTTACTCACAGATCATTTGCAACA 2915  
 Db 2413 TCATTAAGCCAGGTTTCTTCCACTTCCCTGAAATTTTACTCACAGATCATTTGCAACA 2472  
 Qy 2916 AGCATAGCTTACTTATTTGTTTAGGAGCTGAAACATTTATTTGGAGCAAACTTTATAT 2975  
 Db 2473 AGCATAGCTTACTTATTTGTTTAGGAGCTGAAACATTTATTTGGAGCAAACTTTATAT 2532  
 Qy 2976 GCTAGAAAGTACATTTAAAGATGACTACTTACGAGGAGAGTGCAGGTCTCTTAAAG 3035  
 Db 2533 GCTAGAAAGTACATTTAAAGATGACTACTTACGAGGAGAGTGCAGGTCTCTTAAAG 2592  
 Qy 3036 CATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3095  
 Db 2593 CATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2652  
 Qy 3096 GATTAACACAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3155  
 Db 2653 GATTAACACAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2712  
 Qy 3156 TTACATAGTAGACTGTTTGTGGCCAAATCTTGAATGTTCTTTAAAGAACTGAG 3215  
 Db 2713 TTACATAGTAGACTGTTTGTGGCCAAATCTTGAATGTTCTTTAAAGAACTGAG 2772  
 Qy 3216 GTTCAGATACATATCCATGAGAAATCTTACTTTCTTACTTACACAAAGCTATTT 3275  
 Db 2773 GTTCAGATACATATCCATGAGAAATCTTACTTTCTTACTTACACAAAGCTATTT 2832  
 Qy 3276 AAAGAAAGTCTTATGTTGGAGAGAGGCGAAGTTGATATATGACATATCAAT 3330  
 Db 2833 AAAGAAAGTCTTATGTTGGAGAGAGGCGAAGTTGATATATGACATATCAAT 2887

## RESULT 8

ID AAA46328 standard; DNA; 2966 BP.  
 AC AAA46328;  
 XX  
 XX  
 DT 04-SEP-2000 (first entry)

Interphotoreceptor matrix proteoglycan (IPM150) splice variant.

Km Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 Km choroidretinal degeneration; retinal disease; retinal detachment;  
 Km age related macular degeneration; photoreceptor degeneration;  
 Km retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 Km rod-cone dystrophy; cone-rod dystrophy; ss.

Homosapiens.

WO200026367-A2.

11-MAY-2000.

29-OCT-1999; 99WO-US025440.

29-OCT-1998; 98US-00183972.

(IOWA) UNIV IOWA RES FOUND.

Hageman GS, Kuehn MH;  
PI

XX  
 DR MPI; 2000-365616/31.  
 XX  
 PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 PT preventing, diagnosing and treating ocular disorders such as retinal  
 PT detachment and chorioretinal degeneration.  
 XX  
 PS Claim 3; Fig 18; 183pp; English.  
 XX  
 CC The present sequence represents a splice variant of an interphotoreceptor  
 CC matrix (IPM) proteoglycan, designated IPM150. The sequence is missing  
 CC exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs,  
 CC IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome  
 CC 6q13-q15, between markers CHL1, GATTA11F10 and D6S284. The IPM proteins may  
 CC be used to supplement a patient's own production of the protein or to  
 CC rectify alterations in their nucleic acids that result in expression of  
 CC an inactive protein. The IPM nucleic acids may be used in this way to  
 CC treat ocular diseases such as retinal detachment, chorioretinal  
 CC degeneration, retinal degeneration, age related macular degeneration,  
 CC photoreceptor degeneration, RPS (retinal pigment epithelium)  
 CC degeneration, cone degeneration, mucopolysaccharidosis, rod-cone  
 CC dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also  
 CC be used to assay for other modulators of IPM proteoglycan expression and  
 CC activity that may be used as diagnostic reagents to detect the presence  
 CC of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies  
 CC  
 SQ Sequence 2966 BP; 918 A; 687 C; 624 G; 737 T; 0 U; 0 Other;  
 Query Match 81.8%; Score 2724.6; DB 3; Length 2966;  
 Best Local Similarity 96.9%; Pred. No. 0;  
 Matches 245; Conservative 0; Mismatches 24; Indels 66; Gaps 4;  
 Qy 336 TTTTGAAGAGCTTCTCAAGCTTATTTAGATGAGAGTGTGACAGAGAGATGAGAG 455  
 Db 15 TTTTGAAGATTTTCTCAAGTTCAGAGAACCAAGTGTGACAGAGAGATGAGAG 74  
 Qy 456 CATATCGATCTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 515  
 Db 75 CATATCGATCTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 134  
 Qy 516 TCTGCCACAGAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 575  
 Db 135 TCTGCCACAGAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 194  
 Qy 576 AGCAGCTGATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 635  
 Db 195 AGCAGCTGATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 254  
 Qy 636 AAATATCTGACAGAGAGACATTTGGAGAGCTGTGTAACATTTGATCAATTTCAAGAGCA 695  
 Db 255 AAATATCTGACAGAGAGACATTTGGAGAGCTGTGTAACATTTGATCAATTTCAAC----- 309  
 Qy 696 TCTATATTTCAAGAGCTTTGGGACATTTCTAAGAAAACCTTCAGAGAGCAATTTCAAGA 755  
 Db 310 -----AGG 312  
 Qy 756 TGTTCGCAAGCTCACTTGGGCTTTTCCCTCTGACCTGATGACACCTGCTCAATGA 815  
 Db 313 TGTTCGCAAGCTCACTTGGGCTTTTCCCTCTGACCTGATGACACCTGCTCAATGA 372  
 Qy 816 AATTCGATATATACATCAACGACACCAAGATGCTTCAACAGAAAGAAAGCAATTT 875  
 Db 373 AATTCGATATATACATCAACGACACCAAGATGCTTCAACAGAAAGAAAGCAATTT 432  
 Qy 876 CGCTGTGTTGAGAGAGAGAGAGAGCTCAAGCTCTCTCTGATTAACCAAGATTTCA 935  
 Db 433 CGCTGTGTTGAGAGAGAGAGAGAGCTCAAGCTCTCTCTGATTAACCAAGATTTCA 492  
 Qy 936 GGCAGAGCTCGCTGACCTCCAGTCCCATATTTACAGAGAGCTAGAGAGAAATGCCAAT 995  
 Db 493 GGCAGAGCTCGCTGACCTCCAGTCCCATATTTACAGAGAGCTAGAGAGAAATGCCAAT 552

QY 996 TCAGATGCAAAAGATATTTAAGAAACTTCAGAGATTCAAAAAATCAATGTGTAGGATT 1055  
| | | | |  
Db 553 TCGAGTGCAGAAAGATATTTAAGAACTTCAGAGATTCAAAAAATCAATGTGTAGGATT 612  
| | | | |  
QY 1056 TAGACCAAGAAAGAAAAGATGGCTCAAGCTCCAAGAGATGCAATTCAGGCACTCT 1115  
| | | | |  
Db 613 TAGACCAAGAAAGAAAAGATGGCTCAAGCTCCAAGAGATGCAATTCAGGCACTCT 672  
| | | | |  
QY 1116 TAAAGACACAGTGCAGAAAGCAAAAAGCCCTGCAAGTGACTTCCTGTCTTTTGAATTCGA 1175  
| | | | |  
Db 673 TAAAGACACAGTGCAGAAAGCAAAAAGCCCTGCAAGTGACTTCCTGTCTTTTGAATTCGA 732  
| | | | |  
QY 1176 CAAAATTGAAAGTGAAGAGAGTCTATCATGGAACCATGAGAGAGACAAGCAACGAAAT 1235  
| | | | |  
Db 733 CAAAATTGAAAGTGAAGAGAGTCTATCATGGAACCATGAGAGAGACAAGCAACGAAAT 792  
| | | | |  
QY 1236 CTATCTCACAGCTACAGACCTCAAAAAGCTGATCAGCAAAAGCACTAAGAGAAACAATC 1295  
| | | | |  
Db 793 CTATCTCACAGCTACAGACCTCAAAAAGCTGATCAGCAAAAGCACTAAGAGAAACAATC 852  
| | | | |  
QY 1296 TTTGATATGAGGAGCAATTCAATTCATGTAAGAAATGCTGATGATCACTGCCAGCCTTTGG 1355  
| | | | |  
Db 853 TTTGATATGAGGAGCAATTCAATTCATGTAAGAAATGCTGATGATCACTGCCAGCCTTTGG 912  
| | | | |  
QY 1356 TCCTGACACCCCAATCAGAGCTGCCCAATCTTTGCTGTTATAGAGAGATGCTACTTT 1415  
| | | | |  
Db 913 TCCTGACACCCCAATCAGAGCTGCCCAATCTTTGCTGTTATAGAGAGATGCTACTTT 972  
| | | | |  
QY 1416 GAGTCAGAACTTCTCTCTGTTGAAACCCAGCTTGAGACAGTGAACGAGCAGACATGG 1475  
| | | | |  
Db 973 GAGTCAGAACTTCTCTCTGTTGAAACCCAGCTTGAGACAGTGAACGAGCAGACATGG 1032  
| | | | |  
QY 1476 TCTACTGACAACTTCTTGCTCTCCACCTGCTATAGGCTCTTACTCCCTGTGAGAGCTCC 1535  
| | | | |  
Db 1033 TCTACTGACAACTTCTTGCTCTCCACCTGCTATAGGCTCTTACTCCCTGTGAGAGCTCC 1092  
| | | | |  
QY 1536 ACTTTCCTTATGAGATCAAGCATCTTCTCTGACTGATCAAGGACACAGATATACAT 1595  
| | | | |  
Db 1093 ACTTTCCTTATGAGATCAAGCATCTTCTCTGACTGATCAAGGACACAGATATACAT 1152  
| | | | |  
QY 1596 GGCACATGACAGACAAATGCTAGTACAGAGGCTCAACATCCCAAGATGATATTCGTGC 1655  
| | | | |  
Db 1153 GGCACATGACAGACAAATGCTAGTACAGAGGCTCAACATCCCAAGATGATATTCGTGC 1212  
| | | | |  
QY 1656 AATCAGCCAACTGGCTCTGGGAAATTCACATCCACTGTGATCTTCAGATGAGAGCCGATC 1715  
| | | | |  
Db 1213 AATCAGCCAACTGGCTCTGGGAAATTCACATCCACTGTGATCTTCAGATGAGAGCCGATC 1272  
| | | | |  
QY 1716 AAGTCAAGGTGGCAAGATATAGTGCAGACACCTAAGTAAATGGAATCTGTGACATCC 1775  
| | | | |  
Db 1273 AAGTCAAGGTGGCAAGATATAGTGCAGACACCTAAGTAAATGGAATCTGTGACATCC 1332  
| | | | |  
QY 1776 TGCCCCATCTAGATACAGAGCTCAGCGAATATGTTCTGTCCAGATCATTTCTTGA 1835  
| | | | |  
Db 1333 TGCCCCATCTAGATACAGAGCTCAGCGAATATGTTCTGTCCAGATCATTTCTTGA 1392  
| | | | |  
QY 1836 GGAATACCACTCTGTCTCAGCTTTTACAGATATACCAATAGTATCTATGACATTTGGCC 1895  
| | | | |  
Db 1393 GGAATACCACTCTGTCTCAGCTTTTACAGATATACCAATAGTATCTATGACATTTGGCC 1452  
| | | | |  
QY 1896 CAAGGCGCAGAGCTGTAGTGTCTTCAGTCTGCGTGTGCTTAACATGAGCCTTCGCA 1955  
| | | | |  
Db 1453 CAAGGCGCAGAGCTGTAGTGTCTTCAGTCTGCGTGTGCTTAACATGAGCCTTCGCA 1512  
| | | | |  
QY 1956 CGACCTGTTCAAACAAGAGCTCTCTGAGATACCGAGCTCTGAGCAACAATTCACAGCT 2015  
| | | | |  
Db 1513 CGACCTGTTCAAACAAGAGCTCTCTGAGATACCGAGCTCTGAGCAACAATTCACAGCT 1572  
| | | | |  
QY 2016 GCTGGTTCATATCTACATCTCAATCTTACAGATTTTAAAGCACTTGAAATCTTAAGCT 2075  
| | | | |  
Db 1573 GCTGGTTCATATCTACATCTCAATCTTACAGATTTTAAAGCACTTGAAATCTTAAGCT 1632  
| | | | |

QY 2076 CAGAAAACGAGATGATGATGTAAGTAAGCAAAATGAAAGTTTGCTAAGTCTGTCCGATATA 2135  
| | | | |  
Db 1633 CAGAAAACGAGATGATGATGTAAGTAAGCAAAATGAAAGTTTGCTAAGTCTGTCCGATATA 1692  
| | | | |  
QY 2136 CCTCACAAGGCTGTGACACGAGGCTCTTGAGAGATTTTGTTCTGTGACGCCCAACAAT 2195  
| | | | |  
Db 1693 CCTCACAAGGCTGTGACACGAGGCTCTTGAGAGATTTTGTTCTGTGACGCCCAACAAT 1752  
| | | | |  
QY 2196 CCAATCTGAAAATTAACAGACTACTCTCTCCACATTTGAACACAGACTGATCAAGAGATCCCTG 2255  
| | | | |  
Db 1753 CCAATCTGAAAATTAACAGACTACTCTCTCCACATTTGAACACAGACTGATCAAGAGATCCCTG 1812  
| | | | |  
QY 2256 CAAAGTCTGTGCGCGGCGAATTTTGCCCAATGTGTAAAGACGAACGAGCTGAGGAAGC 2315  
| | | | |  
Db 1813 CAAAGTCTGTGCGCGGCGAATTTTGCCCAATGTGTAAAGACGAACGAGCTGAGGAAGC 1872  
| | | | |  
QY 2316 GGAAGTGTGCTGCAACAGAGATATGACAGCCAGGGAGCCTGACCGGTCTGGAACAGG 2375  
| | | | |  
Db 1873 GGAAGTGTGCTGCAACAGAGATATGACAGCCAGGGAGCCTGACCGGTCTGGAACAGG 1932  
| | | | |  
QY 2376 CCTGTGAGCCCTGGCAACAAAGSAATGAGAGTCTCCAGGGGAAAAGGAGCTCCATGCGAG 2435  
| | | | |  
Db 1933 CCTGTGAGG - CCTGGCAACAAAGSAATGAGAGTCTCCAGGGGAAAAGGAGCTCCATGCG - 1989  
| | | | |  
QY 2436 GTTGCAGATCACTCTGAAAATCAAGCATACAAAACCTAGTGTAAAGATTCCAAAATCA 2495  
| | | | |  
Db 1990 GTTGCAGATCACTCTGAAAATCAAGCATACAAAACCTAGTGTAAAGATTCCAAAATCA 2048  
| | | | |  
QY 2496 ACAAATTAACAAGGTATCAGTAAAGAAATTCGAATTAAGTAACTGACCGTGAATATGANA 2555  
| | | | |  
Db 2049 ACAAATTAACAAGGTATCAGTAAAGAAATTCGAATTAAGTAACTGACCGTGAATATGANA 2108  
| | | | |  
QY 2556 ATTTTAACATGAATGAGGAGAAATTAAGAACTGAAATGTAACAATTTATCACTTAAG 2615  
| | | | |  
Db 2109 ATTTTAACATGAATGAGGAGAAATTAAGAACTGAAATGTAACAATTTATCACTTAAG 2168  
| | | | |  
QY 2616 CTATCTCAAGAGATGATGTTGCTCTCAAGAAATGAGAGACAGCATATTCAGGGT 2675  
| | | | |  
Db 2169 CTATCTCAAGAGATGATGTTGCTCTCAAGAAATGAGAGACAGCATATTCAGGGT 2228  
| | | | |  
QY 2676 CATCAAAATCGACATACAGTCAACACTGAGAAATGAGACACACATATTTCAAAATTA 2735  
| | | | |  
Db 2229 CATCAAAATCGACATACAGTCAACACTGAGAAATGAGACACACATATTTCAAAATTA 2288  
| | | | |  
QY 2736 GAAAGTCACTACTCTGGCAACAGTAAATCTGAAAAAAAAGACCTACTCTATTAATTA 2795  
| | | | |  
Db 2289 GAAAGTCACTACTCTGGCAACAGTAAATCTGAAAAAAAAGACCTACTCTATTAATTA 2348  
| | | | |  
QY 2796 AAACCCCAATGCAATCAGCGAACAATATTTTACTATTTCTGATGATGATCAAAATGA 2855  
| | | | |  
Db 2349 AAACCCCAATGCAATCAGCGAACAATATTTTACTATTTCTGATGATGATCAAAATGA 2408  
| | | | |  
QY 2856 TCAATAGCCAGTTTGCTTCACTTCCCTGAAAAATTTTACTCAAGATCAATTTGCAACA 2915  
| | | | |  
Db 2409 TCAATAGCCAGTTTGCTTCACTTCCCTGAAAAATTTTACTCAAGATCAATTTGCAACA 2468  
| | | | |  
QY 2916 AGCATAAGTTACTATGTTTAAAGGATCGAACAATTTATGGAAGCAAACTCTTAATAT 2975  
| | | | |  
Db 2469 AGCATAAGTTACTATGTTTAAAGGATCGAACAATTTATGGAAGCAAACTCTTAATAT 2528  
| | | | |  
QY 2976 GCTAGAAAAGTCAATTTAAAGATGACTACTTACGAGAGGAGATGAGAGGTCTCTAAAG 3035  
| | | | |  
Db 2529 GCTAGAAAAGTCAATTTAAAGATGACTACTTACGAGAGGAGATGAGAGGTCTCTAAAG 2588  
| | | | |  
QY 3036 CATGATATGATGATGATGAGCACTGTAGTAGTATATATGCTCCACATACGTTCT 3095  
| | | | |  
Db 2589 CATGATATGATGATGATGAGCACTGTAGTAGTATATATGCTCCACATACGTTCT 2648  
| | | | |  
QY 3096 GATTAACCAAAACCTCAGATATTCAGTTATTAAGGACACTAAGTTTATACGACATACGTC 3155  
| | | | |  
Db 2649 GATTAACCAAAACCTCAGATATTCAGTTATTAAGGACACTAAGTTTATACGACATACGTC 2708  
| | | | |  
QY 3156 TTACATAGTACAGTTTGTGTCGAATAATCTTTGAATGTGTCTTTAAAGAACTGAG 3215  
| | | | |

Db 2709 TTACATAGAGACTGTTTGTGTCACATATCTTGAAATGTTCTTTAAAGAACTGAG 2768  
 Qy 3216 GTTCAGATACACATACCATGAGAAATCTTACTTTCTGTACTACACAAAGCTATTTT 3275  
 Db 2769 GTTCAGATACACATACCATGAGAAATCTTACTTTCTGTACTACACAAAGCTATTTT 2828  
 Qy 3276 AAGAAGATGCTATGTTGGAGAGAGGCGAAGTTGACTATATGACATTAATCAAT 3330  
 Db 2829 AAGAAGATGCTATGTTGGAGAGAGGCGAAGTTGACTATATGACATTAATCAAT 2883  
 RESULT 9  
 AAA46329  
 ID AAA46329 standard, DNA; 2244 BP.  
 AC AAA46329;  
 XX  
 DT 04-SBP-2000 (first entry)  
 XX  
 DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.  
 XX  
 KM Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 KM chromosome 6q13-q15; ocular disease; retinal detachment;  
 KM choriorretinal degeneration; retinal degeneration; cone degeneration;  
 KM age related macular degeneration; photoreceptor degeneration;  
 KM retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KM rod-cone dystrophy; cone-rod dystrophy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200026367-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 29-OCT-1999; 99WO-US025440.  
 XX  
 PR 29-OCT-1998; 98US-00183972.  
 XX  
 PA (IOWA) UNIV IOWA RES FOUND.  
 XX  
 PI Hageman GS, Kuehn MH;  
 XX  
 DR WPI; 2000-365616/31.  
 XX  
 PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 PT preventing, diagnosing and treating ocular disorders such as retinal  
 PT detachment and choriorretinal degeneration.  
 XX  
 PS Claim 3, Fig 19, 183pp, English.  
 XX  
 CC The present sequence represents a splice variant of an interphotoreceptor  
 CC matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an  
 CC additional intron after exon 5. The protein is an IPM component (IPMC).  
 CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
 CC is located on chromosome 6q13-q15, between markers CHC.GAT11F10 and  
 CC D6S284. The IPM proteins may be used to supplement a patient's own  
 CC production of the protein or to rectify alterations in their nucleic  
 CC acids that result in expression of an inactive protein. The IPM nucleic  
 CC acids may be used in this way to treat ocular diseases such as retinal  
 CC detachment, choriorretinal degeneration, retinal degeneration, age related  
 CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment  
 CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
 CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
 CC also be used to assay for other modulators of IPM proteoglycan expression  
 CC and activity that may be used to treat ocular diseases. The nucleic acids  
 CC and proteins may also be used as diagnostic reagents to detect the  
 CC presence of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies  
 CC  
 SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;  
 Query Match 65.6%; Score 2184.2; DB 3; Length 2244;

Beat Local Similarity 99.5%; Pred. No. 0;  
 Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
 Qy 1 TAAACCAAGAAAGTTATCTCAATCATCTGTATCATATATATATATTTTTCACATTTTC 60  
 Db 22 TAAACCAAGAAAGTTATCTCAATCATCTGTATCATATATATATATATTTTTCACATTTTC 81  
 Qy 61 TGTATCTTTTAAATGAGATTGAGGTGTTCTGTGATTTGTTATTCGAATTTACATTCAC 120  
 Db 82 TGTATCTTTTAAATGAGATTGAGGTGTTG-TCTGTGATTTGTTATTCGAATTTACCAATGCA 140  
 Qy 121 AAAAGCAGAAATGATTTTGGAAACTAGAAAGCTATTTTGTGTTTGGATTTTCTCCA 180  
 Db 141 AAAAGCAGAAATGATTTTGGAAACTAGAAAGCTATTTTGTGTTTGGATTTTCTCCA 200  
 Qy 181 AGTTCAAGAAACCAAGATATCTCCATTATACATATACCATTTCTGAACCTAAAGACATAGA 240  
 Db 201 AGTTCAAGAAACCAAGATATCTCCATTATACATATACCATTTCTGAACCTAAAGACATAGA 260  
 Qy 241 CAATCCCCCAAGAAATGAAACATGAAAGTATCTGAAATTTTCAAAATGTCACATTT 300  
 Db 261 CAATNCCCCCAAGAAATGAAACATGAAAGTATCTGAAATTTTCAAAATGTCACATTT 320  
 Qy 301 GAGACGAATATTCGATTTTGGCAAGCATCGAAACAAAGATCCGATTTTCCAAACGGG 360  
 Db 321 GAGACGAATATTCGATTTTGGCAAGCATCGAAACAAAGATCCGATTTTCCAAACGGG 380  
 Qy 361 GGTAAAGTCTGTCCACAGAAATCCATGAAACAGATTTTAAAGCATCTTCAAGCTTATTA 420  
 Db 381 GGTAAAGTCTGTCCACAGAAATCCATGAAACAGATTTTAAAGCATCTTCAAGCTTATTA 440  
 Qy 421 TAGATTGAGTGTCTCAGAAACATATGGAAGCATATGGAATCTTTCTGGAATGCAT 480  
 Db 441 TAGATTGAGTGTCTCAGAAACATATGGAAGCATATGGAATCTTTCTGGAATGCAT 500  
 Qy 481 CCTGACACAGGGGAATATCAGGACTGGGTGACATCTGCCACAGAGACCTTCTGCT 540  
 Db 501 CCTGACACAGGGGAATATCAGGACTGGGTGACATCTGCCACAGAGACCTTCTGCT 560  
 Qy 541 CTTTGACATTTGAAAAAACTTCAGCAATTTCCAGAGACCTGATCTTCTCCACAGAG 600  
 Db 561 CTTTGACATTTGAAAAAACTTCAGCAATTTCCAGAGACCTGATCTTCTCCACAGAG 620  
 Qy 601 AATTAACAGAGAACTTCCCTGACAGAAAGATGAATATCTGACAGAGAAACATTTGGG 660  
 Db 621 AATTAACAGAGAACTTCCCTGACAGAAAGATGAATATCTGACAGAGAAACATTTGGG 680  
 Qy 661 AGAGCTGTGTAACCATTTGATTTTCAACAGCAATTTCAAGAACTTGGGCAAGT 720  
 Db 681 AGAGCTGTGTAACCATTTGATTTTCAACAGCAATTTCAAGAACTTGGGCAAGT 740  
 Qy 721 ATTCTAAGAAACCTTCAGAGAAAGATTAAGATTTTGCACAGCTCTCACTTGGGCT 780  
 Db 741 ATTCTAAGAAACCTTCAGAGAAAGATTAAGATTTTGCACAGCTCTCACTTGGGCT 800  
 Qy 781 TTCCTCTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATATACCTCAAGAC 840  
 Db 801 TTCCTCTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATATACCTCAAGAC 860  
 Qy 841 ACCAAGATGCTTCAACAGAAAGAAACAAATTCGTGTGTTGGAGAGACAGAGGTTG 900  
 Db 861 ACCAAGATGCTTCAACAGAAAGAAACAAATTCGTGTGTTGGAGAGACAGAGGTTG 920  
 Qy 901 GAGCTCAGAGCTCTCTGTGTAACCAAGATTTCAAGAGCTGCTGATCCAGTCC 960  
 Db 921 GAGCTCAGAGCTCTCTGTGTAACCAAGATTTCAAGAGCTGCTGATCCAGTCC 980  
 Qy 961 CCAATTTTCAAGAGCTTCAAGAAAGTCCCACTTCAGATGCAAAAGATTTTAAGAA 1020  
 Db 981 CCAATTTTCAAGAGCTTCAAGAAAGTCCCACTTCAGATGCAAAAGATTTTAAGAA 1040  
 Qy 1021 CTTCCAGATTTCAAAATTCATGTGTTAGATTTTACCAAGAAAGAAAGATGTC 1080

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Db 1041 CTTCCAGATTCAGAAAAATCCATGTGTATGAGATTAGACCAAGAAAAAGATGGC 1100
Qy 1081 TCAAGCTCCAGAGATGCAATCGGCCATCTTTAGAGACAGAGTGGAGAACAAAA 1140
Db 1101 TCAAGCTCCAGAGATGCAATCGGCCATCTTTAGAGACAGAGTGGAGAACAAAA 1160
Qy 1141 AGCCCTGCAAGTGAAGCTCTGTCTTTTGTATTCACAAATAATGAAAGTGAAGTCTAT 1200
Db 1161 AGCCCTGCAAGTGAAGCTCTGTCTTTTGTATTCACAAATAATGAAAGTGAAGTCTAT 1220
Qy 1201 CATGGAACCATGAGAGAGAGACAGAACCAAGAAATCTATCTCAGAGCTACAGACTCAAA 1260
Db 1221 CATGGAACCATGAGAGAGAGACAGAACCAAGAAATCTATCTCAGAGCTACAGACTCAAA 1280
Qy 1261 AGGCTGATCAGAGAAAGCACTAGAGAGAGAAATCTTTGAGATGTGGAGCAATTCAGTTC 1320
Db 1281 AGGCTGATCAGAGAAAGCACTAGAGAGAGAAATCTTTGAGATGTGGAGCAATTCAGTTC 1340
Qy 1321 ACTGATGAAAATTGCTGATCACTGCACAGCTTTGGTCTTGACACCCCAATCAGAGCTGCC 1380
Db 1341 ACTGATGAAAATTGCTGATCACTGCACAGCTTTGGTCTTGACACCCCAATCAGAGCTGCC 1400
Qy 1381 ACATCTTTTGTCTGTTATTAACAGAGAGATGCTACTTTGAGTCCAGAACTTCTCTGTTGAA 1440
Db 1401 ACATCTTTTGTCTGTTATTAACAGAGAGATGCTACTTTGAGTCCAGAACTTCTCTGTTGAA 1460
Qy 1441 CCCGAGCTTGAGACAGTGAACGAGACAGAGATGTCTTACCTGACACCTTTTGTGCTCCA 1500
Db 1461 CCCGAGCTTGAGACAGTGAACGAGACAGAGATGTCTTACCTGACACCTTTTGTGCTCCA 1520
Qy 1501 CCTGCTATGAGCTCTACCTCCCTGTCAAGAGCTCCACCTTTTATGAGCATCAAGATC 1560
Db 1521 CCTGCTATGAGCTCTACCTCCCTGTCAAGAGCTCCACCTTTTATGAGCATCAAGATC 1579
Qy 1561 TTCTCTCTGAGCTGATCAGAGACCAACAGATACATATGAGCCACTGACCAAGTCTAGTA 1620
Db 1580 TTCTCTCTGAGCTGATCAGAGACCAACAGATACATATGAGCCACTGACCAAGTCTAGTA 1639
Qy 1621 CGAGGAGCTCAGCATCCCAACGAGTATTAATCTGCAATCAGCAACTGCTCTGGAAAT 1680
Db 1640 CGAGGAGCTCAGCATCCCAACGAGTATTAATCTGCAATCAGCAACTGCTCTGGAAAT 1699
Qy 1681 TCACATCCACCTGACATCTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGATC 1740
Db 1700 TCACATCCACCTGACATCTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGATC 1759
Qy 1741 AGACACCTAGATGAATGAGATCTGTCTGACACTCTGCCCCATCTGAGGTACCAAGCTC 1800
Db 1760 AGACACCTAGATGAATGAGATCTGTCTGACACTCTGCCCCATCTGAGGTACCAAGCTC 1819
Qy 1801 AGCGAATATGTTTCTGTCCAGATCATTTCTTGAGAGATACCACTCCCTGTCTCACTTTA 1860
Db 1820 AGCGAATATGTTTCTGTCCAGATCATTTCTTGAGAGATACCACTCCCTGTCTCACTTTA 1879
Qy 1861 CAGTATATCACAACATAGTCTATGACCATTTGCCCAAGGCGCGAAGCTGTAGTGTTC 1920
Db 1880 CAGTATATCACAACATAGTCTATGACCATTTGCCCAAGGCGCGAAGCTGTAGTGTTC 1939
Qy 1921 TTCAGTCTGCGTGTGTTCTAACATGAGCTTTCTCCACGACCTGTTCACAAAGAGCTCTCTG 1980
Db 1940 TTCAGTCTGCGTGTGTTCTAACATGAGCTTTCTCCACGACCTGTTCACAAAGAGCTCTCTG 1999
Qy 1981 GAGTACCGAGCTCTGAGAGAGAAATTCACACAGCTGTGTGTTCCATATCTTACGATTCAT 2040
Db 2000 GAGTACCGAGCTCTGAGAGAGAAATTCACACAGCTGTGTGTTCCATATCTTACGATTCAT 2059
Qy 2041 CTTACAGATTTAAGCACTTGAATACTTAACCTTACAGAAAGGAGTGTGATTTGAT 2100
Db 2060 CTTACAGATTTAAGCACTTGAATACTTAACCTTACAGAAAGGAGTGTGATTTGAT 2119
Qy 2101 AGCAAAATGAAGTTGTCTAAGTCTGTGCGGTATTAACCTTACAGAGGCTGTGACGCGGCTC 2160
Db 2120 AGCAAAATGAAGTTGTCTAAGTCTGTGCGGTATTAACCTTACAGAGGCTGTGACGCGGCTC 2179

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Qy 2161 TTGAGAGATTTTGTCTGCTGACAGCCCAACACTCCATCTGAAATAGACAGCTACTCT 2220
Db 2180 TTGAGAGATTTTGTCTGCTGACAGCCCAACACTCCATCTGAAATAGACAGCTACTCT 2239
Qy 2221 CTC 2223
Db 2240 CTC 2242

RESULT 10
ACCS7948
ID ACCS7948 standard; cDNA; 2244 BP.
XX
ACCS7948;
XX
11-AUG-2003 (first entry)
XX
Human Interphotoreceptor matrix IPM 150, isoform C, cDNA.
XX
Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX
receptor; ophthalmological; gene therapy; gene; ss.
XX
Homo sapiens.
XX
Key Location/Qualifiers
FH CDS 151..747
FT /*tag= a
FT /*product= "IPM 150"
FT sig_peptide 151..210
FT /*tag= b
FT unsure 265..267
FT /*tag= c
FT /*note= "encodes Pro"
FT unsure 346..348
FT /*tag= d
FT /*note= "encodes His"
XX
PN WO2003039346-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036090.
XX
PR 08-NOV-2001; 2001US-00077270.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
WPI; 2003-441440/41.
XX
P-PSDB; ABR42344.
XX
New interphotoreceptor matrix proteins and polynucleotides, useful for
treating or preventing photoreceptor death or retinal detachment, or for
treating ocular disorders.
PS Claim 1; Page 79-80; 105pp; English.
XX
The present sequence is that of cDNA encoding isoform C of novel human
interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
is located on chromosome 6q13-q15, a region that also contains loci for
progressive bifocal choroidretinal atrophy, autosomal dominant Stargardt's
-like macular dystrophy, North Carolina macular dystrophy and Salla
disease. Members of the IPMC gene family have been identified in humans,
monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
Subfamilies are designated IPM 150 (or IMPG1) and IPM 200 (or IMPG2). The
invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
antibodies that specifically bind the polypeptides, and vectors
comprising the polynucleotides. A claimed method of treating or
preventing photoreceptor death or retinal detachment involves
administering an IPMC polynucleotide, polypeptide or antibody. Also

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Db 2060 CTTACAGATTAAACCACTGGAATTAATTACCTTCAAGAAACGGAGTGTGATGTGAAT 2119  
 QY 2101 AGCAAAATGAAGTTGCTAAGCTGTGCGGTATACCTCCACCAAGGCTGTGACGGGGTTC 2160  
 Db 2120 AGCAAAATGAAGTTGCTAAGCTGTGCGGTATACCTCCACCAAGGCTGTGACGGGGTTC 2179  
 QY 2161 TTGAGAGATTTTCTGCTGTGCTGACAGCCCAACCACTCCATCTGGAATAGACAGTACTCT 2220  
 Db 2160 TTGAGAGATTTTCTGCTGTGCTGACAGCCCAACCACTCCATCTGGAATAGACAGTACTCT 2239  
 QY 2221 CTC 2223  
 Db 2240 CTC 2242

## RESULT 11

ADA14844  
 ID ADA14844 standard; cDNA; 2244 BP.

ADA14844;

06-NOV-2003 (first entry)

Human interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.

ss; gene; human; IPMC 150 isoform C; gene therapy;

interphotoreceptor matrix component; IPMC; ocular disorder;

macular degeneration; photoreceptor death; retinal detachment.

Homo sapiens.

Location/Qualifiers

Key CDS

151..747

/\*tag= b

/product= "IPMC 150 isoform C"

151..200

/\*tag= a

/note= "Signal sequence"

201..744

/\*tag= c

/note= "Mature IPMC 150 isoform C"

265..267

/\*tag= d

/note= "Encodes Pro"

346..348

/\*tag= e

/note= "Encodes His"

unSURE

US2002160954-A1.

31-OCT-2002.

08-NOV-2001; 2001US-00007270.

29-OCT-1998; 98US-00183972.

29-OCT-1999; 99US-00430195.

(IOWA ) UNTIV IOWA RES FOUND.

Hageman GS, Kuehn MH;

WPI; 2003-238235/23.

P-PsDB; ADA14845.

New isolated or recombinant interphotoreceptor matrix component

polynucleotide and polypeptide, useful for diagnosing, preventing,

treating or prognosticating ocular disorders, e.g. macular degeneration

or retinal detachment.

Claim 3; Page 36-37; 76pp; English.

The invention relates to an isolated or recombinant interphotoreceptor

CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a present and capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform C.

Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;

Query Match 65.6%; Score 2184.2; DB 10; Length 2244;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 1 TAAACCAAGAAAGTTATCTCAATCATCTGGATCAATATATATATTTTTCACATTTTC 60  
 Db 22 TAAACCAAGAAAGTTATCTCAATCATCTGGATCAATATATATATTTTTCACATTTTC 81  
 QY 61 TGTACTTTTATGAGATTGAGTTGTTCTGTGATTTGTTATCGAATTAACCAATGAC 120  
 Db 82 TGTACTTTTATGAGATTGAGTTGTTCTGTGATTTGTTATCGAATTAACCAATGAC 140  
 QY 121 AAAAGCCGAATGTATTTGGAAGCTAATTTTGTGTTTGTGATTTTCTGCA 180  
 Db 141 AAAAGCCGAATGTATTTGGAAGCTAATTTTGTGTTTGTGATTTTCTGCA 200  
 QY 181 AGTTCAAGAAACCAAGATATCTCATTAACATATACATTTCTGAAACTTAAAGACATGA 240  
 Db 201 AGTTCAAGAAACCAAGATATCTCATTAACATATACATTTCTGAAACTTAAAGACATGA 260  
 QY 241 CAATCCCCCAAGAAATGAAACAACTGAAAGTATGAAATTAATATATATTTTTCACATTTTC 300  
 Db 261 CAATCCCCCAAGAAATGAAACAACTGAAAGTATGAAATTAATATATATTTTTCACATTTTC 320  
 QY 301 GAGACGAATATTCGATTTTGGCAAGCATGAAACAAAGATCCGATTTTTCACACGGG 360  
 Db 321 GAGACGAATATTCGATTTTGGCAAGCATGAAACAAAGATCCGATTTTTCACACGGG 380  
 QY 361 GGTAAAGTCTGTGCAAGCAATCCATGAAACAGATTTTAAACAGTCTTCAAGCTTATTA 420  
 Db 381 GGTAAAGTCTGTGCAAGCAATCCATGAAACAGATTTTAAACAGTCTTCAAGCTTATTA 440  
 QY 421 TAGATTGAGAGTGTGCAAGCAATGTAAGCAATGCAATCTTCTGATCGCAT 480  
 Db 441 TAGATTGAGAGTGTGCAAGCAATGTAAGCAATGCAATCTTCTGATCGCAT 500  
 QY 481 CCTGACACAGGGGAATATCAAGACTGGGTGAGCATCTGCCAGCAGAGACCTTCTGCT 540  
 Db 501 CCTGACACAGGGGAATATCAAGACTGGGTGAGCATCTGCCAGCAGAGACCTTCTGCT 560  
 QY 541 CTTTGAACATTTGGAAGAACTTCAAGCAATTTCCAGAGACCTTGATCTTCTCAGACAG 600  
 Db 561 CTTTGAACATTTGGAAGAACTTCAAGCAATTTCCAGAGACCTTGATCTTCTCAGACAG 620  
 QY 601 AATAAACAAGAAAGTTTCCCTGACAGAAAGATGAATATCTGCAAGAGAGACATTGGG 660  
 Db 621 AATAAACAAGAAAGTTTCCCTGACAGAAAGATGAATATCTGCAAGAGAGACATTGGG 680  
 QY 661 AGAGCTGTGTAACCATTTGTCATTTTCAACAGCAATTTCAAAAGACTTGGGCGAT 720  
 Db 681 AGAGCTGTGTAACCATTTGTCATTTTCAACAGCAATTTCAAAAGACTTGGGCGAT 740  
 QY 721 ATTCTAAGAAAACCTTCAAGAGAGCAATTTCAAGATTTTGGCAAGCTTCACTTGGGCT 780  
 Db 741 ATTCTAAGAAAACCTTCAAGAGAGCAATTTCAAGATTTTGGCAAGCTTCACTTGGGCT 800  
 QY 781 TTCCCTCTCACTCCGATGACACCTCTCTCATATGAATTTCTGATTAATACCTCAAGAG 840  
 Db 801 TTCCCTCTCACTCCGATGACACCTCTCTCATATGAATTTCTGATTAATACCTCAAGAG 860  
 QY 841 ACCAAGATGCTTACAAAGAAAGAAACAGAAATTCGCTGTGTTGAGAGCAGAGGGTG 900

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Db      861 ACCAAGATGCTACAAAGAAAGAGAAACAGAAATGCTGTGTGGAGAGACAGAGGTC 920
Qy      901 GAGCTCAGGCTCTCTGTGTAAACAGAAATTCAAGGACAGCTGCTGATCCCAAGTCC 960
Db      921 GAGCTCAGGCTCTCTGTGTAAACAGAAATTCAAGGACAGCTGCTGATCCCAAGTCC 980
Qy      961 CCATATTACAGAGAGCTACAGAGAAAGTCCCACTTCAGATGCAAGAAAGTATTTAAGAA 1020
Db      981 CCATATTACAGAGAGCTACAGAGAAAGTCCCACTTCAGATGCAAGAAAGTATTTAAGAA 1040
Qy      1021 CTTCCAGAGATTCAAAAAATTCATGTGTAGATTAGACCAAGAAAGAAAGATGTC 1080
Db      1041 CTTCCAGAGATTCAAAAAATTCATGTGTAGATTAGACCAAGAAAGAAAGATGTC 1100
Qy      1081 TCAAGCTCAACAGAGATGCACTTAACGACATCTTTAAGAGACACAGTCAGAGCAAA 1140
Db      1101 TCAAGCTCAACAGAGATGCACTTAACGACATCTTTAAGAGACACAGTCAGAGCAAA 1160
Qy      1141 AGCCCTGCAAGTACCTCTGTCTTTTGAATTCACAAATTTGAAGTGAAGAGTCTAT 1200
Db      1161 AGCCCTGCAAGTACCTCTGTCTTTTGAATTCACAAATTTGAAGTGAAGAGTCTAT 1220
Qy      1201 CATGAAACCATGAGAGAGACCAAGCAACCAAAATCTATCTCAGCTACAGACCTCAA 1260
Db      1221 CATGAAACCATGAGAGAGACCAAGCAACCAAAATCTATCTCAGCTACAGACCTCAA 1280
Qy      1261 AGGCTGATCAGCAAGCACTAAGAGAGAAACAATCTTTGATGTGGGACAAATTCAGTTC 1320
Db      1281 AGGCTGATCAGCAAGCACTAAGAGAGAAACAATCTTTGATGTGGGACAAATTCAGTTC 1340
Qy      1321 ACTGATGAATTTGCTGATCACTGCGACGCTTGGTCTTGACACCAATCAGAGCTGCC 1380
Db      1341 ACTGATGAATTTGCTGATCACTGCGACGCTTGGTCTTGACACCAATCAGAGCTGCC 1400
Qy      1381 ACATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCGAGAACTTCTCTGTGAA 1440
Db      1401 ACATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCGAGAACTTCTCTGTGAA 1460
Qy      1441 CCCCACTTTGAGACAGTGCACGAGCAGAGATGCTTACCTGACACTTCTGTCTCA 1500
Db      1461 CCCCACTTTGAGACAGTGCACGAGCAGAGATGCTTACCTGACACTTCTGTCTCA 1520
Qy      1501 CCTGCTAAGGCTCTTACCTCTCTGTCAGAAAGTCCACCTTTTATGAGCATCAAGCATC 1560
Db      1521 CCTGCTAAGGCTCTTACCTCTCTGTCAGAAAGTCCACCTTTTATGAGCATCAAGCATC 1579
Qy      1561 TTCTCTGACTGATCAAGGACCAAGATACATGATGCGACCTGACCAAGCATGCTAGTA 1620
Db      1580 TTCTCTGACTGATCAAGGACCAAGATACATGATGCGACCTGACCAAGCATGCTAGTA 1639
Qy      1621 CCAAGGCTCACCATCCCAACAGTATTATCTGCAATCAGCCAACTGCTCTGGAAT 1680
Db      1640 CCAAGGCTCACCATCCCAACAGTATTATCTGCAATCAGCCAACTGCTCTGGAAT 1699
Qy      1681 TCACATCCACCTGCACTTCAGATGACAGCCGATCAAGTCAGGTCGAGAGATATGTC 1740
Db      1700 TCACATCCACCTGCACTTCAGATGACAGCCGATCAAGTCAGGTCGAGAGATATGAC 1759
Qy      1741 AGACACCTAGATGAATGATCTGCTGACATCTGCGCCCACTGAGGTAACAGAGCTC 1800
Db      1760 AGACACCTAGATGAATGATCTGCTGACATCTGCGCCCACTGAGGTAACAGAGCTC 1819
Qy      1801 AGCGAATATGTTCTGTCCAGATCATTTCTTGAAGATACCACTCTGTCTCAGCTTTA 1860
Db      1820 AGCGAATATGTTCTGTCCAGATCATTTCTTGAAGATACCACTCTGTCTCAGCTTTA 1879
Qy      1861 CAGTATATCAACCACTAGTTCTATGACATTTGCCCAAGGCGCGAGAGCTGTAGTTC 1920
Db      1880 CAGTATATCAACCACTAGTTCTATGACATTTGCCCAAGGCGCGAGAGCTGTAGTTC 1939
Qy      1921 TTCAGTCTGCGTGTGTAAACATGCGCTTCTCAACGACCTGTTCAACAAAGAGCTCTG 1980

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Db      1940 TTCAGTCTGCGTGTGTAAACATGCGCTTCTCCAAACGACCTGTTCACAGAGCTATTTC 1999
Qy      1981 GAGTACCAAGCTCTGAGCAACAATTCACACAGCTGCTGTTCATATCTACGATCCAAT 2040
Db      2000 GAGTACCAAGCTCTGAGCAACAATTCACACAGCTGCTGTTCATATCTACGATCCAAT 2059
Qy      2041 CTTAAGAGATTTAAGCACTTGAATTAATCTTAATCTTCAAGAAAGGAGTGTATTTGAAAT 2100
Db      2060 CTTAAGAGATTTAAGCACTTGAATTAATCTTAATCTTCAAGAAAGGAGTGTATTTGAAAT 2119
Qy      2101 AGCAAAATGAAGTTTGTCTAAGTCTGCGATTAACCTCAACCAAGGCTGTGACGGGTC 2160
Db      2120 AGCAAAATGAAGTTTGTCTAAGTCTGCGATTAACCTCAACCAAGGCTGTGACGGGTC 2179
Qy      2161 TTGAGAGATTTTCTGCTGCTGACGCCCAACAATCTTCATTTGAAATAGACAGTACTCT 2220
Db      2180 TTGAGAGATTTTCTGCTGCTGACGCCCAACAATCTTCATTTGAAATAGACAGTACTCT 2239
Qy      2221 CTC 2223
Db      2240 CTC 2242

RESULT 12
ACCS7950
ID ACCS7950 standard; cDNA, 3668 BP.
XX
XX ACCS7950;
AC AC
XX
XX 11-AUG-2003 (first entry)
DT
XX
DE Mouse Interphotoreceptor matrix IPM 150, isoform A, cDNA.
XX
XX Mouse Interphotoreceptor matrix; IPM 150; chromosome 9; IPM; receptor;
KW ophthalmological; gene therapy; gene; ss.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH 196. .2592
FT /*tag= a
FT /product= "IPM 150"
XX
XX WO2003039346-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002MO-US036090.
XX
XX 08-NOV-2001; 2001US-00077270.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-441440/41.
XX
XX P-P8DB; ABR42345.
XX
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX
XX Claim 1; Page 81-82; 105pp; English.
XX
XX The present sequence is that of cDNA encoding isoform A of novel mouse
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 9. Members of the IPMC gene family have been
XX identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and
XX rat IPM. 2 Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or
XX IPMG2). The invention provides IPM 150 and IPM 200 polynucleotides and
XX polypeptides, antibodies that specifically bind the polypeptides, and
XX vectors comprising the polynucleotides. A claimed method of treating or

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CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression

XX Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;

Query Match 41.3%; Score 1375.6; DB 9; Length 3668;  
Best Local Similarity 70.7%; Pred. No. 0;  
Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19;

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Oy 1 TAAACCAAGAGGTTATCTCAATCATCTGTATCATATATATATATTTTTCACATTTT 60
Db 62 TAAACCAAGAGGTTATCTCAATCATCTGTATCATATATATATATTTTTCACATTTT 121
Oy 61 TGTATCTTTT-----AATGAGATTGAGGTTGTTCTGTGATGTTATCGAATTACC 113
Db 122 AGTCACCTTATTTCTTTAAGTGTGACTGTATTTGTTCTGTGATTTT--TCGAATTTAC 179
Oy 114 AATGACAAAGCCAGAAATGTATTTGAAACTAGAAAGCTATTTTGTGTTTGGATTT 173
Db 180 AGTATACAGAA--CCGAATGAATTTTCAATTTAAATGCTATCTTTGTTTGGATTT 238
Oy 174 TTCTCAAGTTCAAGAAACCAAGATATCTCCATTACATATATACATTTCTGAACTAAG 233
Db 239 TTCTCAAGTTCAAGAAATCAAGATACCTCTATTTAAATTTCAAGTTCTGAAATTTAAA 298
Oy 234 ACATGACATCTCCCAAGAAATGAAACACTGAAAGTCTGAAATTTTCAAAATGT 293
Db 299 ACATGACAAACCCCAAGAAATGAAACATTTGAAAGTACTTCAACAGTGCACAAAGGT 358
Oy 294 CAATCATGAGACGAATATTCGATTTGGCAAGCATCGAAACAAAGATCCGATTTTCC 353
Db 359 CAACCATGAAGAAATATTTGATTTGCAAGCTTCGAACCAAGATCAGACTTTTCC 418
Oy 354 CAACGGGGGTTAAAGTCTGTCCACAGAAATCCATGAAACAGATTTTGAACAGTCTTCA 413
Db 419 CA---GCTGCTAACTGTGTCCACAGAAATCCTTGAGACAGATTTTGAAGATCTTCAAG 475
Oy 414 CTATTTATATGATTTGAGAGTGTCTGAGAAAGCATATGGAAGCATATGAGATCTTTCC 473
Db 476 AATATTTATAGACTGAGAGATATGTCAAGAGTGTGTGGAAACATATGATCTTTCCGG 535
Oy 474 ATCGATCCCTGACACAGAGGAATATCAGGACTGGGTGAGATCTGCCAGCAGAGACT 533
Db 536 ACCGAATTCCTACACAGAGAAATATCAAGACTGGGTGAGCTCTGCCAGAAAGAACT 595
Oy 534 TCTGCTCTTTGACATTTGAAAAAACTTCAGCAATTTCCAGAGACCTGATCTTCTCC 593
Db 596 TCTGCTCTTTGACATTTGAAAAAACTTCAGCAATTTCCAGAGACCTGATCTTCTCC 655
Oy 594 AGCAAGAAATAAACAGAGAAATTTCCCTGACAGAAAAAGATGAATATTTGACAGAAAG 653
Db 656 AGCAAGAAATAAACAGAGAAATTTCCCTGAGGAGAAAGATGACAGCTTCATCAGGAG 715
Oy 654 CATTTGGAGAGCTGGTGAACCATTTGTCAATTTCACAGCAATCTAATTCAAGAGACT 713
Db 716 CACTGAAGACCTTACTGAAGCCCTGTGTGTAACCCAC----- 752
Oy 714 GGGGAGTATTTCTAAGAAAAACCTCAGAAAGCAAAATTCAGATGTTGCCAAGTCTCACT 773
Db 753 -----AGATGTTTCCAGAGATGCTCT 773
Oy 774 TGGGCTTTCTCTCTCACTCTGATGACACCTCTCTCAATGAATTTCTGATTAATACCT 833
Db 774 GGGGCTCTCTCTCTCTCTGATGACACACCTCTCAAGAGATTTCTCAAGTGTCACTCT 833
Oy 834 CAACGACACCAAGATGCTTACAAAGAAAGAAAGAAACAGAA-----TTGGCTGT 881
Db 834 CAAGGACATTTCAAAAGCCACACAGAAAGTAAACAGAACTTATCAGTGTCTGAAT 893
Oy 882 GTTGAAGAGCAGAGGTGAGCTCAGCTCTCTCTGTTAAACAGAAAGTTCAAGGACAG 941
Db 882 GTTGAAGAGCAGAGGTGAGCTCAGCTCTCTCTGTTAAACAGAAAGTTCAAGGACAG 941
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Db 894 CTCATCAGAGAGAGGATGATTAATTCAGCATCTCTCTGCCAAACACACAGATTCAAGGACAG 953
Oy 942 GCTGCTGATCTCCAGTCCCATATTAACAGAGCTGACAGAAAGTCCCAATTCATAT 1001
Db 954 GCTCAACACTCTGGGTACATCTACACAGAACTGTGGACAGCTCCAACTGCAAT 1013
Oy 1002 GCAAAAGATATTTAAGAACTTCCAGATTCAGAAAAATTCATGTGTTAGATTTAGAC 1061
Db 1014 GCAAAAGATATTTAAGAACTTCCAGATTCAGAAAAATTCGTGTATTTAGATTTAGAC 1073
Oy 1062 AAGAAAGAAAGATGAGCTCAAGCTCCACAGAGATGCACTTAAGGCAATCTTTAAG 1121
Db 1074 AAGAAAGAAAGATGAGCTCAAGCTCCACAGAAATACAGCTTATGAGCAATCTTTAAG 1133
Oy 1122 ACACAGTCAAGAACCAAAAGCCCTGCAAGTACCTCTGTCTTTTGAATTTCAAAAT 1181
Db 1134 GACACATGACAAACCAAAAGCCCTGATGATCTACTGTCTCTTGAATTTCAACAAAT 1193
Oy 1182 TGAAGTGAAGAGCTTATCATGGAACCATGAGAGAGACAAAGCAACCAAAATCTATCT 1241
Db 1194 TGAAGTGAAGAGATTCATCTAGAGTCTATGA---GACAAACACCAAGAACTTACT 1250
Oy 1242 CACAGCTACAGACTCAAAAGGCTGATGACAAAGCACTAGAGAAACAACTTTTGA 1301
Db 1251 CACAGCTACAGACTCAAAAGGCTGATGATCACTAATGATGAGAGCTGTCTTGT 1310
Oy 1302 TGTGGGACAAATTCAGTTCACTGATGAATTTGCTGATCACTGCCAGCTTTGTCTCGA 1361
Db 1311 AGAAGGAGAAATTCATTTGAGTGAATGAAATTAAGTCACT-----CTTCAAGCTGT 1364
Oy 1362 CACCAATCAGAGCTGCCACATCTTTTGTGTTAATACAGAGATGCTACTTTGAGTCC 1421
Db 1365 CACTGAACCAATCTGCCCAAGCCCTTGTGATGTCTACAGAGATGCTCACTTTGAGTCC 1424
Oy 1422 AGAATCTCTCTGTTGAACCCAGCTTGAGACAGTGAACGAGACAGATGTCTAAC 1481
Db 1425 AGAATCTCTCTGTTGAACCCAGCTTGAGACAGTGAACAGAGATGCTGAGTCC 1484
Oy 1482 T-----GACATCTCTGTGCTCCACCTGCTATGCTCTACTCCCTGCTC 1526
Db 1485 TGAATGTCTCTCAAGACAGTCTTGTGCTCCACCTGATCAAGCTCAATTTCCGATC 1544
Oy 1527 AGAAGCTCACCTTTCTTTATGAGCATCAAGCATCTTCTCTGACTGATCAAGGACAC 1586
Db 1545 AGAATATCTACTCTGTTT---CACCTAGCATCTTCTCTAGATGCTCAAAAGCCCC 1601
Oy 1587 AGATACAAATGACCTGACAGACATGATGATGATGATGATGATGATGATGATGATGAT 1646
Db 1602 TCCCTGATGACCACTGGCCCAACAGCACTATCCCAAGCCCACTCTCCCACTATG 1661
Oy 1647 TTAATTTGCAATTCAGCCCACTGGCTCTGGGAATTTCAATCCACTGATCTTCAGATGA 1706
Db 1662 TTAATTTGCAATTCAGCCCACTGGCTCTGGGAATTTGATGATGATGATGATGATGAT 1721
Oy 1707 CAGCCGATCAAGTCAAGTGGCGAAGATATGATGACACCTAGATGAATGATGATGATGAT 1766
Db 1722 CAGAGAGTGAATCAAGAGACATGACACATGACACATGACACATGACATGATGATGAT 1781
Oy 1767 TGAACCTCTGCCCCATCTGAGTACAGAGCTCAGCAATATGTTCTGTCTCCAGATCA 1826
Db 1782 TGAACCTCTGCCCCATCTGAGTACAGAGCTCAGCAATATGTTCTGTCTCCAGATCA 1841
Oy 1827 TTTCTTGAAGATACCACTCTGTCTGATGATGATGATGATGATGATGATGATGATGAT 1886
Db 1842 GTTCTTGAAGATACCACTCTGTCTGATGATGATGATGATGATGATGATGATGATGAT 1901
Oy 1887 CATTTGCCCCCAAGGCGAGAGCTGTGATGTTCTTCAAGTCTGAGTGTGATCAATGAC 1946
Db 1902 CATTTGCCCCCAAGGCGAGAGCTGTGATGTTCTTCAAGTCTGAGTGTGATCAATGAC 1961
Oy 1947 GTTCTTCAAGACCTGTTCAACAGAGCTCTCTGAGTACAGAGCTCTGAGACCAAT 2006
Db 1962 GTTCTTCAAGACCTGTTCAACAGAGCTCTCTGAGTACAGAGCTCTGAGACCAAT 2021
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QY 2007 CACACAGCTGCTGTTCCATATCTAGSANTCAATCTTACAGGATTTAAGCACTTGAAT 2066
DB 2022 CACAGACTGCTGTTCCATATCTAGSANTCAATCTTACAGGATTTAAGCACTTGAAT 2081
QY 2067 ACTTAATTCAGAAACGGAGTGTGATTTGTAATAGCAAAATGAAATTTGCTAGCTGT 2126
DB 2082 ACTGAGCTTCAGAAACGGAGTGTGATTTGTAATAGCAAAATGAAATTTGCTAGCTGT 2141
QY 2127 GCCGATTAATCTCACCAGGCTGTGACGGGGCTTTGAGAGATTTTCTGCTGCACG 2186
DB 2142 ACCCTTCAACCTCACCAGGCTGTGACGGGGCTTTGAGAGATTTTCTGCTGCACG 2201
QY 2187 CCAACATCCCATCTGGAATATAGACGATCTCTCAACATTTGAACCGCTGATCAACG 2246
DB 2202 TCAGAGGCTCAATCTGGAATATAGACGATCTCTCAACATTTGAACCGCTGATCAACG 2261
QY 2247 AGATCCCTGCAAGTTCTGCGCTGCGGCGAATTTGCCCAATGTGTAAAGAACGAACG 2306
DB 2262 GGAATCCCTGCAAGTTCTGCGCTGCGGCGAATTTGCCCAATGTGTAAAGAACGAACG 2321
QY 2307 TGAGGAAGGAGTGTGCTGTGCAAAACGAGATATGACAGCCAGGGAGCTTGAAGCT 2366
DB 2332 AGAGGAACGAGTGTGCTGTGCAAAACGAGATATGACAGCCAGGGAGCTTGAAGCT 2381
QY 2367 GGAACGAGGCTGTGCGCTGCGGCGAATTTGCCCAATGTGTAAAGAACGAACG 2426
DB 2382 GACCTTGAACCTGTGCTGCGGCGAATTTGCCCAATGTGTAAAGAACGAACG 2438
QY 2427 TCCATGAGAGTTGCGAGATCACTCTGAAATATCAAGCATCAAAATGATGTTAAAGAT 2486
DB 2439 TCCATGAGAGTTGCGAGATCACTCTGAAATATCAAGCATCAAAATGATGTTAAAGAT 2498
QY 2487 CCAAAATCAAAATTAACAGGTATGTAAGAAATTTCTGAATTAATGACCGTGA 2546
DB 2499 ACGTCAGCAA-----AATAGGTAGTCAAGAAAGAAATTTCTAATCATGATATAG 2552
QY 2547 AATAGGAATTTAATCAATCAAGATTTGGAAGAAATTTAAATCTGAAA----- 2595
DB 2553 AATGGAAGATTTGGAAGATCAAGATCTGAGGAAATTTAAATCTGGAATCATGAT 2612
QY 2596 -----ATGTCAATATATCACTAGGCTATCTCAAGAGATGATTTGGCT 2640
DB 2613 ATGTGCAAACTCTGTGAAAGAAATTTATTTCTTAAAGAAAGTGTATCTGTCTGT 2672
QY 2641 TCTCAAGAAATGAGACAGGATATTCATGGGTCACTCAAAATCAGACATACATCA 2700
DB 2673 TAACTTCTGAAACAGAGGAGATTCAGGTCACTTGAATACAGGCAATGATATCA 2732
QY 2701 CACTGAGATCAGCACACCATATTTCAATATATGAAAGATCATGATCTTGGCAACAG 2760
DB 2733 CTGTAAGACTAG-----CATGCTTGAACAAAGGACAGGCGTGTATTTGATGA-CAG 2784
QY 2761 TAAATTTGAAACAAAGCACTTACTTATTAATTA--AAACCCAAATGACATGAGCA 2818
DB 2785 TTAAGCTGTGTTGGGCGGGGGGCAATATTTTGTCAAACTCAAGCAATCACTGGA 2844
QY 2819 ACATATTTTACTATTTCTGATGATGATCAAAATGATCATAGCCAGGTTTGTCTCAC 2878
DB 2845 ACACA-TTGAATAATTTTGAAGATGATC--AAGTGAAGAAAGATAGGATGATTTT 2901
QY 2879 CTTCCTGAAATTTTACTCAGATCATTTGCAACAGCATAGCTTACTTATTTAG 2938
DB 2902 CTTCCTGAAATTTTACTCAGATCATTTTCAAAATTAATACMC-----TTGTTAG 2954
QY 2939 GGAATGAACATTTATGGAAGCAAACTTTATATGCTAGAAAGTACATTTAAAGT 2998
DB 2955 TGGGTGTACATATTTGAGATCTGATCTTTTATATGTTAGAAATATACAGTTAAAGT 3014
QY 2999 GACTACTTACGC 3010
DB 3015 TATCATTTGGGC 3026

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RESULT 13
ADAL4847
ID ADAL4847 standard; cDNA, 3668 BP.
XX
AC ADAL4847;
XX
AC 06-NOV-2003 (first entry)
XX
DB Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX
KW ss; gene; mouse; IPMC 150 isoform A; gene therapy;
KW interphotoreceptor matrix component; IPMC; ocular
KW macular degeneration; photoreceptor death; retinal detachment.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 196..2592
FT /tag= a
FT /product= "IPMC 150 isoform A"
XX
PF US2002160954-A1.
XX
PD 31-OCT-2002.
XX
PF 08-NOV-2001; 2001US-00007270.
XX
PR 29-OCT-1998; 98US-00183972.
PR 29-OCT-1999; 99US-00430195.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2003-238235/23.
XX
DR P-PSDB; ADAL4848.
XX
PT New isolated or recombinant interphotoreceptor matrix component
PT polynucleotide and polypeptide, useful for diagnosing, preventing,
PT treating or prognosticating ocular disorders, e.g. macular degeneration
PT or retinal detachment.
XX
PS Claim 3; Page 39-41; 76pp, English.
XX
CC The invention relates to an isolated or recombinant interphotoreceptor
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC gene operatively linked to the IPMC polynucleotide. The IPMC
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC preventing, treating or prognosticating ocular disorders, e.g. macular
CC degeneration, photoreceptor death or retinal detachment. They are also
CC useful for identifying a compound capable of modulating IPMC gene
CC expression in a cell. The present sequence represents cDNA encoding mouse
CC interphotoreceptor matrix component, IPMC, 150 isoform A.
XX
SQ Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;
XX
Query Match 41.3%; Score 1375.6; DB 10; Length 3668;
Best Local Similarity 70.7%; Pred. No. 0;
Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19;
QY 1 TAAACCAAGAGGTATCTCAATCATCTGATCATATATATATTTTTCACATTTTC 60
DB 62 TAAACCAAGAGGTGCTGTGATCTCAGCCGACCTGATTTGATTTTTCATATTTTC 121
QY 61 TGTACTTTT-----AATGAGATTTGAGTTGTTGTGATGTTTATCAGAAATACC 113
DB 122 AGTACCTTATTTCTTAAAGTGTACCTGTGATTTGTTGATTTT--TCGAATATACC 179
QY 114 AATGACAAAGCCAGATGATTTGGAACATAGAAAGACTATTTTGTGTTTGGATTT 173
DB 180 AGTATACGAA--CCAGATGAAATTTTCAAAATTAACATGCTATCTTTGTTGGATTT 238

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174 TTCTCAAGTTCAAGGAACCAAGATATCTCCATTACATATACCATTTCTGAAGCTTAAG 233  
239 TTCTCAAGTTCAAGGAATCAAGATACCTCTATTTAAATATTCAGTTCTGAATTTAAA 298  
234 ACATGACATCTCCCAAGAAATGAAACAATGAAAGTACTGAAAAATTTGTAACAATGT 293  
239 ACATGACAAAAACCAAGAAATCGAAACAATTTGAAAGTACTTCAACAGTGCACAAAGTGT 358  
234 CAACATGAGAGATATTCGATTTGGCAAGCAATCGAAACAAAGATCCGATTTTTC 353  
339 CAACATGAAACGAATATTCGATTTGGCAAGCAATCGAAACAAAGATCGACATTTTTC 418  
334 CAACGGGGGTTTAAAGTCTGTCCACAGAAATCCATGAAACAAGTTTAAAGATCTTCAAG 413  
419 CA---GCTGCTAACATCTGTCCACAGAAATCTTGAACAGATTTTAAAGATCTTCAAG 475  
414 CTATTTATGATTTGAGAGTGTGTCAAGAAAGCATTTGGAAAGCATATCGATCTTTCTGG 473  
476 AATATTTATGACTGAGAGATATGTCAAGAAAGTGTGTGGGAAGCATATCGATCTTTCTGG 535  
474 ATCGATCCCTGACACAGGGGAAATATCAAGACTGGGTGAGCATCTTGGCAGCAGAGACT 533  
536 ACCGATTTCTGACACAGAGAAATATCAAGACTGGGTGAGCATCTTGGCAGGAAAGAACT 595  
534 TCTGCTCTTTTGACATTTGAAAAAACTTCAGCAATTTCCAGAGGACCTGTGATCTTCTCC 593  
536 TCTGCTCTTTTGACATTTGAAAAAACTTCAGCAATCTCCAGAGGACCTGTGATCTTCTCC 655  
534 ACCAGAGATTAACAGAGAAAGTCTTCCCTGACAGAAAAAGATGAAATATCTGACAGAAAG 653  
656 AGCAGAGATTAACAGAGAAAGTCTTCCCTGAGAGAAAGATGAGACAGCTCCATGAGAG 715  
654 CATTTGGAGAGCTGTGTGAACCATTTGATTTCAACAGCAATCTATCATTTCAAGACTT 713  
716 CACTGAGAGACCTTACTGAAAGCCCTGTGTGTACCAAC----- 752  
714 GGGCAGTATTTCAAGAAAAACCTCAGAAAGCAAAATTCAGAGATGTTGCCAAGTCTCACT 773  
753 -----AGATGTTTCCAGATGTCTCT 773  
774 TGGGCTTTTCCCTCTCACTCTGATGACACCTCTCTCAATGAAATTTCTGATTAATACCT 833  
774 GGGGCTTTTCCCTCTCTGATGACACAGACTCAAGAGATTTCTCAGTGTCACTCT 833  
834 CAACGACACCAAGATGCTTACGACAGAAAGAAACAGAA-----TTGCTGT 881  
834 CAAGGACATTTCAAAAGCCCAACAGAAAGTAAACAGAACTTATTCAGTGTCTGAATT 893  
882 GTTGGAGAGCAGAGGGTGGAGTCAAGCTCTCTGTGTTAAACAGAAATTCAGAGCAGA 941  
884 CTCATCAAGAGAGAAAGTGGATTTCAAGCATCTCTGTGCAACCAAGATTTCAAGGACAG 953  
942 GCTGCTGATCTCCAGTCCCATATTTACAGAGAGTCAAGAGAAAGTCCCACTTCAAGT 1001  
954 GCTCAACCACTCTGGGTCACTACATCTACCAAGAACTGTGGGACAGTCCCACTCAAGT 1013  
1002 GCAAAAGATTTTAAGAACTTCCAGAGATTTCAAAAAATTCATGTGTGTTAGATTTAGAC 1061  
1014 GCAAAAGATTTTAAGAACTTCCAGAGATTTCAAAAAATTCGTTGTTAGATTTAGACC 1073  
1062 AAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCACTTACGGCATCTTTAAGAG 1121  
1074 AAAGAAAGAAAGATGCTCAAGCTCCACAGAAATACAGCTTTAAGGCTTTTAAAG 1133  
1122 ACACAGTGCAGAGCAAAAGCCCTGCAAGTGAAGCTCTGTCTTTGATTTCCAAACAAAT 1181  
1134 GCACCATGCGAAGCAAAAGCCCTGATAGTCACTGATCTCTTGAATTTCAACAAAT 1193  
1182 TGAAGTGAAGAGTCTATCATGGAACCATGAGAGAGCAAGCAACCGAATCTATCT 1241  
1194 TGAAGTGAAGAGATTCATCATGAGTCTATGAA---GACAAACACAGAAACCTTACT 1250

1242 CACAGCTACAGACCTCAAAAGGCTGATCAAGCAAGACATAGAGAGAAACAATCTTTGA 1301  
1251 CACAGCTACAGACCTCAAAAGGCTGATCAAGCAAGACATAGAGAGAAACAATCTTTGA 1310  
1302 TGTGGGAGCAATTCAGTTCACTGATGAAATTTGTGATGATCTGCGCAGCTTTGTCTGA 1361  
1311 AGAAGGGAATTTCCATTCGGTGAATGAAATTTGTGAGACACT-----CTTCAGACTGT 1364  
1362 CACCAATCAGAGCTGCCACATCTTTGCTGTTATTAACAGAGATGCTACTTTGAGTCC 1421  
1365 CACTGAACCAATCTGCGCAAGCCCTTGTGATGTCACAGAGATGCTCAGCTTGAATTC 1424  
1422 AGAATCTCTCTGTGAAACCCAGCTTGAGACAGTGAACGAGAGAGACATGTCTACC 1481  
1425 AGAATCTCTCTGTGAAACCCAGCTTGAGACAGTGAACGAGAGAGACATGTCTACC 1484  
1482 T-----GACACTTCTGTGTCCACCTGTCTATGAGCTTCACTCTCTGTCT 1526  
1485 TGAATGTCTCCAAAGACAGATTTGTGTCTCACCTGTATCAGCTCAATTTCCGATTC 1544  
1527 AGAAGCTCCAGCTTTCTTTATGAGATCAAGATCTTCTCTGACTGATCAAGAGACAC 1586  
1545 AGAAATCTTACCTCTGTTTA---CAGCTGACATCTTCTCTGAGATGCTCAAAAGCCCTCC 1601  
1587 AGATCAATGAGCCACTGACACAGACATGCTAGTACCAAGGGCTCACACATCCCAACAGTGA 1646  
1602 TCCCTGATGACACATGAGCCCAAGAGACATCATCCCAAGCCCACTCTCCCACTATGGA 1661  
1647 TTATTTGCAATCAAGCAATGAGCTCTGGGAAATTTACATCAACCTGATCTTCAGATGA 1706  
1662 TTATTTCTACATCGCCCAATTTGCTGTGAATTCGTCATTTGGCTGTGATCTCCAGTGA 1721  
1707 CAGCGATCAAGTGAAGTGGGCAAGATATGATGACAGACCTGATGAAATGGAATCTGTC 1766  
1722 CAGAGAGTGAATCAACAGCAAGCCATGACACATCCGAACCTGATGAGATGATGTTC 1781  
1767 TGACATCTCTGCCCCATCTGAGTACAGAGCTCAGCAATATGTTCTGTCTCCAGATCA 1826  
1782 TGACAGGCTGATCTGTCTGAGAAATTCAGAACTGATGATGATGATCTGTCTCGGATCA 1841  
1827 TTTCTTGAAGATACCACTCTGTCTGATGATGATGATGATGATGATGATGATGATGATG 1886  
1842 GTTCTTGAAGATGACACACCAATCCCAAGTACAGGTTCAACACACAGCTCCGAGAC 1901  
1887 CATTTGCCCCCAAGGCGCAGAGCTGTGATGTTCTTCAAGTCTGCTGTGCTCAAGATGC 1946  
1902 CATTTGCCCCCAAGGCGCAGAGCTGTGATGTTCTTCAAGCTGTGCTGTGCTCAAGATGC 1961  
1947 GTTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2006  
1962 GTTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2021  
2007 CACACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2066  
2022 CACACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2081  
2067 ACTTAATCTTCAAGAAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2126  
2082 ACTTAATCTTCAAGAAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2141  
2127 GCGGTATTAATCTTCAAGAGCTGTGACAGGAGTCTTGAAGATTTTCTGTCTGACAGC 2186  
2142 ACCCTTCAACCTTCAACAGGCTGTGACAGGAGTCTTGAAGATTTTCTGTCTGACAGC 2201  
2187 CCAACATCTCATCTGAAATGACAGCTACTCTTCAACATTTGAACCAAGCTGATCAAGC 2246  
2202 TCAAGGCTCATCTGAAATGAAAGCTACTCTCTCAACATTTGAACCAAGCTGATCAAGC 2261  
2247 AGATCTCTGCAAGTCTCTGAGCTGTGAGGATTTTCCCAATGTGTTAAAGAAAGCAAGAC 2306  
2262 GATCTCTGCAAGTCTCTGAGCTGTGAGGATTTTCCCAATGTGTTAAAGAAAGCAAGAC 2321  
2307 TGAAGAGCGAGATGTGCTGCAAAACAGATATGACAGCCAGAGGAGCTTGAAGCTGT 2366

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Db 2322 AGAGGAGAGAGTCTCGCTGACAGAGGACATGAGACCCAGGACCTTGATACCA 2381
Qy 2367 GGAACACAGGCTCTGTGGGCTCTGGGCAAGAAATGCGAGTCTTCCAGAGGAAGGAGC 2426
Db 2382 GACCCCTGAACCTCTGTCCCTGG---AAAGACTGTGTGGCCGGCCGAGAACAGCAAC 2438
Qy 2427 TCCAGGAGGTTGCCAGATCACTCTGAAATTCAGCATACAAACTAGTGTAAAAAGTT 2486
Db 2439 TCCAGGAGGCCACAGATCACTCAAAACCAACTCGAGAACTGGGTGTAAAAAGCT 2498
Qy 2487 CCAAAATCAACAAATTAACAAGTATCATGTAAGAAATTCGATTACTGACCGTGA 2546
Db 2489 AGCTGACGA-----AATAGGTAGTCAAGAAAAGAAATTTAAACTATGCTATAG 2552
Qy 2547 ATATGAGAAATTTAAACATCAAGATTTGGAGAAATTTAAAACTGAAA----- 2595
Db 2553 ATTTGAGAAATTTGAAGACCAAGACTGGGAGGAAATTTAAAGCTGAAATCATATG 2612
Qy 2596 -----ATGTACAAATTAATCATCTTAGCTATCTCAAGAGATGATTGGCT 2640
Db 2613 ATGTGCAAACTCTGTGAAGAAAATTTATTTCTTAAAGAAAGTGTATCTGTCT 2672
Qy 2641 TCTCAAGGAAATGAGACAGGCAATATTCATGGGTCAATCAAAATCAGACATACGTA 2700
Db 2673 TAACTTCTGAAAAACAGAGGAGAGATTCAGTGTCAATTCAGGATGATATCA 2732
Qy 2701 CACTGAGAAATCAGACACACATATTTCAATATATGAAAGTCAATGATCTTGGAACCG 2760
Db 2723 CTTTGAGACTGAG-----CATGCTTGAACAGAGCAGCGGTATTTGATGA-CA 2784
Qy 2761 TAAATTCGAAAAAAAGACACTTACTTATTTA--AAACCCCAATGCATCAGCGAA 2818
Db 2785 TTAACTCTGTGGGCGGGGACATATTTTGTCAAACTCAAAACATCATCTTGA 2844
Qy 2819 ACATATTTTACTATTTCTTGATGATGATCAAAATGATCATAGGAGTTGCTTCAC 2878
Db 2845 ACAC-TTTTACTATTTTGGACAGTCTC--AAGTAGCAAAAGATAGGTAGCTTTT 2901
Qy 2879 CTTCCTGAAATTTTACTCAGATTCATTTGCAACAGATAGCTTACTTATTTAG 2938
Db 2902 CTTCCTTAAATATTAACATAARCTTATTTCAATTAATACAC-----TTGTTAG 2954
Qy 2939 GACTGAAACATTTATTTGGGAACAACTCTTATATGCTAGAAAGTCAATTAAGAT 2998
Db 2955 TGGGTGTACATATTTGAGATCTGATCTTATATGTTAGAAATATACAGTTAAAGAT 3014
Qy 2999 GACTACTTACGC 3010
Db 3015 TATCATTTGGGC 3026

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## RESULT 14

AAA46309  
ID AAA46309 standard; cDNA, 3206 BP.

AC AAA46309;

DT 04-SEP-2000 (first entry)

DE cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).

XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;

KM chromosome 6q13-q15; ocular disease; retinal detachment;

KM choroidretinal degeneration; retinal degeneration; cone degeneration;

KM age related macular degeneration; photoreceptor degeneration;

KM retinal pigment epithelium degeneration; mucopolysaccharidosis;

XX rod-cone dystrophy; cone-rod dystrophy; ss.

OS Mus sp.

XX Key

PH Location/Qualifiers

FT CDS 1..2130

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FT FT /tag= a
FT FT /transl_except= (pos: 16..18, aa: Val)
FT FT /transl_except= (pos: 55..57, aa: Ala)
FT FT /transl_except= (pos: 58..60, aa: Tyr)
FT FT /transl_except= (pos: 73, aa: Asp)
FT FT /transl_except= (pos: 234..236, aa: Xaa)
FT FT /transl_except= (pos: 271..272, aa: Xaa)
FT FT /transl_except= (pos: 403..405, aa: Xaa)
FT FT /transl_except= (pos: 2107..2109, aa: Xaa)
FT FT /product= "interphotoreceptor matrix proteoglycan IPM150"
FT FT /note= "Xaa is an unspecified amino acid"

W0200026367-A2.
11-MAY-2000.
29-OCT-1999; 99WO-US025440.
29-OCT-1998; 98US-00183972.
(IOWA ) UNIV IOWA RES FOUND.
Hageman GS, Kuehn MH;
WPI: 2000-355616/31.
P-PSDB; AAY93338.

Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
preventing, diagnosing and treating ocular disorders such as retinal
detachment and choroidretinal degeneration.

Claim 2, Fig 6A; 183pp; English.

The present sequence encodes an interphotoreceptor matrix (IPM)
proteoglycan, designated IPM150. The protein is an IPM component (IPMC).
Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
is located on chromosome 6q13-q15, between markers CHIC.GAT11P10 and
D6S284. The IPM proteins may be used to supplement a patient's own
production of the protein or to rectify alterations in their nucleic
acids that result in expression of an inactive protein. The IPM nucleic
acids may be used in this way to treat ocular diseases such as retinal
detachment, choroidretinal degeneration, retinal degeneration, age related
macular degeneration, photoreceptor degeneration, RPE (retinal pigment
epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
also be used to assay for other modulators of IPM proteoglycan expression
and activity that may be used to treat ocular diseases. The nucleic acids
and proteins may also be used as diagnostic reagents to detect the
presence of IPM nucleic acids and their products in samples from patients
according to standard methodologies

SQ Sequence 3206 BP; 937 A; 778 C; 686 G; 793 T; 0 U; 12 Other;
Query Match 33.8%; Score 1127.2; DB 3; Length 3206;
Beet Local Similarity 68.9%; Pred. NO. 1.6e-290; Indels 152; Gaps 15;
Matches 1824; Conservative 5; Mismatches 665;

Qy 418 TTATGATTGAGAGTGTGTCAGAAAGCATATGGAACATATGATCTTTCTGGATCG 477
Db 18 TCAAGAAATCAAAATATCTCAAGAAAGTGTGTCAGAAAGATATCTTCTTGGANNAG 77
Qy 478 CATCCTGACACAGGGGAATATCAGACTGGGTGATGCTGTCAGACAGAGAACCTTCTG 537
Db 78 AATTCCTGACACAGAGAAATATCAAGGCTGGGTGATGCTGTCAGAGAAAGAACCTTCTG 137
Qy 538 CCTCTTTGACATTTGGAAGAAATTTCCAGAGAGACCTTGGATCTTTTCCAGCA 597
Db 138 CCTCTTTGACATTTGGAAGAAATTTCCAGAGAGACCTTGGATCTTTTCCAGCA 197
Qy 598 GAGATATAAACAAGAGATTCCCTGACAGAAAGATATATCTGACAGAGAGACATT 657
Db 198 GAGATATAAACAAGAGATTCCCTGAGAGAGAAAGATGACACCTCTCAAGAGACACT 257

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Oy	658	GGGAGAGCCTGGTGA	AACCATTTGTCATTTTCAACGACAACTTCAACATTTCAAGACTTGGC	717
Db	258	GGAGCACCTTCTGAG	CGCCCTGGTAGTCCAC-----	290
Oy	718	AGTATTCTAAGAAA	CCTCAGAAAGCAAAATTCAGATGTGGCAACGTCTCACTTGGG	777
Db	291	-----	-----AGATGTTTCCAGGATGTCCCTGGG	315
Oy	778	CCTTTCCTCTCACT	CTGTGATGACACCTCCTCAATGAAATTTCTGATTAATACACTCAAC	837
Db	316	CCMTTCCCACTCTCT	CTGTGATGACACAGACTCAAGAGATTTCTCAGTGTCAACCTCAAG	375
Oy	838	GACGCCAAGATGCC	TCAACACAGAAAGAAAAGAAAAGAA-----TTGGCTGTGTGG	885
Db	376	GACATTCAAAAGCC	CAACAGAAAGTMAACAGAACCTATTCATGATGAAATTTCTCA	435
Oy	886	GAGAGCAGAGGGT	GAGACTCAGAGCTCCTCTGTGGTAAACAGAAAGTTCAAGGACAGAGTC	945
Db	436	TCAGAGGAGAGT	GGATTTCAAGCATCTCTGTCCAAACCAAGGTTCAAGGACAGAGTCC	495
Oy	946	GCTGACTCCAGT	CCCCATATTATCCAGAGCTAGCAGAGAAAGTCCCACTTCAGATGCA	1005
Db	496	ACCAACTCTGGGT	TCACATACAGAGAACTGATGGAGCAGTCCCACTGCAAGTTGCA	555
Oy	1006	AAGATATTTAAGAA	CTTCCAGATTTCAAAAAATTCATGTGTTAAGATTTTAGACCAAG	1065
Db	556	AAGATATTTAAGAA	CTTCCAGATTTCCAGAAATCCGTATTAAGATTTTAGACCAAG	615
Oy	1066	AAAGAAAAGAT	GTGCTCAAGCTCCACAGAGATGCAACTTACGGGCATCTTTAAGAGCAC	1125
Db	616	AAAGAAAAGAT	GTGCTCAAGCTCCACAAATATACGCTTATGGCATTTTAAAGGGAC	675
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Oy	1246	GCTACAGA	CCTCCAAAAGGCTGATCGCAAGACATGAGAGAAACAATCTTGGATGTG	1305
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Db	853	GGGACAA	TTCAAGTTCACTGATGAATTTGCTGGATCACTGCGCAGCTTGTGCTGTACACT	906
Oy	1366	CAATCAGAG	CTGCCCAACATCTTTTGCTGTATACAGAGATGCTATCTTTGATGTCAGAA	1425
Db	907	GAAACGAG	ATCTGCCCAAGCCCCCTGCTATGTGCACAGAGATGTCCACTTTGATGTCAGAA	966
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Db	1144	TTGATGAC	CACTGACCACTCAATCCCAAGGCCACTCTCCCACTATGATTAAT	1203
Oy	1651	TCTGCAAT	CAGCACTGGCTCTGGGAAATTTCAATCACTGCATCTTTCAGATGACAGC	1710
Db	1204	TCTTACAT	CTCCGCAATTTGCTCTTGGAAATGTCTACATTTGGCTGTACTCTCCAGTATACGA	1263
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[illegible]

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Qy	2885	TGAAATTTTCTCTCAGATCATTTTGCAACAAGCATACCTTACTTCTTGTTTAGGACTG2944
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RESULT 15

ID	ACC57951	ACC57951 standard; cDNA; 1726 BP.
XX	ACCS7951,	
XX	ACCS7951,	
XX	11-AUG-2003	(first entry)
DE	Mouse interphotoreceptor matrix IPM 150, isoform D, cDNA.	
XX		
KM	Mouse; interphotoreceptor matrix; IPM 150; chromosome 9; IPMC; receptor;	
XX	ophthalmological; gene therapy; gene; ss.	
XX	Mus sp.	
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XX	WO2003039346-A2.	
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PD	15-MAY-2003.	
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PF	08-NOV-2002; 2002WO-US036090.	
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PR	08-NOV-2001; 2001US-00077270.	
XX		
XX	(IOWA ) UNIV IOWA RES FOUND.	
XX		
PI	Hageman GS, Kuehn MH;	
XX		
XX	WPI; 2003-441440/41.	
DR	P-PSDB; ABR42346.	

New interphotoreceptor matrix proteins and polynucleotides, useful for treating or preventing photoreceptor death or retinal detachment, or for treating ocular disorders.

Claim 1; Page 82-83; 105pp; English.

The present sequence is that of cDNA encoding isoform D of novel mouse interphotoreceptor matrix 150 (IPM 150), a member of the newly identified interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene is located on chromosome 9. Members of the IPMC gene family have been identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2 Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The invention provides IPM 150 and IPM 200 polynucleotides and polypeptides, antibodies that specifically bind the polypeptides, and vectors comprising the polynucleotides. A claimed method of treating or preventing photoreceptor death or retinal detachment involves administering an IPMC polynucleotide, polypeptide or antibody. Also

[illegible]

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OY 1344 GCCAGCCTTGGTCCTGACACCCAAATCAGAGCTGCCACATCTTTGCTGTATAACAGA 1403
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OY 1404 GGATGCTACTTTGAGTCCAGAACTTCTCTGTTGAAACCCAGCTTGAAGACAGTGAACGG 1463
Db 1120 GGATGCCACTTTGAGTCCAGAACTTCTCTGTTGAGCCTAAGCTTGAAGGAGTGAACAG 1179
OY 1464 AGCAGAGCATGSGTCTACCTG 1483
Db 1180 AGAAGATCTGAGCTGCTG 1199
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Search completed: January 14, 2006, 08:42:38  
Job time : 1928 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2006, 07:25:30 ; Search time 16555 Seconds  
(without alignment)

11433.929 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 26421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_ph:\*  
9: gb\_ph:\*  
10: gb\_ph:\*  
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12: gb\_ph:\*  
13: gb\_ph:\*  
14: gb\_ph:\*  
15: gb\_ph:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3196	96.0	3268	8 AF047492	AF047492 Homo sapi
2	1713.2	51.4	3552	4 AB047844	AB047844 Bos tauri
3	1604.2	48.2	2009	6 CQ725539	CQ725539 Sequence
4	1375.6	41.3	3668	9 AF266478	AF266478 Mus muscu
5	1366.4	41.0	2924	9 BC022970	BC022970 Mus muscu
6	1287.2	38.7	2850	9 AB047843	AB047843 Rattus no
7	1255.2	37.7	3675	9 AF229929	AF229929 Mus muscu
8	823.6	24.7	90766	8 AL392166	AL392166 Human DNA
9	823.6	24.7	132145	14 AL359817	AL359817 Homo sapi
10	814.2	24.5	1235	8 HSIMPG17	HSIMPG17 Homo sapi
11	535.8	16.1	816	8 HSIMPG13	HSIMPG13 Homo sapi
12	535.8	16.1	160719	14 AL157379	AL157379 Homo sapi
13	481.2	14.5	4953	5 AB070714	AB070714 Gallus ga
14	439	13.2	555	5 AF047491	AF047491 Macaca fa
15	317.8	9.5	259413	14 AC161554	AC161554 Bos tauri
16	282.6	8.5	157596	9 AC120388	AC120388 Mus muscu
17	274.6	8.2	248573	14 AC096467	AC096467 Rattus no
18	249	7.5	444	8 HSIMPG10	HSIMPG10 Homo sapi

19	236.4	7.1	537	8 HSIMPG02	AF017761 Homo sapi
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21	236.4	7.1	186301	8 AL359817	AL359817 Homo sapi
22	226	6.8	448	8 HSIMPG14	HSIMPG14 Homo sapi
23	210.4	6.3	477	8 HSIMPG15	HSIMPG15 Homo sapi
24	204.6	6.1	310	8 HSIMPG01	AF017760 Homo sapi
25	203.4	6.1	3326	6 CQ728190	CQ728190 Sequence
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27	203.4	6.1	4165	6 CQ870600	CQ870600 Sequence
28	203.4	6.1	4165	8 AF173155	AF173155 Homo sapi
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30	198.8	6.0	4010	9 AY174061	AY174061 Mus muscu
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32	198.2	6.0	259413	14 AC161554	AC161554 Bos tauri
33	169.8	5.1	422	8 HSIMPG03	HSIMPG03 Homo sapi
34	153	4.6	41220	8 AC148244	AC148244 Mus muscu
35	145.6	4.4	159816	14 AC136044	AC136044 Rattus no
36	143.2	4.3	214606	14 AC161819	AC161819 Gallus ga
37	142.4	4.3	377	8 HSIMPG07	HSIMPG07 Homo sapi
38	121.4	3.6	187351	5 CR788305	CR788305 Zebrafish
39	110.4	3.3	311	8 HSIMPG06	HSIMPG06 Homo sapi
40	110	3.3	60914	14 AC135246	AC135246 Rattus no
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44	103	3.1	160042	14 AC027757	AC027757 Homo sapi
45	103	3.1	178064	14 AC023311	AC023311 Homo sapi

## ALIGNMENTS

RESULT 1	AF047492	3268 bp	mRNA	linear	PRI 26-OCT-1999
LOCUS	AF047492				
DEFINITION	Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)				
ACCESSION	AF047492.2	GI:6118565			
VERSION	AF047492.2	GI:6118565			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Kuehn, M.H. and Hageman, G.S.				
TITLE	Expression and characterization of the IPM 150 gene (IMPG1) product, a novel human photoreceptor cell-associated chondroitin-sulfate proteoglycan				
JOURNAL	Matrix Biol. 18 (5), 509-518 (1999)				
PUBMED	10601738				
REFERENCE					
AUTHORS	Kuehn, M.H. and Hageman, G.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-FEB-1998) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 11150E PFP, Iowa City, IA 52240, USA				
REFERENCE					
AUTHORS	Kuehn, M.H. and Hageman, G.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-OCT-1999) Ophthalmology and Visual Sciences, University of Iowa, 200 Hawkins Drive, 11150E PFP, Iowa City, IA 52240, USA				
REMARK	Sequence update by submitter				
COMMENT	On Oct 26, 1999 this sequence version replaced gi:2906231.				
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## ORIGIN

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Best Local Similarity 75.1%; Pred. No. 0;
Matches 2558; Conservative 0; Mismatches 638; Indels 212; Gaps 25;
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DEFINITION
ACCESSION      AF266478
VERSION      AF266478.1 GI:9844921
KEYWORDS
SOURCE
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS      Kuehn,M.H., Mielecki,D.T. and Hageman,G.S.
TITLE      Molecular characterization of the murine orthologue of the human
retinal proteoglycan IPM 150
Mol. Vis. 6 (2000) In press
2 (bases 1 to 3668)
Kuehn,M.H., Mielecki,D.T. and Hageman,G.S.
Direct Submission
Submitted (10-MAY-2000) Ophthalmology, University of Iowa, 2501
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 REFERENCES  
 AUTHORS  
 Kluksner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
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LOCUS

AB047843

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mRNA

linear

ROD 30-AUG-2000

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VERSION AB047843.1 GI:9955917  
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Sciuronomachi; Muridae; Murinae; Rattus.  
REFERENCE 1 (sites)  
AUTHORS Uehara, F., Ohba, N. and Ozawa, M.  
TITLE Core Protein of rat Mucinlike Glycoprotein Associated with  
Photoreceptor Cells  
JOURNAL Published Only in Database (2000)  
AUTHORS Uehara, F., Ohba, N. and Ozawa, M.  
TITLE Direct Submission  
JOURNAL Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University  
Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,  
Kagoshima 890-8520, Japan  
(E-mail: f.uehara@meds.kufm.kagoshima-u.ac.jp, Tel: 81-99-275-5402,  
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 90766)
AUTHORS
Clark,S.
TITLE
Direct Submision
JOURNAL
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Mar 20, 2001 this sequence version replaced gi:13224983.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi, EMBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information

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on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RPI1-758017 is from the library RPI1-11.3 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6

----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [vegas@sanger.ac.uk](mailto:vegas@sanger.ac.uk)

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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

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AUTHORS  
TITLE  
JOURNAL  
COMMENT

McLay, K.  
Direct Submission  
Submitted (09-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
Requests: clonerequest@sanger.ac.uk  
On Jan 14, 2001 this sequence version replaced gi:12214326.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: BA505B21  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
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Consensus quality: 126505 bases at least Q20  
Insert size: 12645; sum-of-contigs  
Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality  
coverage: 2.65x in Q20 bases; agarose-tp  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
\* 8913 8912: contig of 8912 bp in length  
\* 9013 9012: gap of 100 bp  
\* 12665 12665: contig of 3653 bp in length  
\* 12765 12765: gap of 100 bp  
\* 16825 16825: contig of 4060 bp in length  
\* 16925 16925: gap of 100 bp  
\* 22958 22958: contig of 6033 bp in length  
\* 23058 23058: gap of 100 bp  
\* 23059 23059: gap of 100 bp  
\* 25080 25080: contig of 2022 bp in length  
\* 25081 25081: gap of 100 bp  
\* 27372 27372: contig of 2092 bp in length  
\* 27373 27372: gap of 100 bp  
\* 40754 40754: contig of 13382 bp in length  
\* 40755 40754: gap of 100 bp  
\* 40855 45147: contig of 4233 bp in length  
\* 45148 45247: gap of 100 bp  
\* 48493 48493: contig of 3246 bp in length  
\* 48494 48593: gap of 100 bp  
\* 48594 52881: contig of 4288 bp in length  
\* 52882 52881: gap of 100 bp  
\* 52982 57112: contig of 4111 bp in length  
\* 57113 57212: gap of 100 bp  
\* 60637 60637: contig of 3425 bp in length  
\* 60638 60737: gap of 100 bp  
\* 62738 62745: contig of 2008 bp in length  
\* 62746 62845: gap of 100 bp  
\* 62846 70684: contig of 7839 bp in length  
\* 70685 70784: gap of 100 bp  
\* 74560 74560: contig of 3776 bp in length  
\* 74561 74660: gap of 100 bp  
\* 77242 77242: contig of 2582 bp in length  
\* 77243 77342: gap of 100 bp  
\* 77343 81104: contig of 3762 bp in length  
\* 81105 81204: gap of 100 bp  
\* 81205 83750: contig of 2546 bp in length  
\* 83751 83850: gap of 100 bp  
\* 83851 92962: contig of 9112 bp in length  
\* 92963 93062: gap of 100 bp  
\* 93063 106092: contig of 13030 bp in length  
\* 106093 106192: gap of 100 bp

FEATURES  
source

\* 106193 110995: contig of 4803 bp in length  
\* 110996 111095: gap of 100 bp  
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\* 114863 114962: gap of 100 bp  
\* 114963 118827: contig of 3665 bp in length  
\* 118828 118927: gap of 100 bp  
\* 118928 124084: contig of 5157 bp in length  
\* 124085 124184: gap of 100 bp  
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 Best Local Similarity 97.8%; Pred. No. 2.3e-176;  
 Matches 835; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 3257 TACTACACAAAGCTATTTTAAAGAAAGATGATGTTGGAGAGAGGCCAGTTGACTAT 3316
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DB 40503 TACTACACAAAGCTATTTTAAAGAAAGATGATGTTGGAGAGAGGCCAGTTGACTAT 40562
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QY 3317 ATGACATATCAAT 3330
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DB 40563 ATGACATATCAAT 40576
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RESULT 10
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DEFINITION Homo sapiens Interphotoreceptor matrix gene (IPM150), exon 17 and
complete cds.
ACCESSION AF017776.1 GI:3800731
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1235)
Felbor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
Genomic organization and chromosomal localization of the
Interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
9691169
2 (bases 1 to 1235)
Gehrig,A., Felbor,U., Kelseil,R., Hunt,D.M., Maumenee-Huselle,I.E.
and Weber,B.H.F.
Assessment of a novel Interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bifocal choroidoretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCRI)
Unpublished
3 (bases 1 to 1235)
Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
Direct Submission
Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
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AF017768.1:1..294,AF017769.1:1..444,AF017770.1:1..347,
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AF017768.1:153..173,AF017769.1:97..339,
AF017770.1:148..224,AF017771.1:271..349,
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## ORIGIN

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 2537 TGACCGTGAATATGAGAAATTTAAACATCAAGATTGGAGAGAAATTTAAACTGAAA 2596  
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 501 TGTACATATTCATAGGCTATCTCAAGAGAGATGATTTGCTTCTCAAGAGAAATGGA 560  
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 2657 GACAGGCAATTCATAGGCTATCAAAATTCAGACATACGTAACATGAGAAATCAGCAC 2716  
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 801 CTCACAGATCATTTGCAACAGCATAGCTTACTTATGTTTGAAGGCTGAAACAATTTAT 860  
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 Homnidae; Homo.  
 1 (bases 1 to 816)  
 Felbor,U.; Gehrig,A.; Sauer,C.G.; Marquardt,A.; Kohler,M.;  
 Schmid,M. and Weber,B.H.  
 Genomic organization and chromosomal localization of the  
 interphotoreceptor matrix proteoglycan-1 (IMPg1) gene: a candidate  
 for 6q-linked retinopathies  
 Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
 9691169  
 2 (bases 1 to 816)  
 Gehrig,A.; Felbor,U.; Kessel,R.; Hunt,D.M.; Maunee-Huesels,I.B.  
 and Weber,B.H.F.  
 Assessment of a novel interphotoreceptor matrix gene (IPM150)  
 localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
 macular dystrophy, progressive bilateral choroidretinal atrophy  
 (PBCRA), and North Carolina macular dystrophy (MCDRI)  
 Unpublished  
 3 (bases 1 to 816)  
 Felbor,U.; Kuehn,M.; Hegeman,G.S. and Weber,B.H.F.  
 Direct Submision  
 Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am  
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ORIGIN  
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 Qy 1541 TCTTTATGGCATCAAGCATCTTCTCTGACGTATTAAGGCAACACAGATTAAGTGGCA 1600  
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 Qy 1601 CTGACAGACAAATGCTAGTACCAAGGGCTGACATCCCGACGATGATTAATTCGCAATTA 1660  
 Db 261 CTGACAGACAAATGCTAGTACCAAGGGCTGACATCCCGACGATGATTAATTCGCAATTA 320  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1  
 Wall, M.  
 Direct Submission  
 Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 Requester: clonerequest@sanger.ac.uk  
 On Sep 12, 2001 this sequence version replaced gi:11991356.  
 ----- Genome Center  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: duf62L18  
 ----- Summary Statistics  
 Sequencing program: XGAP4; version 4.5  
 Sequencing vector: pLacmid; 108752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 160382 bases at least Q40  
 Consensus quality: 160493 bases at least Q30  
 Consensus quality: 160578 bases at least Q20  
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 Insert size: 158939; 9.3% error; agarose-fp  
 Quality coverage: 8.32x in Q20 bases; sum-of-contigs Quality  
 coverage: 8.41x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 Location/Qualifiers

## FEATURES

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## misc\_feature

## ORIGIN

Query Match 16.1%; Score 535.8; DB 14; Length 160719;  
 Best Local Similarity 99.6%; Pred. No. 6.4e-111;  
 Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 7704 TCTTTATGGCATCAAGCATCTTCTCTGACGTATTAAGGCAACACAGATTAAGTGGCA 7645  
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 Db 7524 CAGGTGGCGAAGATATGCTCAACACCTTGAATGAATGATGCTGTGACACTCTGCCC 7465  
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 Db 7404 CCACCTCTGCTCAGCTTACAGTATATGACCACTAGTCTTATGACCATTTGCCCAAG 7345  
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 Db 7344 GCCGAGAGCTGTAGTCTTCTTCACTGCTGCTGTTGCTTAACTAGGCTTCTCCAGAC 7285  
 Qy 1961 TGTTCACAGAGCTCTCTGAGTACCGAGCTCTGAGAGCAATTCACACAGCTGTG 2019  
 Db 7284 TGTTCACAGAGCTCTCTGAGTACCGAGCTCTGAGAGCAATTCACACAGCTGTG 7226

## RESULT 13

AB070714 4953 bp mRNA linear VRT 10-JUL-2002  
 LOCUS AB070714  
 DEFINITION Gallus gallus mRNA for SPACR, complete cds.  
 ACCESSION AB070714  
 VERSION AB070714.1 GI:21623676

KEYWORDS  
 SOURCE  
 ORGANISM

Gallus gallus (chicken)  
 Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
AUTHORS  
REFERENCE  
TITLE  
JOURNAL  
FEATURES  
source  
1  
Zako,M., Iwaki,M., Yoneda,M., Miyaiishi,O., Zhao,J., Suzuki,Y.,  
Takeuchi,M., Miyake,G., Ikagawa,H. and Kimata,K.  
Molecular Cloning and Characterization of Chick Sialoprotein  
Associated with Cones and Rods, a Developmentally Regulated  
Glycoprotein of Interphotoreceptor Matrix  
J. Biol. Chem. 277 (28), 25592-25600 (2002)  
1191949  
2 (bases 1 to 4953)  
Zako,M. and Iwaki,M.  
Direct Submission  
Submitted (28-Aug-2001) Masehiro Zako, Aichi Medical University,  
Department of Ophthalmology, Nagakute-cho, Aichi-gun, Aichi  
480-1195, Japan (E-mail:zako@aiichi-med-u.ac.jp.  
Tel:81-52-264-4811(ex.2181), Fax:81-561-63-7255)  
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Matches 875; Conservative 0; Mismatches 488; Indels 71; Gaps 3;

QY 279 AAATGTCAAAAATGTCAACTATGAGAGATATTGATTTGGCAAGCATGAAACAAA 338  
DB 374 AGAGGTCCAGAGTGCACCTAATAGAGAGATATTGACATGACCAACACGACAAAGA 433  
QY 339 GATCCGACATTTTCCCAACGGGAGGTAAAGTCTGTCCACAGAAATCCATGAACAGATT 398  
DB 434 GATCACCTTTTCTTCTATCTGTGTGAAAATTTGGCCCAAGAAATCACTGAAGCAGATT 493  
QY 399 TAGACATCTTCAAGCTTATTATATGATTGAGAGTGTCCAGAAACAGTATGGAAAGAT 458  
DB 494 TAGCCAGTCAACCAAGCTTACTATGATTAAAGCTGACAGAAAGCTGTGTGGAAAGCT 553  
QY 459 ATCCGATCTTCTGATGTCATCCCTGACACAGGAGAAATATCAGGACTGGGTACGATCT 518  
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QY 519 GCCACAGAGACCTTCTGCTCTTGTGACATTTGAAAAAACTTCAGCAATTCACAGAGC 578  
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DB 786 -----TACAGGTCC 794  
QY 759 TGCACAGTCTCATTGGGCTTTCCCTCTCACTCTGATGACACCTCTCTCAATGAAT 818  
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QY 879 TGTGTGGAGAGCAGAGGATGAGCTCAGGCTCTCTGTGTAAACCAAGATTCAGAGC 938  
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DB 969 TGAACCTTAGTATCCAACTCCCAAGTATCGAATTAAGCTGCAAAATTCACATGCA 1028  
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DB 1089 ACAGAAAGAGGAAAGATGGGTCAAGCAGACCTATAGACGATCATGTGTAACCTTGA 1148  
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RESULT 14  
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 DEFINITION  
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 KEYWORDS  
 SOURCE  
 ORGANISM  
 Macaca fascicularis (craab-eating macaque)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Cercopithecoidea; Cercopithecinae; Macaca.  
 1 (bases 1 to 555)  
 Kuehn,M.H. and Hageman,G.S.  
 Characterization And Complete cDNA Sequence Of IPM 150, A Novel  
 Human Photoreceptor Cell-Associated Chondroitin-Sulfate  
 Proteoglycan  
 Unpublished  
 2 (bases 1 to 555)  
 Kuehn,M.H. and Hageman,G.S.  
 Direct Submission  
 Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,  
 University of Iowa, 200 Hawkins Drive, 1190E PPP, Iowa City, IA  
 52240, USA

FEATURES  
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ORIGIN  
 Query Match 13.2%; Score 439; DB 8; Length 555;  
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 Matches 526; Conservative 0; Mismatches 25; Indels 62; Gaps 1;

DB 244 CTTCCTCCAGCAGAAATTAACAGAAATTTCCCTGAGAGAAATGATATCTACA 303  
 QY 647 GAGAAACATTTGGAGAGAGCTGTGTGAAACATTTGTCATTTCAACAGCAATCTACATTTCA 706  
 DB 304 GAGAAACATTTGGAGAGAGCTGTGTGAAACATTTGTCATTTCAACAGCAATCTACATTTCA 347  
 QY 707 AAGACTTGGGCGATTTCTTAAGAAAAACCTCAAGAAAGCAATTTCAAGTCTTCCCAAGC 766  
 DB 348 -----AGATGTTCGACAGC 361  
 QY 767 TCTCACTTGGGCTTTCCCTCTCACTCTCGATGACACCCCTCTCAATGAATTTCTGATA 826  
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 1 (bases 1 to 259413)  
 Murny,D.Marie, Metzker,M.Lee, Abramson,S., Adams,C., Alder,J.,  
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 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
 Weinstein, G. and Gibbs, R.A.  
 Unpublished  
 Direct Submission  
 2 (bases 1 to 259413)  
 Morley, K.C.  
 Direct Submission  
 Submitted (17-MAY-2005) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 259413)  
 Cow Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (01-JUN-2005) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jun 29, 2005 this sequence version replaced gi:65811890.  
 The sequence in this assembly is a combination of BAC-based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Project name: PCOV  
 Center clone name: CH240-104J3  
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 Assembly program: Atlas 3.0  
 Consensus quality: 237131 bases at least Q40  
 Consensus quality: 240855 bases at least Q30  
 Consensus quality: 244386 bases at least Q20  
 Estimated insert size: 249035; sum-of-contigs estimation  
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 47 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
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 \* 15572 15621: gap of 50 bp  
 \* 15622 28748: contig of 13127 bp in length  
 \* 28749 28798: gap of 50 bp  
 \* 28799 38157: contig of 9358 bp in length  
 \* 38157 38207: gap of 50 bp  
 \* 38207 45141: contig of 6334 bp in length  
 \* 45141 45817: gap of 676 bp  
 \* 45817 56270: contig of 10453 bp in length  
 \* 56270 56671: gap of 401 bp  
 \* 56671 65734: contig of 9063 bp in length  
 \* 65734 65783: gap of 50 bp  
 \* 65783 67664: contig of 1880 bp in length  
 \* 67664 70264: gap of unknown length  
 \* 70264 70314: contig of 2501 bp in length  
 \* 70314 70315: gap of 50 bp  
 \* 70315 75340: contig of 5026 bp in length  
 \* 75340 75391: gap of 50 bp  
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 \* 77341 77392: gap of 50 bp  
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 \* 88986 89946: gap of 50 bp  
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\* 235504 236821: contig of 1318 bp in length  
\* 236822 236922: gap of unknown length  
\* 236922 238542: contig of 1621 bp in length  
\* 238543 238642: gap of unknown length

Query Match 9.5%; Score 317.8; DB 14; Length 259413;  
Best Local Similarity 76.4%; Pred. No. 2.4e-61;  
Matches 404; Conservative 0; Mismatches 122; Indels 3; Gaps 1;

QY 1491 TTGGTCTCCACCTGTATGAGCCTTACCTCCCTGTCAGAGCTCCACCTTTCTTTATGCG 1550  
DB 205793 TTGGTCTCCACCTGTATGAGCCTTACCTCCCTGTCAGAGCTCCACCTTTCTTTATGCG 205734  
QY 1551 ATCAAGCATCTTCTCTCTGATGATGAGGACACAGATACATGCGCATGACCGAC 1610  
DB 205733 ATCAAGCGCTTCTCTCTGATGATGAGGACACAGATACATGCGCATGACCGAC 205674  
QY 1611 AATGCTAGTACAGGAGCTCACCATCCCACTGATTAATTTGCAATCAGCCAACTGGC 1670  
DB 205673 AATGCTAGTACAGGAGCTCACCATCCCACTGATTAATTTGCAATCAGCCAACTGGC 205614  
QY 1671 TCTGGAAATTTTCAATCCACCTGATCTTCAGATGACAGCCGATCAAGTGACAGTGGCA 1730  
DB 205613 TCTGGAAATTTTCAATCCACCTGATCTTCAGATGACAGCCGATCAAGTGACAGTGGCA 205557  
QY 1731 AGATATGGTCAGACACTGATGAAATGATGATCTGTGACACTCTGCCCCATCTGAGGT 1790  
DB 205556 AGATATGGTCAGACACTGATGAAATGATGATCTGTGACACTCTGCCCCATCTGAGGT 205497  
QY 1791 ACCAGAGCTCAGGAGATATGTTTCTGTCCAGATCATTTCTTGAGGATACCACTCCCTGT 1850  
DB 205496 ACCAGAGCTCAGGAGATATGTTTCTGTCCAGATCATTTCTTGAGGATACCACTCCCTGT 205437  
QY 1851 CTCAGCTTTACAGTATATCACCAGCTAGTCTATGACATTTGCCCAAGGCGGAGAGCT 1910  
DB 205436 CTCAGCTTTACAGTATATCACCAGCTAGTCTATGACATTTGCCCAAGGCGGAGAGCT 205377  
QY 1911 GGTAGTGTCTTCAAGTCTGCGGTGCTAAACATGCGCTTCTCCAAAGACCTGTTCAACA 1970  
DB 205376 GGTAGTGTCTTCAAGTCTGCGGTGCTAAACATGCGCTTCTCCAAAGACCTGTTCAACA 205317  
QY 1971 GAGCTCTCTGAGAGTACCGAGCTCTGAGAGACAAATTCAACAGCTGCTG 2019  
DB 205316 GAGCTCTCTGAGAGTACCGAGCTCTGAGAGACAAATTCAACAGCTGCTG 205268

Search completed: January 14, 2006, 13:18:42  
Job time : 16589 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2006, 16:49:15 ; Search time 532 Seconds  
(without alignments)  
5066.034 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taacacgaagaggtatctc.....tactatgatcatcatcat 3330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- Published Applications NA New:\*
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  - 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
  - 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
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  - 7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
  - 8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
  - 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*
  - 10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119.4	3.6	1219	US-10-750-185-30474	Sequence 30474, A
2	119.4	3.6	1219	US-10-750-623-30474	Sequence 30474, A
3	84.8	2.5	554	US-10-750-185-30481	Sequence 30481, A
4	84.8	2.5	554	US-10-750-623-30481	Sequence 30481, A
5	46.6	1.4	1288	US-10-750-185-46240	Sequence 46240, A
6	46.6	1.4	1288	US-10-750-623-46240	Sequence 46240, A
7	44.8	1.3	8607	US-10-240-708-63	Sequence 63, Appl
8	43.2	1.3	8607	US-10-240-708-72	Sequence 72, Appl
9	42.8	1.3	105550	US-10-995-561-13235	Sequence 13235, A
10	41.6	1.2	1902	US-10-750-185-29751	Sequence 29751, A
11	41.6	1.2	1902	US-10-750-623-29751	Sequence 29751, A
12	41.6	1.2	7304	US-10-240-708-43	Sequence 43, Appl
13	41.2	1.2	10467	US-10-240-708-2	Sequence 2, Appl
14	41.2	1.2	53641	US-10-995-561-13238	Sequence 13238, A
15	41.2	1.2	1125000	US-10-995-561-13286	Sequence 13286, A
16	40.6	1.2	316	US-11-000-688-348	Sequence 348, App
17	40.6	1.2	1045	US-10-750-185-49935	Sequence 49935, A
18	40.6	1.2	1045	US-10-750-623-49935	Sequence 49935, A
19	40	1.2	6306	US-10-240-708-50	Sequence 50, Appl
20	39.6	1.2	600	US-11-136-527-4832	Sequence 4832, Ap
21	39.6	1.2	2475	US-11-136-527-736	Sequence 736, App
22	39.6	1.2	6113	US-10-240-708-14	Sequence 14, Appl
23	39.6	1.2	19513	US-10-240-708-39	Sequence 39, Appl

C 24	39.6	1.2	645179	6	US-10-995-561-13293	Sequence 13293, A
C 25	39.2	1.2	135019	6	US-10-849-438-11	Sequence 11, Appl
C 26	39	1.2	2419	6	US-10-750-185-49215	Sequence 49215, A
C 27	39	1.2	2419	6	US-10-750-623-49215	Sequence 49215, A
C 28	39	1.2	100000	7	US-11-124-368A-2883	Sequence 2883, Ap
C 29	39	1.2	148935	6	US-10-995-561-13308	Sequence 13308, A
C 30	39	1.2	285300	6	US-10-857-780-6	Sequence 6, Appl
C 31	38.8	1.2	5152	6	US-10-240-708-74	Sequence 74, Appl
C 32	38.8	1.2	8537	6	US-10-240-708-41	Sequence 41, Appl
C 33	38.6	1.2	5360	6	US-10-240-708-65	Sequence 65, Appl
C 34	38.4	1.2	134499	7	US-11-117-187-192	Sequence 192, App
C 35	38.2	1.1	57073	6	US-10-995-561-13275	Sequence 13275, A
C 36	37.8	1.1	1240	6	US-10-750-185-60335	Sequence 60335, A
C 37	37.8	1.1	1240	6	US-10-750-623-60335	Sequence 60335, A
C 38	37.8	1.1	1483	6	US-10-750-185-39052	Sequence 39052, A
C 39	37.8	1.1	1483	6	US-10-750-623-39052	Sequence 39052, A
C 40	37.8	1.1	4128	6	US-10-995-561-253	Sequence 253, App
C 41	37.8	1.1	95832	6	US-10-995-561-13273	Sequence 13273, A
C 42	37.6	1.1	600	6	US-10-750-185-809	Sequence 809, App
C 43	37.6	1.1	600	6	US-10-750-623-809	Sequence 809, App
C 44	37.6	1.1	1741	6	US-10-750-185-26423	Sequence 26423, A
C 45	37.6	1.1	1741	6	US-10-750-623-26423	Sequence 26423, A

## ALIGNMENTS

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RESULT 1
US-10-750-185-30474
; Sequence 30474, Application US/10750185
; Publication No. US20050260603M1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30474
; LENGTH: 1219
; TYPE: DNA
; ORGANISM: Bovine 19868880607526
US-10-750-185-30474

Query Match      3.6%  Score 119.4; DB 6; Length 1219;
Best Local Similarity 89.0%; Pred.No. 5.2e-23;
Matches 129; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 430 AGTGTGAGAGAGAGATGGAAGCATTCGATCTTTGATCGATCCCTGACAC 489
    |||
DB 1075 AGTGTGAGAGAGAGAGATGGAAGCATTCGATCTTTGATCGATCCCTGACAC 1134
    |||

OY 490 AGGGAATATATGAGACTGGTTCAGCATTCGACAGAGAGACCTTTCCTTTGACAT 549
    |||
DB 1135 GGGGGAATATATGAGACTGGTTCAGCATTCGACAGAGAGACCTTTCCTTTGACAT 1194
    |||

OY 550 TGGAAAAAATTCGACATTCGACAG 574
    |||
DB 1195 CGGGAATATTCGACATTCGACAG 1219
    |||

RESULT 2
US-10-750-623-30474
; Sequence 30474, Application US/10750623

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/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30474
/ LENGTH: 1219
/ TYPE: DNA
/ ORGANISM: Bovine 19866880607526
US-10-750-623-30474

Query Match      3.6%; Score 119.4; DB 6; Length 1219;
Best Local Similarity 89.0%; Pred. No. 5.2e-23;
Matches 129; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 430 AGTGTGTCAAGAGACGATGTGGAAAGCATATTCGATTCGATCCGATCCGACAC 489
DB 1075 AGTGTGCCGAGAGCGGTGTGGAAAGCCCTACCGAGATCTTTCGATTCGCTCCCGACCC 1134

QY 490 AGGGAATATCAGAGCTGGGTGACGATCTGCAGAGAGAGACCTTCTGCTCTTGGACAT 549
DB 1135 GGGGGAATACAGAGCTGGGTGACGATCTGCAGAGAGAGACCTTCTGCTCTTGGACAT 1194

QY 550 TGGAAAAAATTCAGCAATTCGACG 574
DB 1195 CGGAAAAAATTCAGCAATTCGACG 1219

RESULT 3
US-10-750-185-30481/c
/ Sequence 30481, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30481
/ LENGTH: 554
/ TYPE: DNA
/ ORGANISM: Bovine 19866881169584
US-10-750-185-30481

Query Match      2.5%; Score 84.8; DB 6; Length 554;
Best Local Similarity 81.7%; Pred. No. 1.6e-13;
Matches 98; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 888 GGAGCAGAGGTTGAGCTCAGCGTCTCTGTGTAACGAAAGTTCAAGCAGAGCTGCG 947
DB 369 GGAGCAGAAAGTAGAGCTAAGTATCTCTGCGCAAACTCAAGTCAAGTCAAGCTGGA 310
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QY 948 TGACTCCAGTCCCGCATATTACAGAGAGCTAGCAGAAAGTCCCAACTTCAGATGCAAAA 1007
DB 309 TAATCCCGATCCCGCATATTACAGAGAGTGCAGAGCCCAAGTCTCAAGTTCAGGTGAGCAA 250

RESULT 4
US-10-750-623-30481/c
/ Sequence 30481, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30481
/ LENGTH: 554
/ TYPE: DNA
/ ORGANISM: Bovine 19866881169584
US-10-750-623-30481

Query Match      2.5%; Score 84.8; DB 6; Length 554;
Best Local Similarity 81.7%; Pred. No. 1.6e-13;
Matches 98; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 888 GGAGCAGAGGTTGAGCTCAGCGTCTCTGTGTAACGAAAGTTCAAGCAGAGCTGCG 947
DB 369 GGAGCAGAAAGTAGAGCTAAGTATCTCTGCGCAAACTCAAGTCAAGTCAAGCTGGA 310

QY 948 TGACTCCAGTCCCGCATATTACAGAGAGCTAGCAGAAAGTCCCAACTTCAGATGCAAAA 1007
DB 309 TAATCCCGATCCCGCATATTACAGAGAGTGCAGAGCCCAAGTCTCAAGTTCAGGTGAGCAA 250

RESULT 5
US-10-750-185-46240/c
/ Sequence 46240, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 46240
/ LENGTH: 1288
/ TYPE: DNA
/ ORGANISM: Bovine 19866881819734
US-10-750-185-46240

Query Match      1.4%; Score 46.6; DB 6; Length 1288;
Best Local Similarity 59.4%; Pred. No. 0.016;
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;; PRIOR APPLICATION NUMBER: DE 10032529.7  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: DE 10043826.1  
;; PRIOR FILING DATE: 2000-09-01  
;; NUMBER OF SEQ ID NOS: 98  
;; SEQ ID NO 72  
;; LENGTH: 8607  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-240-708-72

Query Match 1.3%; Score 43.2; DB 6; Length 8607;  
Best Local Similarity 50.4%; Pred. No. 0.54;  
Matches 131; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

QY 2454 AATCATGATTCACAACTGATGTTAAAGTTCCAAATCAACAATTAACAGATAT 2513  
DB 7055 AA 6996  
QY 2514 CAGTAAAGAAATTCGATTAACGCTAGATTAATGAAGATTAAACCATCAAGATTG 2573  
DB 6995 AAAAAAAAAAAAAAAAAAAAAAAAAACCATATCAAAATTAACATTAACATTAACATTA 6936  
QY 2574 GGAAGAAATTTAAATCGAAATGTACATTA-TCAGTTAGGCTATCTCAAGAGATG 2632  
DB 6935 CAATTTCTCTCACTATATAATCCATTAATCTCTTACCAATCTTATTAATAAATA 6876  
QY 2633 ATTGCTCTTCAAGAAATGAGACAGCATATTCAGGTCAATCAAAATCCAGACAT 2692  
DB 6875 TTTTAACTAAACCGATTAATCACATCTATATCCACACCTTAAAAAATCTAAAT 6816  
QY 2693 ACAGTCAACATCGAATCA 2712  
DB 6815 AACAAGATCACTTAATCA 6796

RESULT 9  
US-10-995-561-13235  
;; Sequence 13235, Application US/10995561  
;; Publication No. US20050272054A1  
;; GENERAL INFORMATION:  
;; APPLICANT: CARGILL, Michele et al.  
;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
;; TITLE OF INVENTION: DETECTION AND USES THEREOF  
;; FILE REFERENCE: CL001559  
;; CURRENT APPLICATION NUMBER: US/10/995,561  
;; CURRENT FILING DATE: 2004-11-24  
;; NUMBER OF SEQ ID NOS: 85702  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 13235  
;; LENGTH: 105550  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-995-561-13235

Query Match 1.3%; Score 42.8; DB 6; Length 105550;  
Best Local Similarity 45.1%; Pred. No. 4;  
Matches 155; Conservative 1; Mismatches 188; Indels 0; Gaps 0;

QY 14 TTATCTCATCATCTGATCATATATATATTTTTCACATTTCTGTACTTTTAA 73  
DB 48951 WTATATTTAAAT 49010  
QY 74 TGAGATTTGAGGTGTTCTGTGATTTGTTATCAAGATTACCAATGACAAAGCCAGATG 133  
DB 49011 AT 49070  
QY 134 TATTGGAACTGGAAGACATATTTTGTGTTTGTGATTTTCTCCAAAGTCAAGAAC 193  
DB 49071 TAT 49130

QY 194 AAGATATCTCCATTAAATATACATTCGAAACTTAAGACATAGACATCCCAAGA 253  
DB 49131 AATTTATATTTAT 49190  
QY 254 AATGAACCACTGAAAGTACTGAAAAATGTCAAAATGTCAACTATGAGCAATATTC 313  
DB 49191 AAAATCAAGATATACAGATATATATATATATATATATATATATATATATATAT 49250  
QY 314 GATTGGAAAGCATCGAAGAAAGATCCGATTTTCCCAAC 357  
DB 49251 TATATATGATGATAAATATATATATATATATATATATATATATATATATAT 49294

RESULT 10  
US-10-750-185-29751  
;; Sequence 29751, Application US/10750185  
;; Publication No. US20050260603A1  
;; GENERAL INFORMATION:  
;; APPLICANT: MMI GENOMICS, INC.  
;; APPLICANT: DENIS, Sue K.  
;; APPLICANT: KERR, Richard  
;; APPLICANT: ROSENFELD, David  
;; APPLICANT: HOLM, Tom  
;; APPLICANT: BATES, Stephen  
;; APPLICANT: FANTIN, Dennis  
;; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
;; FILE REFERENCE: MM1100-2  
;; CURRENT APPLICATION NUMBER: US/10/750,185  
;; CURRENT FILING DATE: 2003-12-31  
;; PRIOR APPLICATION NUMBER: US 60/437,482  
;; PRIOR FILING DATE: 2002-12-31  
;; NUMBER OF SEQ ID NOS: 64922  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 29751  
;; LENGTH: 1902  
;; TYPE: DNA  
;; ORGANISM: Bovine  
US-10-750-185-29751

Query Match 1.2%; Score 41.6; DB 6; Length 1902;  
Best Local Similarity 49.5%; Pred. No. 0.54;  
Matches 107; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 2517 TAAAGAAATCTGATTAACGCGTAGAATATGAAGATTAACATCAAGATGGGA 2576  
DB 459 TAAAGAAATCTGATTAACGCGTAGAATATGAAGATTAACATCAAGATGGGA 518  
QY 2577 AGGAATTTAAATCTGAAATGTACATTAATCACTTAGGCTATCTCAAGAGATGATTT 2636  
DB 519 ATGTCATCATCAAGAGAAATGTAAAGTTTCTGTTTGTGTTTCAACACAAACATTT 578  
QY 2637 GCCTTCTCAAGAAATGGAAGACAGCATATTCATGAGTCAATCAAAATCCAGACTACG 2696  
DB 579 GAAATTTCAAGAAATGAGGTAGGCTTCTTACTTAAAGCTCAAGAAAGTCTAGACAT 638  
QY 2697 TCAACACTGAGATCAGACACACCATATTTCAAT 2732  
DB 639 CTGGTCTGGGCAATTCGTGAGGTTCAATGTTCAAT 674

RESULT 11  
US-10-750-623-29751  
;; Sequence 29751, Application US/10750623  
;; Publication No. US20050287531A1  
;; GENERAL INFORMATION:  
;; APPLICANT: MMI GENOMICS, INC.  
;; APPLICANT: DENIS, Sue K.  
;; APPLICANT: KERR, Richard  
;; APPLICANT: ROSENFELD, David  
;; APPLICANT: HOLM, Tom  
;; APPLICANT: BATES, Stephen  
;; APPLICANT: FANTIN, Dennis

QY	2447	ACTGTGAAATCAAGCATACAAA	CTGTGTTAAAAAGTCCAAATCA	CAAAATACA	2504
Db	8453	ACTATATAATTTAAAAATAAAAA	AAAAATCAATTCAAAAA	AAAAATTA	8194
QY	2507	AGGAATCAGTAAAGAAATTC	ATAATCGACCGTAGAT	TAGAGAAATTAACAT	2566
Db	8193	AAAAAACACGTAAAAA	AAAAATTAATAAACA	AAATATATATATCCAA	8134
QY	2567	AAAGTTGGAAGAAATTA	AAAACTGAAATGTCAATTA	CACTTAGGCTATCTCA	2628

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Db      8133 TATTGATTAATCGAATTAATAA-TTATTAAGTCCAAACAAAAAATTAATCAAC 8075
Qy      2627 GAGATGATTTGCTTCTCAAGAAATGAGACAGGCATATTCATGGTCATCAAAATCC 2686
Db      8074 CAAATATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8015
Qy      2687 AGACATACAGTCACAGTCAGAGTACAGACACACCATATTTTCAAAATATAGAGAGTCATG 2746
Db      8014 TAAAAAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7955
Qy      2747 TACTGGGACACACGATTAATTTGAAAAAAGACACTTATTTATTAATTAATTAATTAAT 2806
Db      7954 ATAAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 7895
Qy      2807 GCATACAGGAAACATATTTTACTATCTTGATGATAGTCAAAATGAT 2856
Db      7894 TTCTCCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 7845

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## RESULT 14

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US-10-995-561-13238
; Sequence 13238, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13238
; LENGTH: 53641
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13238

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Query Match 1.2%; Score 41.2; DB 6; Length 53641;

Best Local Similarity 48.0%; Pred. No. 7; Matches 118; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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Qy      2581 AATTAAAACTGAAAAATGACATTTATCTAGGCTATCTCAAGAGATGATTTGCT 2640
Db      14714 AAGCAACAAAGCAAACTAGCAAGTAGGTTACGTAAATTAATTAATTAATTAATTA 14773
Qy      2641 TCTCAAGAAAATGAGACAGGCATATTCATGGTCATCAAAATCCAGATACAGTCA 2700
Db      14774 TAAAGAAAACAATCAAGACATGAAGGCAAGCTCAAAATATGTAATTAATTAATTA 14833
Qy      2701 CACTGGAATCAGACACACCATATTTCAAAATATAGAGATGATCTTGGCAACG 2760
Db      14834 ACCTCATTAAGTATGTTGTTATTCCAAAATATATATAGAACTCTTAATTAATTAATTA 14893
Qy      2761 TAAATTTGAAAAAAGACACTTATTTATTAATTAATTAATTAATTAATTAATTAATTA 2820
Db      14894 AAAAAAAAAAAAAAAAAAAGCAAGATTTTAAATTAATTAATTAATTAATTAATTAATTA 14953
Qy      2821 ATATTT 2826
Db      14954 AATTCT 14959

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## RESULT 15

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US-10-995-561-13286/c
; Sequence 13286, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13286
; LENGTH: 1125000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)..(1125000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13286

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Query Match 1.2%; Score 41.2; DB 6; Length 1125000;

Best Local Similarity 48.0%; Pred. No. 55; Matches 118; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

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Qy      2581 AATTAAAACTGAAAAATGACATTTATCTAGGCTATCTCAAGAGATGATTTGCT 2640
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Qy      2641 TCTCAAGAAAATGAGACAGGCATATTCATGGTCATCAAAATCCAGATACAGTCA 2700
Db      66177 TAAAGAAAACAATCAAGACATGAAGGCAAGCTCAAAATATGTAATTAATTAATTA 66118
Qy      2701 CACTGGAATCAGACACACCATATTTCAAAATATAGAGATGATCTTGGCAACG 2760
Db      66117 ACCTCATTAAGTATGTTGTTATTCCAAAATATATATAGAACTCTTAATTAATTAATTA 66058
Qy      2761 TAAATTTGAAAAAAGACACTTATTTATTAATTAATTAATTAATTAATTAATTAATTA 2820
Db      66057 AAAAAAAAAAAAAAAAAAAGCAAGATTTTAAATTAATTAATTAATTAATTAATTAATTA 65998
Qy      2821 ATATTT 2826
Db      65997 AATTCT 65992

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Search completed: January 14, 2006, 22:47:11  
Job time : 538 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	3330	100.0	3330	5	US-10-007-270-1	Sequence 1, Appl1
2	3124.6	93.8	3261	5	US-10-007-270-27	Sequence 27, Appl1
3	2765.8	83.1	2887	5	US-10-007-270-3	Sequence 3, Appl1
4	2184.2	65.6	2244	5	US-10-007-270-5	Sequence 5, Appl1
5	1375.6	41.3	3668	5	US-10-007-270-8	Sequence 8, Appl1
6	534	16.0	1726	5	US-10-007-270-10	Sequence 10, Appl1
7	491.6	14.8	1321	5	US-10-007-270-12	Sequence 12, Appl1
8	439	13.2	555	5	US-10-007-270-14	Sequence 14, Appl1
9	204.6	6.1	536	5	US-10-027-632-186848	Sequence 186848, Appl1
10	204.6	6.1	1858	5	US-10-007-270-7	Sequence 7, Appl1
11	204.6	6.1	4165	8	US-10-783-528-9	Sequence 9, Appl1
12	203.4	6.1	4165	5	US-10-007-270-15	Sequence 15, Appl1
13	203.4	6.1	4165	5	US-10-007-270-23	Sequence 23, Appl1
14	197.8	5.9	4204	5	US-10-007-270-23	Sequence 23, Appl1
15	184.8	5.5	2964	5	US-10-007-270-18	Sequence 18, Appl1
16	103.4	3.1	592	9	US-10-972-079-61156	Sequence 61156, Appl1
17	103.4	3.1	599	9	US-10-972-079-61152	Sequence 61152, Appl1
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19	103.4	3.1	600	9	US-10-972-079-61154	Sequence 61154, Appl1
20	103.4	3.1	600	9	US-10-972-079-61155	Sequence 61155, Appl1
21	79	2.4	428	4	US-09-925-065A-223807	Sequence 223807, Appl1
22	69	1.9	458	4	US-09-925-065A-462444	Sequence 462444, Appl1
23	62.4	1.1	438	9	US-10-972-079-61157	Sequence 61157, Appl1

C	24	61	1.8	113515	6	US-10-311-455-2147	Sequence 2147, Ap
C	25	60	1.8	60	3	US-09-908-975-1639	Sequence 1639, A
C	26	56.4	1.7	4634	8	US-10-357-930-5850	Sequence 5850, A
C	27	54.6	1.6	3683	8	US-10-473-126-339	Sequence 339, App
C	28	53.2	1.6	6255	6	US-10-311-455-833	Sequence 833, App
C	29	52.6	1.6	5178	5	US-09-960-352-5785	Sequence 5785, A
C	30	52.6	1.6	673	7	US-10-424-599-57885	Sequence 57885, A
C	31	52.6	1.6	6575	7	US-10-433-793-189	Sequence 189, App
C	32	52.2	1.6	5596	7	US-10-237-166-86	Sequence 86, App
C	33	52.2	1.6	11155	6	US-10-311-455-577	Sequence 577, App
C	34	52.2	1.6	15674	6	US-10-311-455-335	Sequence 335, App
C	35	52.2	1.6	15674	6	US-10-240-485-29	Sequence 29, App1
C	36	52.2	1.6	3673778	6	US-10-312-841-2	Sequence 2, App1
C	37	52	1.6	4654	6	US-10-311-455-1196	Sequence 2196, App
C	38	52	1.6	4654	7	US-10-221-714A-508	Sequence 508, App
C	39	51.8	1.6	1243	6	US-10-425-115-17217	Sequence 11271, A
C	40	51.6	1.5	5328	6	US-10-311-455-533	Sequence 533, App
C	41	50.6	1.5	2308	8	US-10-602-494-264	Sequence 264, App
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C	43	50.4	1.5	15387	6	US-10-311-455-157	Sequence 157, App
C	44	50.2	1.5	424	6	US-10-108-846-2925	Sequence 2257, App
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QY 241 CAATCCCCAGAAATGAAACAACTGAAAGTACTGAAAAATGTACAAATGTCAACTAT 300  
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QY 301 GAGACGAATATTGCAATTGGCAAAAGCATTGAAACAAAAGATCCGATTTTCCCAACGGG 360  
DB 301 GAGACGAATATTGCAATTGGCAAAAGCATTGAAACAAAAGATCCGATTTTCCCAACGGG 360  
QY 361 GGTTAAAGCTGTGTCACAGGAATGCAATGAAACAGATTTTGAACAGCTTCAAGCTTATTA 420  
DB 361 GGTTAAAGCTGTGTCACAGGAATGCAATGAAACAGATTTTGAACAGCTTCAAGCTTATTA 420  
QY 421 TAGATTGAGAGTGTGTCAAGAAAGCATATGAGAAAGCATTCGGATCTTCTGGAATCGCAT 480  
DB 421 TAGATTGAGAGTGTGTCAAGAAAGCATATGAGAAAGCATTCGGATCTTCTGGAATCGCAT 480  
QY 481 CCTTGAACACAGGGGAATATCAGAGCTGGGTCAAGCATCTGCCAGACAGAGACCTTCTGCTT 540  
DB 481 CCTTGAACACAGGGGAATATCAGAGCTGGGTCAAGCATCTGCCAGACAGAGACCTTCTGCTT 540  
QY 541 CTTTGCATTTGAAAAAACTTGACGAATCCGAGAGACCTGGATCTTCTGACAGAG 600  
DB 541 CTTTGCATTTGAAAAAACTTGACGAATCCGAGAGACCTGGATCTTCTGACAGAG 600  
QY 601 AATAAAAACAGAAAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAAAGCATTTGGG 660  
DB 601 AATAAAAACAGAAAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAAAGCATTTGGG 660  
QY 661 AAGAGCTGGTGAACCATTTGTCTCAACAGCAATCTACATTTCAAGACTTTGGGCACT 720  
DB 661 AAGAGCTGGTGAACCATTTGTCTCAACAGCAATCTACATTTCAAGACTTTGGGCACT 720  
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DB 721 ATTCTAAGAAAAACCTCAGAAAGCAAAATTCAGAAAGTGGCAAGTCTCACTTGGGCACT 780  
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DB 781 TTCCCTCTCACTCTGTAGTACACCTCTCTCAATGAAATTCGATTAATCACTCAACGAC 840  
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DB 841 ACCAAGATGCTTACCAACAGAAAGAGAAACAAATTCGCTGTGTGAGAGACAGAGGCTG 900  
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DB 961 CCATATTACAGAGAGCTACAGAGAAAGTCCCAACTTCAGATCAAAAGATTTTAAGAA 1020  
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DB 1021 CTTTCCAGGATTTCAAAAAATCCATGTGTTAGATTGACCAAGAAAGAAAGATGGC 1080  
QY 1081 TCAAGCTCACAAGAGTGAAGCTTACGAGCATCTTTAAGAGACAGCTGCAAGAGAA 1140  
DB 1081 TCAAGCTCACAAGAGTGAAGCTTACGAGCATCTTTAAGAGACAGCTGCAAGAGAA 1140  
QY 1141 AGCCCTGCAAGTGAACCTCTGTCTTTGATTCACAAAAATTTGAAAGTGAAGTCTAT 1200  
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DB 1501 CTTGCTATGAGCTTCACTCTCTGTCAAGAGCTCCACTTTCTTTATGAGCATCAAGATC 1560  
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DB 1621 CGAGGAGCTCAGCATCCCAAGAGTATTTCTGCAATCAGGCAACTGGCTCTGGGAAAT 1680  
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DB 1921 TTCAATCTGAGTGTGTTGCTTAACATGGCTTCTTCCACAGACCTGTTCACAGAGCTCTG 1980  
QY 1981 GAGTACGAGCTCTGGAGCAACATTTCAACAGAGCTGTGTTCAATCTAGATCAAT 2040  
DB 1981 GAGTACGAGCTCTGGAGCAACATTTCAACAGAGCTGTGTTCAATCTAGATCAAT 2040  
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DB 2101 AGCAAAATGAAGTTGCTTAAGTCTGTGCGCTTAACCTTCAACAGAGCTGTGACGGGTC 2160  
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DB 2341 GACAGCAGGGGAGCTGAGAGGCTGGAACAGGCTCTGTGAGCTTGGGCAAGAGAA 2400  
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Db 2401 TCGAGAGTCTCCAGGAGAAAGGAGCTCCATGCGAGGTGCGAGTCACTCTGAAATCA 2460  
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Qy 2761 TAAATTCGAAAGAAAGCACTTACTTATTAATTAACCCCAATGCAATGAGGAAAC 2820  
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Qy 2821 AATTTTCTATTTCTGATGATGATCAAAATGATCAATAGCAGGTTGCTTCCACT 2880  
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Db 2941 ACTGAACAATTTATGGAAGCAACTCTTATATGCTAGAAAGTACATTTAAAGATGA 3000  
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Db 3001 CTACTTACGAGGAGATGACAGGCTCTCTAAACGATGATGATGATGATGAGCA 3060  
Qy 3061 CTGATGAGTATATATGCTCCACAGATGATGATGATGATGATGATGATGATGATG 3120  
Db 3061 CTGATGAGTATATATGCTCCACAGATGATGATGATGATGATGATGATGATGATG 3120  
Qy 3121 TTATTAAGGACACTAGTTTATAGCACTACTGCTTATAGTATGATGATGATGATG 3180  
Db 3121 TTATTAAGGACACTAGTTTATAGCACTACTGCTTATAGTATGATGATGATGATG 3180  
Qy 3181 AATTAATCTTGAATGTTCTTTAAAGAACTGAGGTTCAATACATACATGAGAAA 3240  
Db 3181 AATTAATCTTGAATGTTCTTTAAAGAACTGAGGTTCAATACATACATGAGAAA 3240  
Qy 3241 ATCTTACTTTTCTGTTATACAAAGTATTTTAAAGAAAGTATGTTGGAGAG 3300  
Db 3241 ATCTTACTTTTCTGTTATACAAAGTATTTTAAAGAAAGTATGTTGGAGAG 3300  
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RESULT 2  
US-10-007-270-27  
; Sequence 27, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US

; CURRENT APPLICATION NUMBER: US/10/007,270  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 3261  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: CDS  
; LOCATION: (128)..(2440)  
US-10-007-270-27  
Query Match 93.8%; Score 3124.6; DB 5; Length 3261;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 3256; Conservative 0; Mismatches 5; Indels 69; Gaps 6;  
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Db 59 TTTTACTTTTATGAGATTTGAGGTTGTTCTGATTTTATCAGAAATTTAC -ATGAC 117  
Qy 121 AAAAGCCGAATGATTTTGGAAATGAAAGCTATTTTGTGTTTGGATTTTCTCA 180  
Db 118 AAAAGCCGAATGATTTTGGAAATGAAAGCTATTTTGTGTTTGGATTTTCTCA 177  
Qy 181 AGTTCAAGAAACCAAGATCTCCATTAATCAATATCAATCTGAACTGAAAGATGAA 240  
Db 178 AGTTCAAGAAACCAAGATCTCCATTAATCAATATCAATCTGAACTGAAAGATGAA 237  
Qy 241 CAATCCCCCAAGAAATGAAACACTGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 300  
Db 238 CAATCCCCCAAGAAATGAAACACTGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 297  
Qy 301 GAGACGAATATTCGATTTTGGCAAGATGCAAAAGATTCGATTTTCCAAACGGG 360  
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Qy 361 GGTAAAGTCTGTCACAGGAATCCATGAACAGATTTTGAACATCTTCAAGCTTATTA 420  
Db 358 GGTAAAGTCTGTCACAGGAATCCATGAACAGATTTTGAACATCTTCAAGCTTATTA 417  
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Db 418 TAGATTTGAGATGTTGTCAGAAAGTATGGAAGCATATCGATCTTTTGGATGCGAT 477  
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Qy 541 CTTTGAACATTTGAAAGAACTTCAAGATTTCCAGAGAGACTTCTTCCACAGAG 600  
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Db	716	TTCCCTCTCACTCTGATGACAACCTTCTCAATGAATTCGATATATACACTCAACGAC	775
Qy	841	ACCAAGATGCTTACCAACAGAAAAGAAAACAGAAATTCGCTGTGTGTTGAGAGCAAGGGTG	900
Db	776	ACCAAGATGCTTACCAACAGAAAAGAAAACAGAAATTCGCTGTGTGTTGAGAGCAAGGGTG	835
Qy	901	GAGCTCAGGGCTCTCTCTGTTAAACGAAAGTTCAAGGCAAGCTGCTGCTCCAGTCC	960
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Qy	961	CCATATTAACAGAGCTAGCAGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA	1022
Db	896	CCATATTAACAGAGCTAGCAGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA	955
Qy	1021	CTTCCAGGATTCAAAAAAATCCATGTGTGAATTTAGACCAAGAAAGAAAAGATGCG	1088
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Qy	1081	TCAAGCTCCACAGAGATGCAATCTTACGGCATCTTTAAGACAACAGTCCAGAGCAAAA	1144
Db	1016	TCAAGCTCCACAGAGATGCAATCTTACGGCATCTTTAAGACAACAGTCCAGAGCAAAA	1077
Qy	1141	AGCCCTGCAGAGTCACTCTGTCTTTTGAATTCCAACAAATTTGAAAGTAGAGAGTCTAT	1200
Db	1076	AGCCCTGCAGAGTCACTCTGTCTTTTGAATTCCAACAAATTTGAAAGTAGAGAGTCTAT	1133
Qy	1201	CATGGAAACAATGAGAGAGACAAGCAACCAAAATTTATCTCAAGCTTCAAGCTCTAAA	1267
Db	1136	CATGGAAACAATGAGAGAGACAAGCAACCAAAATTTATCTCAAGCTTCAAGCTCTAAA	1199
Qy	1261	AGGCTGATCAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGGACAATTCAGTTC	1322
Db	1196	AGGCTGATCAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGGACAATTCAGTTC	1255
Qy	1321	ACTGATGAAATTCCTGATCACTGCCCCCTTTGTGCTTGACACCAATCAGAGTGGCC	1381
Db	1256	ACTGATGAAATTCCTGATCACTGCCCCCTTTGTGCTTGACACCAATCAGAGTGGCC	1311
Qy	1381	ACATCTTTTGGCTGTTATTAACAAGAGATGCTACTTTGATGCCAAGACTTCTCTGTTGAA	1444
Db	1316	ACATCTTTTGGCTGTTATTAACAAGAGATGCTACTTTGATGCCAAGACTTCTCTGTTGAA	1377
Qy	1441	CCCCAGCTTGAAACAGTGAACGAGACGAGAGCAATGCTACCTGACACTTCTTGCTCCAA	1500
Db	1376	CCCCAGCTTGAAACAGTGAACGAGACGAGAGCAATGCTACCTGACACTTCTTGCTCCAA	1433
Qy	1501	CCGTGATAGGCTCTTACCTCCCTGTACAGAACTCCACTTTCTTTATGGCATCAAGCATC	1566
Db	1436	CCGTGATAGGCTCTTACCTCCCTGTACAGAACTCCACTTTCTTTATGGCATCAAGCATC	1499
Qy	1561	TTCTCTCTGATCTGATCAAGGACCAACAGATTAACAATGAGCACTGACCAACAATGCTAGTA	1622
Db	1496	TTCTCTCTGATCTGATCAAGGACCAACAGATTAACAATGAGCACTGACCAACAATGCTAGTA	1555
Qy	1621	CCAGGGCTCAACATCCCAACAGTGAATTAATTCGCAATCAAGCCAACTGGCTCTGGGAAAT	1688
Db	1556	CCAGGGCTCAACATCCCAACAGTGAATTAATTCGCAATCAAGCCAACTGGCTCTGGGAAAT	1611
Qy	1681	TCACATCCACTGCACTTCAAGATGACACCGCATCAAGTGCAGGTGGCAAGATATGTC	1744
Db	1616	TCACATCCACTGCACTTCAAGATGACACCGCATCAAGTGCAGGTGGCAAGATATGTC	1677
Qy	1741	AGACACTGATGAAATGATCTGTGACACTCTGCCCACTGAAGGTACCAAGGCTC	1800
Db	1676	AGACACTGATGAAATGATCTGTGACACTCTGCCCACTGAAGGTACCAAGGCTC	1733
Qy	1801	AGGGAATAGTTTCTGTCCCAATCATTTCTTGAGAGATACCACTCTCTCTCAAGCTTTA	1866
Db	1736	AGGGAATAGTTTCTGTCCCAATCATTTCTTGAGAGATACCACTCTCTCTCAAGCTTTA	1799

QY	1861	CAGTATATACCACTAGTTCTATATACCATTCGCGCCCAAGGGCCGAGAGCTGTAGTTC	192
Db	1796	CAGTATATACCACTAGTTCTATATACCATTCGCGCCCAAGGGCCGAGAGCTGTAGTTC	1855
QY	1921	TTCAAGTCCGCTGTGTGCTTAACATGAGCTCTTCCACACGACCTGTTCACACAGAGCTCTG	1980
Db	1856	TTCAAGTCCGCTGTGTGCTTAACATGAGCTCTTCCACACGACCTGTTCACACAGAGCTCTG	1915
QY	1961	GAGTACCGAGCTCTGAGACACAAATTCACACAGCTGCTGTTCATATCTACGATCCAA	2040
Db	1916	GAGTACCGAGCTCTGAGACACAAATTCACACAGCTGCTGTTCATATCTACGATCCAA	1975
QY	2041	CTTACAGGATTTAAGCAACTTGAATATCTTAATCTTCAAAAACGGAGGTGATGTGCAAT	2100
Db	1976	CTTACAGGATTTAAGCAACTTGAATATCTTAATCTTCAAAAACGGAGGTGATGTGCAAT	2035
QY	2101	AGCAAAATGAAGTTTGCTAAGTCTGTGCGGTATTAACCTCACCAAGGCTGTGCAAGGGCTC	2166
Db	2036	AGCAAAATGAAGTTTGCTAAGTCTGTGCGGTATTAACCTCACCAAGGCTGTGCAAGGGCTC	2095
QY	2151	TTGAGAGATTTTTCGTTCTGCTGACGAGCCCAACAACTCCATCTGAGAAATGAGAGCTACTCT	2220
Db	2096	TTGAGAGATTTTTCGTTCTGCTGACGAGCCCAACAACTCCATCTGAGAAATGAGAGCTACTCT	2155
QY	2221	CTCAACATTTGAAACCGAGCTGATCAAGCAGATCCCTGCAGATTCTGTGCGCGGCAATTT	2280
Db	2156	CTCAACATTTGAAACCGAGCTGATCAAGCAGATCCCTGCAGATTCTGTGCGCGGCAATTT	2215
QY	2281	GCCCAATGTGTAAAGAACGAACGACCTGAGGAACGGAGTCCGTCCGTGAACCAAGATAT	2340
Db	2216	GCCCAATGTGTAAAGAACGAACGACCTGAGGAACGGAGTCCGTCCGTGAACCAAGATAT	2275
QY	2341	GACAGCCAGGGAGGCTGAGCGGTCTGGAACCAAGGCTCTGTGCGCTGTGCAACAAAGAA	2400
Db	2276	GACAGCCAGGGAGGCTGAGCGGTCTGGAACCAAGGCTCTGTGCGCTGTGCAACAAAGAA	2334
QY	2401	TGCGAGTCTCTCCAGGAAAGGAGCTCCATGCAAGTTGCCAGATCACTTGAAAAATCA	2460
Db	2335	TGCGAGTCTCTCCAGGAAAGGAGCTCCATGCG -- GGTTCAGATCACTTGAAAAATCA	2392
QY	2461	GCAATCAAAAATAAGTTAAAAAGTTCAAAAATCAAAAAATTAACAAGATATCAAGTAA	2520
Db	2393	GCAATCAAAAATAAGTT -- AAAAGTTCAAAAATCAAAAAATTAACAAGATATCAAGTAA	2451
QY	2521	AGAAATTCGTGAATTAATCAGCCGTGAATATGAGAAATTTAAACAATCAAGATTGGAAGAA	2580
Db	2452	AGAAATTCGTGAATTAATCAGCCGTGAATATGAGAAATTTAAACAATCAAGATTGGAAGAA	2511
QY	2581	AATTAATAAATCTGAAAAATGATCAATTAATCACTTAAGCTATCTCCAGAGATGATTTGCT	2640
Db	2512	AATTAATAAATCTGAAAAATGATCAATTAATCACTTAAGCTATCTCCAGAGATGATTTGCT	2571
QY	2641	TCTCAAGAAAAATGAGACAGGACATATCATGGGCTATCAAAATTCACACATACAGTCAA	2700
Db	2572	TCTCAAGAAAAATGAGACAGGACATATCATGGGCTATCAAAATTCACACATACAGTCAA	2633
QY	2701	CACGTAGATGACACACCAATTTCAAAATATGAAAGAGTCATGTATCTTGCAACCAAG	2760
Db	2632	CACGTAGATGACACACCAATTTCAAAATATGAAAGAGTCATGTATCTTGCAACCAAG	2691
QY	2761	TAAATTTCTGAAAAAAGACCTTAATTAATTTAAAAACCCCAATGCAATCAGGAAAC	2820
Db	2692	TAAATTTCTGAAAAAAGACCTTAATTAATTTAAAAACCCCAATGCAATCAGGAAAC	2751
QY	2821	ATAATTTTACTAATCTTGTGATGATATGCAAAATGATCAATGACCAAGTTTGCTTCACT	2880
Db	2752	ATAATTTTACTAATCTTGTGATGATATGCAAAATGATCAATGACCAAGTTTGCTTCACT	2811
QY	2881	TCCCTGAAAAATTTTACTCAAGATATATTTGCAACAAGATAGCTTAATTTGTTTAAGG	2940
Db	2812	TCCCTGAAAAATTTTACTCAAGATATATTTGCAACAAGATAGCTTAATTTGTTTAAGG	2871



OY	1716	AAGGCAAGGTGGCCGAAGATATGGTCTCAGCAACCTTGAATGAAATGCAATCTGTCTGCACTCC	1775
Db	1273	AAGTGCAGGTGGCGAAGATATGGTGTGACACCTTGATGAAATGGAATCTGTCTGCACTCC	1332
OY	1776	TGCCCAATCTGAGGTTACCAAGACTCAGCGAAATATGTTCTGTCTCCAGATCAATTTCTTGGA	1835
Db	1333	TGCCCAATCTGAGGTTACCAAGGAGCTCAGGAAATACGTTCTGTCTCCAGATCAATTTCTTGGA	1392
OY	1836	GGATACCACTCTGTCTCAGCTTTTACAGTATATCACCACTAGTTCTATGACCAATTTGCCCC	1895
Db	1393	GGATACCACTCTGTCTCAGCTTTTACAGTATATCACCACTAGTTCTATGACCAATTTGCCCC	1452
OY	1896	CAAGGCGCGAGAGCTGATGTTCTTCAGTCTGCGTGTGTACTAATATGCGCTTCTCCAA	1955
Db	1453	CAAGGCGCGAGAGCTGATGTTCTTCAGTCTGCGTGTGTACTAATATGCGCTTCTCCAA	1512
OY	1956	CGACTGTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAGCT	2015
Db	1513	CGACTGTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAGCT	1572
OY	2016	GCTGGTTTCATATCTACGATCCAAATCTTACAGGAATTAAGCACTGGAATAACTTAATCTT	2075
Db	1573	GCTGGTTTCATATCTACGATCCAAATCTTACAGGAATTAAGCACTGGAATAACTTAATCTT	1632
OY	2076	CAGAAACGGGAGTGTGATTTGTGAATAGCAAAATGAAATTTGCTAAGTCTGTCCGTATTA	2135
Db	1633	CAGAAACGGGAGTGTGATTTGTGAATAGCAAAATGAAATTTGCTAAGTCTGTCCGTATTA	1692
OY	2136	CCTCAACCAAGGCTGTGCACGGAGTCTTGGAAGATTTTGTGTGTGTGACGCCCAACAAT	2195
Db	1693	CCTCAACCAAGGCTGTGCACGGAGTCTTGGAAGATTTTGTGTGTGTGACGCCCAACAAT	1752
OY	2196	CCATCTGAAATATGACAGCTACTCTCTCAACATTGAACACAGCTATCAAGCAGATCCCTG	2255
Db	1753	CCATCTGAAATATGACAGCTACTCTCTCAACATTGAACACAGCTATCAAGCAGATCCCTG	1812
OY	2256	CAAGTTCTGTGCTGTGCGCGGAATTTTGCCCAATGTGTAAAGAACGACGGACTGAGAAAGC	2315
Db	1813	CAAGTTCTGTGCTGTGCGCGGAATTTTGCCCAATGTGTAAAGAACGACGGACTGAGAAAGC	1872
OY	2316	GGAAGTGTGCTGTGCAAAACGAGATATGACAGCAAGGAGGCGCTGACCGTCTGGAACAAG	2375
Db	1873	GGAAGTGTGCTGTGCAAAACGAGATATGACAGCAAGGAGGCGCTGACCGTCTGGAACAAG	1932
OY	2376	CCTCTGTGGCCCTGTGCAAAAGGAATGCGAGTCTCCAGGGAAAGGAGCTCCATGAG	2435
Db	1933	CCTCTGTGGCCCTGTGCAAAAGGAATGCGAGTCTCCAGGGAAAGGAGCTCCATGAG	1992
OY	2436	GTTGCGCAATCACTCTGAAAAATCAAGCATCAAAAATATGTGTATAAAAAGTTCCAAAATCA	2495
Db	1993	GTTGCGCAATCACTCTGAAAAATCAAGCATCAAAAATATGTGTATAAAAAGTTCCAAAATCA	2052
OY	2496	ACAAATATTAACAAGGTATCAGTATTAAGAAATTCGAAATTACTGACCGTGAATATGAGA	2555
Db	2053	ACAAATATTAACAAGGTATCAGTATTAAGAAATTCGAAATTACTGACCGTGAATATGAGA	2112
OY	2556	ATTTAACCATCAAGATTTGGGAAAGGAATTTAAAACTGAAAAATGTACATTAATCACTTAGG	2615
Db	2113	ATTTAACCATCAAGATTTGGGAAAGGAATTTAAAACTGAAAAATGTACATTAATCACTTAGG	2172
OY	2616	CTATCTCAAGAGAGATGATTTTGCCCTTCAAGGAAAAATGGAGACAGGATATTCATGGGT	2675
Db	2173	CTATCTCAAGAGAGATGATTTTGCCCTTCAAGGAAAAATGGAGACAGGATATTCATGGGT	2232
OY	2676	CATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGACACACACATATTCGAAATTA	2735
Db	2233	CATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGACACACACATATTCGAAATTA	2292
OY	2736	GAAAGTATATGTACTTTGGCAACCAAGTAATTTCTGAAAAAAAAGACACTTAATTAATTA	2795
Db	2293	GAAAGTATATGTACTTTGGCAACCAAGTAATTTCTGAAAAAAAAGACACTTAATTAATTA	2352

QY	2796	AAACCCCAATGCAATGAGGAAACATATTTTATCTATTTCTGGATGATGTGCAAAATGA	2855
Db	2253	AAACCCCAATGCAATGAGGAAACATATTTTATCTATTTCTGGATGATGTGCAAAATGA	2412
QY	2856	TCATTAAGCCAGGTTTGCTTCCACTTCCCTGAAATTTTATCTCAGATCATTTTGACAA	2915
Db	2413	TCATTAAGCCAGGTTTGCTTCCACTTCCCTGAAATTTTATCTCAGATCATTTTGACAA	2472
QY	2916	AGCATAGCTTACTATTTGTTTAAAGGACTGAACATTTATATGGGAAGGAAACCTCTTATAT	2975
Db	2473	AGCATAGCTTACTATTTGTTTAAAGGACTGAACATTTATATGGGAAGGAAACCTCTTATAT	2532
QY	2976	GCTAGAAAGTACATTTAAAGATGACTTACGACGAGGAGATGACAGTCTCTCTAAACG	3035
Db	2533	GCTAGAAAGTACATTTAAAGATGACTTACGACGAGGAGATGACAGTCTCTCTAAACG	2592
QY	3036	CATATAATGTATGTATGTGTATGAGGACTGTAGTGTAGTGTATATATATGCTCCACATACGCTT	3095
Db	2593	CATATAATGTATGTATGTGTATGAGGACTGTAGTGTATATATATATGCTCCACATACGCTT	2652
QY	3096	GATAAACACAAACCTCAGTATTACGATTATTAAGGACACTAGTTTATACGCAACTACTGTC	3155
Db	2653	GATAAACACAAACCTCAGTATTACGATTATTAAGGACACTAGTTTATACGCAACTACTGTC	2712
QY	3156	TTACATAGTATAGCTGTTTTGTTGGCAATTAATCTTTGATTTGTTTAAAAAGAACTGAG	3215
Db	2713	TTACATAGTATAGCTGTTTTGTTGGCAATTAATCTTTGATTTGTTTAAAAAGAACTGAG	2772
QY	3216	GTTCAGATATACATATCCATGGAATAATCTTATCTTTCTTGTTACTACACAAGCTATTTT	3275
Db	2773	GTTCAGATATACATATCCATGGAATAATCTTATCTTTCTTGTTACTACACAAGCTATTTT	2832
QY	3276	AAAGAAGATGCTATGTTGGGAGAAAGGGCGAAGTTGTACTATATGACATAATCAAT	3330
Db	2833	AAAGAAGATGCTATGTTGGGAGAAAGGGCGAAGTTGTACTATATGACATAATCAAT	2887

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RESULT 4
US-10-007-270-5
; Sequence 5, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2244
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IPM 150 CDNA sequence, isoform C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2244)
; OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-5

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Query Match	65.6%	Score 2184.2	DB 5	Length 2244
Best local Similarity	99.5%	Pred. No. 0		
Matches 2211, Conservative	0	Mismatches 10	Indels 2	Gaps 2

QY 1 TAAACCAAGAGTATCTCAATCATCTGGTATCAATATTAATTTATTTTCACATTTC 60

Db 22 TAAACCAAGAGTTATCTCAATCATCTGTATCAATATATATATATTTTCACATTTTC 81  
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Qy 1861 CAGTATATCAACACTAGTTCTATGACATTTGCCCCCAAGGGCCGAGAGCTGTAGTTC 1920  
Db 1880 CAGTATATCAACACTAGTTCTATGACATTTGCCCCCAAGGGCCGAGAGCTGTAGTTC 1939  
Qy 1921 TTCAGTCTGCGTGTGCTAACAATGCGCTTCTCCACAGACCTGTTCAAGAAGCTCTCTG 1980  
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DB 1602 TCCCTTGATGACATGCGCCCAACAGACATCAATCCCAAGCCCACTCCCACTATGCA 1661
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QY 1827 TTTCTTGGAGATACCACTCTGCTCAGCTTTTACAGTATACCACTAGTTCTATGAC 1886
DB 1842 GTTCTTGGAGATGACCAACCCATCCCAAGATAGGTTTATACACCAACAGCTCCGAGAC 1901
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DB 1902 CATTGCCACCAAGGGCCAGAGACTAGTGTATTTCTTCAAGCTGCGCTGTTGCTTAATGCC 1961
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DB 2022 CACAGACTGCTGTTTCTTCTATCTATCTAGATCAATCTTACAGGATTTTAAAGCACTGGAAT 2081
QY 2067 ACTTAACTTCAAGAAACGGAAGTGTATGTAATGACAAATGAAGTTTGTACTGCTGT 2126
DB 2082 ACTCAGCTTCAAGAAACGGAAGTGTATGTAATGACAAAGTGGGTTTGAACAAAGCGGT 2141
QY 2127 GCCGTATACCTCACCAGAGCTGTGACAGGGGCTTGTGAGATTTTCTGCTGCTGAC 2186
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DB 2553 ATTGAAGAAATTTGAAGACAGGACTGGAGGGAATTTAAAGCTGGAATCAATATGACT 2612
QY 2596 -----ATGTACAATTTTCACTTGGCTTCTCAAGAGAGATGATTTGCT 2640
DB 2613 ATGTTCGAACCTCTGTTGAAGGAACCTTATTTCTTAAAGAAAGTATCTGTTCTGT 2672

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QY 2641 TCTCAAGAAATATGAGACAGGCATATTCATGCGTCAATCAAAATCCAGACATACAGTCA 2700
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QY 2701 CACTGAGATACAGACACACATATTTTCAAAATATGAAAGATCATGTACTTGGCAACGAG 2760
DB 2733 CTTTGAAGCTCAG-----CATGCTTGAACAAGAGCACAGCGGTATTTTGAATGA-CAG 2784
QY 2761 TAAATCTGAAATAAAGACACTTACTATTTATTA--AAACCCCAATGCAATCAGCGAA 2818
DB 2785 TTAAGCCTGTTGGGGCGCGGGGACATATTTTATGTCAAATCTAAAGCAATCATTTGGA 2844
QY 2819 ACAAATTTTCTATTTCTTGAATGATGATCAAAATGATCATAGCCAGTTTCTTCCAC 2878
DB 2845 ACACA-TTGTACTATTTTGTGACAGTACTC--AGTACCAAAAGATMAAGTTAGCTTTTT 2901
QY 2879 CTTCCCTGAAATTTTACTCAGATCAATTTGCAACAAGCATAGCTTACTTATTTGTTAG 2938
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QY 2939 GAACTGAACAATTTATTTGGAAGCAAACTTTTATATGCTAGAAATGATCATTTAAAGAT 2998
DB 2955 TGGGTGTGACAATATTTGAGATCTGATTTCTTTATATGTTGAATATACATTAAGAT 3014
QY 2999 GACTACTTACGC 3010
DB 3015 TATCATTTGGGC 3026

RESULT 6
US-10-007-270-10
; Sequence 10, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 CDNA sequence, isoform D
US-10-007-270-10

Query Match 16.0%; Score 534; DB 5; Length 1726;
Beech Local Similarity 72.0%; Pred. No. 1,2e-11;
Matches 792; Conservative 0; Mismatches 225; Indels 83; Gaps 4;

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Db	2392	CCGAGTCGTGCCCTCCTCATATGTCAACAAAGCCATGTATAGATTTTGGAAAGCTTTGTGA	2455
Qy	2177	CTGCTGCACGCCCAACACTCCATCTGGAAATGACAGCTACTCTCTCAACATTGAACAG	2236
Db	2452	CCACTGCTCTAACCAACCATGAACTTGGATATCGAATAGTAATACCTCCGTGACGGTGAATCAG	2511
Qy	2237	CTGATTCACGACGATCCCTGCAGAGTTCCATGGCCCTGGCGGAATTTGCCAATGTGTAAAGA	2296
Db	2512	GTGATGAGGCCAACCTTGGCAAGTTTCAGGCTGTATGAATTTTCTGAGTGTTTGGTAA	2571
Qy	2297	ACGAAACGACTGAGAGAACGGAGTGTGCGCTGGCAAAACAGATATGACACGCCAGGGAGCC	2356
Db	2572	ATCATGTGAGATGGAGAACCAAGTCAATGCTACCTCGGGTACTGAGTGTGATGAAC	2631
Qy	2357	TGGACGGTTC	2365
Db	2632	TGCCTTGTTC	2640

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RESULT 15
US-10-007-270-18
; Sequence 18, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2964
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: Human IPW 200 cDNA sequence, isoform C
US-10-007-270-18

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Query Match	5.5%	Score 184.8;	DB 5;	Length 2964;
Best Local Similarity	66.1%;	Pred. No. 8.1e-38;		
Matches 267;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0

Qy	1883	TGACCATTGCCCCCCAGAGCGAGAGCTGTAGTTCCTTCAGTGTGCTGTGTGTAC	1944	CA
Db	2520	TGAGTTATACCAAGCTTCAGAGGCTTTGGTGGTTTCTTCAGCCTCCGAGTACTACA	2579	TA
Qy	1943	TGGCCTTCCAGACGACTGTTCACACAAAGAGCTCTCTGGAGTACCGAGCTCTGAGCAAC	2002	TA
Db	2580	TGATGTTTTCAGAAAGATCTGTTTATATAAAACTCCTTGGAGTATATAAACCCCTGGAGCAAA	2639	TA
Qy	2003	AATTCACACAGCTGTGGTTCATCTACGATTCATCAATCTTACAGATTTATAGCAACTTG	2062	TA
Db	2640	GATTCCTTAGAATGTGTGGTTCCTTATCTCCAGTCAAACTCACGCGGTTCCAGAACTTAG	2699	TA
Qy	2063	AAATTACTTAACCTTCAGAAAACGGAGGTGTGATTGTGATATAGCAAAATGAAGTTTGCTAAGT	2122	TA
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Qy	2123	CTGTGCCGTATTAACCTTCACAAAGGCTGTGCACGCGGCTCTTGAGAGATTTTCGTTCTGCTG	2182	TA
Db	2760	CTGTGCCCTCTTAACGTCAACAAATGGCGGTGTACATGATTTCTGGAAGACCTTTTGTACACATG	2819	TA
Qy	2183	CAGCCCAACAACCTCATCTGTGAAATAGACAGCGTACTCTTCTCAACATTGAACCAAGCTGATC	2242	TA

Db 2820 CCTACATACCATGAACCTTGCTATTTGATAATACCTCTTGGATGTGGAATCAGTGTATG 2875

Qy 2243 AAGCAGATCCCTGCAAGTTCCTGGCCTGGCGGCAATTTGCCAA 2286

Db 2880 AAGCAACCCCTTGCAAGTTTCAGGCTGTATATGAAATTTTCGAA 2923

Search completed: January 14, 2006, 22:38:23  
Job time : 2567 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2006, 14:24:40 ; Search time 12641 Seconds  
(without alignments)  
12325.052 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaacacaaagaagttatcct.....tactatatgacataatcaat 3330

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 2339354128 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*  
1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_hic:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_esc7:\*  
9: gb\_gse81:\*  
10: gb\_gse82:\*  
11: gb\_gse83:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2472	74.2	5829	4	CR749572 Homo sapi
2	1456	43.7	1665	10	AY415971 Homo sapi
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4	626	18.8	626	5	BQ639265 h33d04.y
5	558	16.8	675	5	BM650735 UI-E-CKO-
6	450	14.4	633	3	BM695987 UI-E-CKO-
7	472	14.2	472	5	BX097138 BX097138
8	469	14.1	622	5	BQ638902 h429406.y
9	467	14.0	653	3	BM685921 UI-E-CKO-
10	433	13.0	836	3	BT752112 603022362
11	409	12.3	422	3	BM726533 UI-E-EJO-
12	342	12.1	508	6	CA393958 c844g04.y
13	335	11.9	801	2	BG196799 RST16026
14	380	11.4	598	5	BQ636596 h411h02.y
15	373	11.2	683	5	BT732814 UI-E-COI-
16	340	10.2	698	5	BT792227 UI-E-COI-
17	322	9.4	405	8	H38604 yP4604.r1
18	306	9.2	448	8	BM681190 UI-E-EJO-
19	294	8.8	368	3	BM694699 UI-E-CII-
20	282	8.5	521	3	BM691879 UI-E-CL1-
21	282	8.5	548	5	BT728582 UI-E-CL1-
22	268	8.0	515	5	BT726282 UI-E-CKO-

23	266	8.0	561	8	W26960
24	263	7.9	618	6	CA391789
25	249	7.5	340	1	AV656968
26	241	7.2	510	1	AL713229
27	228	6.8	641	5	BT734170 UI-E-CK1-
28	213	6.4	298	1	AA296278 RST10795
29	204	6.1	393	5	BQ636351 h407h06.y
30	188	5.6	1587	10	AY415972 Pan trogl
31	168	5.0	309	8	H38594
32	156	4.7	322	1	AA326863 RST30113
33	152	4.6	527	5	BT731220 UI-E-CII-
34	113	3.4	701	10	AG128736
35	81	2.4	647	9	AQ234080 HS 2057.A
36	40	1.2	626	5	BK646053 DKFZp781B
37	32	1.0	624	7	CK619878 mk29d09.y
38	32	1.0	754	8	CX568203 UI-M-IBO-
39	32	1.0	797	4	AK020862 Mus muscu
40	32	1.0	802	3	BT735091 603356230
41	32	1.0	1647	10	AY415973 Mus muscu
42	30	0.9	654	10	CS64832
43	28	0.8	753	3	BT735383
44	25	0.8	393	6	CB774211 AMGNNUC:S
45	25	0.8	409	6	CB770207 AMGNNUC:S
46	24	0.7	269	7	CO506867 CGEZR201
47	24	0.7	400	5	BU255882 603745523
48	24	0.7	471	5	BU201300 60415385
49	24	0.7	866	3	BY742200 BY742200
50	24	0.7	624	5	BT738733 603358767
51	24	0.7	851	3	BT733865 603353151
52	24	0.7	963	5	BU506195 AGENCOURT
53	24	0.7	1090	5	BU295512 603742306
54	23	0.7	779	9	BH357376 CH230-175
55	23	0.7	814	10	CB814676 OC_Ba019
56	22	0.7	320	2	BB251690 BB251690
57	22	0.7	387	1	A1632451 WP09C01.x
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62	22	0.7	503	1	AM303461 xv19d01.x
63	22	0.7	520	3	BM168779 RST571302
64	22	0.7	549	3	BT509853 BB170024B
65	22	0.7	562	7	CO617781 DG9-179e1
66	22	0.7	569	7	CN694482 E0351C10-
67	22	0.7	611	7	CK621236 ml12a05.y
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69	22	0.7	646	5	BU736728 UI-E-CK1-
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72	22	0.7	682	5	BU681181 UI-CF-ECL1
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74	22	0.7	732	9	BX871618 BX871618
75	22	0.7	781	11	CR806529 Sus scrofa
76	22	0.7	917	10	CS2525050 GMM2-64N1
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78	22	0.7	1305	9	CC314264 TAM32-311
79	22	0.6	201	6	CA931592 MTU2TA.P9
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81	21	0.6	269	2	BB279156 BB279156
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83	21	0.6	310	6	CB921817 VVD075H12
84	21	0.6	312	6	CA304907 Ag adfo.2
85	21	0.6	333	11	AL99588 Tetradon
86	21	0.6	343	6	CB379587 rqt7d07.y
87	21	0.6	364	10	CE317252 t19f-g88-
88	21	0.6	379	5	BO797217 EST_6155
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92	21	0.6	474	8	DT035848 VTL109B05
93	21	0.6	483	8	CX917235 JGI_CAA66
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535	19	0.6	444	8	DR566736	DR566736	WS0268.B2	C 608	19	0.6	504	1	AV523816	AV523816
536	19	0.6	446	1	AM465903	AM465903	BE230021A	C 609	19	0.6	504	2	BF402435	BF402435
537	19	0.6	446	8	DR576573	DR576573	WS00743.C	C 610	19	0.6	504	3	BJ381538	BJ381538
538	19	0.6	447	1	DR586481	DR586481	WS0342.B2	C 611	19	0.6	506	5	BK474504	BK474504
C 539	19	0.6	447	11	TA230D1P	TA230D1P	AL481019 T. Brucei	C 612	19	0.6	506	9	AK391032	AK391032
C 540	19	0.6	450	9	B2158538	B2158538	CH230-244	C 613	19	0.6	507	3	BJ380941	BJ380941
C 541	19	0.6	452	2	BF407032	BF407032	UI-R-BJ2-	C 614	19	0.6	507	3	BJ382102	BJ382102
C 542	19	0.6	452	9	AQ820005	AQ820005	HS_5270_A	C 615	19	0.6	507	3	BP422579	BP422579
C 543	19	0.6	453	3	BJ440205	BJ440205	BJ440205	C 616	19	0.6	508	3	BJ443622	BJ443622
C 544	19	0.6	453	7	CK873672	CK873672	SGP134825	C 617	19	0.6	508	6	CD286790	CD286790
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C 546	19	0.6	454	3	BJ443131	BJ443131	BJ443131	C 619	19	0.6	509	3	BD043220	BD043220
C 547	19	0.6	454	6	CB785072	CB785072	AMGNNUC:N	C 620	19	0.6	509	10	CE718291	CE718291
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C 549	19	0.6	455	3	BJ440612	BJ440612	UI-M-BZ1-	C 622	19	0.6	511	10	CL661095	CL661095
C 550	19	0.6	458	9	AZ720214	AZ720214	RPCI-24-1	C 623	19	0.6	512	3	BJ444162	BJ444162
C 551	19	0.6	459	9	CE053899	CE053899	t1gr-g88-	C 624	19	0.6	512	3	BJ446579	BJ446579
C 552	19	0.6	460	2	BE206908	BE206908	bs05g11.Y	C 625	19	0.6	512	5	BJ085439	BJ085439
C 553	19	0.6	461	1	AA143625	AA143625	z065g08.T	C 626	19	0.6	512	6	CA768372	CA768372
C 554	19	0.6	461	9	AZ769335	AZ769335	IM0569H19	C 627	19	0.6	513	3	AM249387	AM249387
C 555	19	0.6	462	1	AM740850	AM740850	uq93e08.X	C 628	19	0.6	513	1	BJ439229	BJ439229
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C 557	19	0.6	462	3	BM942848	BM942848	UI-M-BZ1-	C 630	19	0.6	514	2	BB764576	BB764576
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C 559	19	0.6	463	2	BG126428	BG126428	EST472074	C 632	19	0.6	514	11	TA101D06P	TA101D06P
C 560	19	0.6	463	3	BJ445943	BJ445943	BJ445943	C 633	19	0.6	516	6	BJ442338	BJ442338
C 561	19	0.6	464	8	DN162818	DN162818	SGP268789	C 634	19	0.6	516	6	CD007461	CD007461
C 562	19	0.6	466	3	BJ436797	BJ436797	BS436797	C 635	19	0.6	517	6	CA755154	CA755154
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C 564	19	0.6	467	5	BY015974	BY015974	BS015974	C 637	19	0.6	518	3	BJ442523	BJ442523
C 565	19	0.6	468	8	DR564838	DR564838	WS02631.C	C 638	19	0.6	518	3	BJ444638	BJ444638
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C 567	19	0.6	470	8	T21911	T21911	3919_Lambda	C 640	19	0.6	519	3	BJ445343	BJ445343
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C 569	19	0.6	472	2	BE314829	BE314829	601147484	C 642	19	0.6	520	6	CF603787	CF603787
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C 571	19	0.6	473	8	DR544945	DR544945	WS01045.B	C 644	19	0.6	521	3	BJ446264	BJ446264
C 572	19	0.6	474	2	BI041006	BI041006	113-NT028	C 645	19	0.6	521	10	CM446004	CM446004
C 573	19	0.6	475	9	AZ272169	AZ272169	RPCI-23-4	C 646	19	0.6	522	2	BG299088	BG299088
C 574	19	0.6	476	2	BE991683	BE991683	UI-M-BZ1-	C 647	19	0.6	522	9	AO958704	AO958704
C 575	19	0.6	476	3	BJ437568	BJ437568	BJ437568	C 648	19	0.6	522	9	AO381225	AO381225
C 576	19	0.6	477	11	BH060297	BH060297	RPCI-24-2	C 649	19	0.6	523	2	BE110065	BE110065
C 577	19	0.6	477	11	CR332264	CR332264	mtel-61P3	C 650	19	0.6	523	7	CK225617	CK225617
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C 579	19	0.6	478	8	BM413828	BM413828	EST00750	C 652	19	0.6	524	9	AG255062	AG255062
C 580	19	0.6	479	8	DR806621	DR806621	ZM_BRF003	C 653	19	0.6	524	9	AZ074207	AZ074207
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C 582	19	0.6	480	7	CK534974	CK534974	rwg9D_00	C 655	19	0.6	525	10	CE570788	CE570788
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C 584	19	0.6	481	5	BX865430	BX865430	BX865430	C 657	19	0.6	526	8	CK215834	CK215834
C 585	19	0.6	482	3	BJ351397	BJ351397	BJ351397	C 658	19	0.6	527	10	CM287043	CM287043
C 586	19	0.6	483	3	BJ445152	BJ445152	BJ445152	C 659	19	0.6	529	8	CK509438	CK509438
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C 593	19	0.6	487	5	BX909101	BX909101	BX909101	C 666	19	0.6	535	3	BJ442578	BJ442578
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C 595	19	0.6	488	3	BJ381314	BJ381314	BJ381314	C 668	19	0.6	537	2	BE581117	BE581117
C 596	19	0.6	489	3	BJ439213	BJ439213	BJ439213	C 669	19	0.6	537	3	BJ378637	BJ378637
C 597	19	0.6	490	7	CM438285	CM438285	BE04015B1	C 670	19	0.6	537	5	BK474495	BK474495
C 598	19	0.6	495	1	AA116463	AA116463	mp95e12.X	C 671	19	0.6	539	8	CK223301	CK223301
C 599	19	0.6	495	9	AO153617	AO153617	BS246_A	C 672	19	0.6	541	3	BJ438578	BJ438578
C 600	19	0.6	496	3	BJ442310	BJ442310	WS02610.B	C 673	19	0.6	541	3	BK438578	BK438578
C 601	19	0.6	498	8	DR557071	DR557071	WS02610.B	C 674	19	0.6	541	5	BK885283	BK885283
C 602	19	0.6	500	3	BP114396	BP114396	BP114396	C 675	19	0.6	542	3	BJ446522	BJ446522
C 603	19	0.6	500	3	BP114684	BP114684	BP114684	C 676	19	0.6	543	10	CM099409	CM099409
C 604	19	0.6	500	3	BP114685	BP114685	BP114685	C 677	19	0.6	543	3	BJ438952	BJ438952
C 605	19	0.6	500	3	BP114716	BP114716	BP114716	C 678	19	0.6	545	2	BP723252	BP723252
C 606	19	0.6	500	6	CD568290	CD568290	RK04CA110	C 679	19	0.6	545	3	BJ371709	BJ371709

C 680	19	0.6	545	9	BZ212961	BZ212961 CH230-342	753	19	0.6	591	7	CK534355	CK534355 rawb0.00
C 681	19	0.6	546	10	CZ812620	CZ812620 OC_Ba018	C 754	19	0.6	592	2	BG815534	BG815534 dad8e03.
C 682	19	0.6	547	10	B1301062	B1301062 UI-R-CV2-	C 755	19	0.6	592	2	B435364	B435364 B435364
C 683	19	0.6	547	9	AZ764151	AZ764151 1M0559N20	C 756	19	0.6	592	5	B0521154	B0521154 N19C_n109
C 684	19	0.6	548	1	AL387243	AL387243 McBC41C07	C 757	19	0.6	593	2	BG047109	BG047109 8aa76h02.
C 685	19	0.6	548	1	AM423908	AM423908 sh57f08.Y	C 758	19	0.6	593	3	BM308006	BM308006 8ak40f06.
C 686	19	0.6	548	7	CR551424	CR551424 CR551424	C 759	19	0.6	593	6	CA768485	CA768485 8aa1p1C15
C 687	19	0.6	549	7	CK225700	CK225700 704374711	C 760	19	0.6	594	5	BX304856	BX304856 BX304856
C 688	19	0.6	550	11	DR140386	DR140386 f0yz1ae 1	C 761	19	0.6	595	3	B1383602	B1383602 B1383602
C 689	19	0.6	552	10	CM485250	CM485250 f8db000f2	C 762	19	0.6	595	10	CM349401	CM349401 B18b001f0
C 690	19	0.6	554	3	B0383700	B0383700 B0383700	C 763	19	0.6	595	11	DE040648	DE040648 Branch10b
C 691	19	0.6	554	3	BQ630245	BQ630245 sakp9g05.	C 764	19	0.6	596	3	B0383496	B0383496 B0383496
C 692	19	0.6	556	5	BM528831	BM528831 sakp9a04.	C 765	19	0.6	596	7	CJ417931	CJ417931 Cj417931
C 693	19	0.6	556	5	BQ637599	BQ637599 hel2b08.Y	C 766	19	0.6	596	9	AQ722909	AQ722909 HS_5309_A
C 694	19	0.6	556	7	CK536785	CK536785 rawb0.00	C 767	19	0.6	597	3	B1378587	B1378587 B1378587
C 695	19	0.6	556	9	CE262345	CE262345 t1gr-g88-	C 768	19	0.6	598	5	BX315421	BX315421 BX315421
C 696	19	0.6	557	3	B0444030	B0444030 B0444030	C 769	19	0.6	598	5	BX861372	BX861372 BX861372
C 697	19	0.6	557	5	BX304857	BX304857 BX304857	C 770	19	0.6	598	5	BX912644	BX912644 BX912644
C 698	19	0.6	557	8	DN165680	DN165680 SGP275253	C 771	19	0.6	598	6	CA162195	CA162195 SC08R2303
C 699	19	0.6	557	8	AZ889361	AZ889361 RPCI-24-1	C 772	19	0.6	598	7	CK534393	CK534393 rawb0.00
C 700	19	0.6	559	1	AM019857	AM019857 f457g06.x	C 773	19	0.6	598	8	CK693547	CK693547 yd-c83A09.
C 701	19	0.6	560	7	CM075137	CM075137 EC1CBA002	C 774	19	0.6	598	8	B1987071	B1987071 3191-40_M
C 702	19	0.6	560	8	CV889994	CV889994 4141586_B	C 775	19	0.6	600	3	A2835957	A2835957 2M0130P20
C 703	19	0.6	560	9	AZ271596	AZ271596 RPCI-23-1	C 776	19	0.6	601	1	AM027901	AM027901 AM027901
C 704	19	0.6	560	9	BH873279	BH873279 hp43g03.b	C 777	19	0.6	602	8	CK193949	CK193949 25-802357
C 705	19	0.6	561	9	BH327557	BH327557 CH230-80L	C 778	19	0.6	603	2	B1198736	B1198736 602759748
C 706	19	0.6	562	8	CK215179	CK215179 MNS22917	C 779	19	0.6	603	2	B2887048	B2887048 CH240_189
C 707	19	0.6	563	5	BM888281	BM888281 BM888281	C 780	19	0.6	604	7	CK716729	CK716729 16450_Swo
C 708	19	0.6	563	8	DR448999	DR448999 VMS062.B2	C 781	19	0.6	604	7	BF296000	BF296000 0328P12
C 709	19	0.6	564	6	CD009721	CD009721 VVB059D12	C 782	19	0.6	605	2	BF297106	BF297106 047PB812
C 710	19	0.6	564	6	CD510832	CD510832 onerfxy00	C 783	19	0.6	606	1	AM263637	AM263637 xm81b12.x
C 711	19	0.6	565	3	B046382	B046382 B0446382	C 784	19	0.6	606	3	B0414429	B0414429 B0414429
C 712	19	0.6	565	7	CV046303	CV046303 RST_8010	C 785	19	0.6	607	9	A0552773	A0552773 RPCI-11-3
C 713	19	0.6	566	3	B1855827	B1855827 603382776	C 786	19	0.6	610	9	A0523119	A0523119 HS_5225_A
C 714	19	0.6	566	3	BH453773	BH453773 BOH1H93TR	C 787	19	0.6	611	1	AL786354	AL786354 AL786354
C 715	19	0.6	567	3	B0398523	B0398523 B0398523	C 788	19	0.6	611	1	CK888756	CK888756 SGP160753
C 716	19	0.6	567	5	BX315420	BX315420 BX315420	C 789	19	0.6	611	8	DR109168	DR109168 USDA-FP.1
C 717	19	0.6	568	3	B0441773	B0441773 B0441773	C 790	19	0.6	612	2	BB346790	BB346790 BB346790
C 718	19	0.6	568	3	BM102179	BM102179 fvi4a11.x	C 791	19	0.6	612	10	C2664314	C2664314 OM_Ba021
C 719	19	0.6	570	3	B1501908	B1501908 tm06f08.Y	C 792	19	0.6	613	11	DE038834	DE038834 Branch10b
C 720	19	0.6	570	8	DR017499	DR017499 STRS1_16-	C 793	19	0.6	614	3	B1871167	B1871167 603395056
C 721	19	0.6	571	3	BP257239	BP257239 BP257239	C 794	19	0.6	615	5	B0379464	B0379464 603812195
C 722	19	0.6	571	6	CB501492	CB501492 8aa1ga504	C 795	19	0.6	615	7	CK225711	CK225711 704377058
C 723	19	0.6	571	9	AZ491333	AZ491333 1M0324P16	C 796	19	0.6	615	10	CM169909	CM169909 104_580_1
C 724	19	0.6	572	2	B1196895	B1196895 602756042	C 797	19	0.6	616	5	B0383652	B0383652 N19C-tm02
C 725	19	0.6	572	11	DR4U16T	DR4U16T Danio rer	C 798	19	0.6	616	5	B2517267	B2517267 BOMR709TR
C 726	19	0.6	574	3	B0446758	B0446758 B0446758	C 799	19	0.6	619	3	B0381554	B0381554 B0381554
C 727	19	0.6	575	2	BF520075	BF520075 EST457543	C 800	19	0.6	619	3	CR339582	CR339582 m0e1-71E7
C 728	19	0.6	575	9	AZ981550	AZ981550 2M0262G03	C 801	19	0.6	619	11	FR0005517	FR0005517 F_rubripdes
C 729	19	0.6	577	8	CV993112	CV993112 IpcGRF2.1	C 802	19	0.6	620	1	B0382952	B0382952 B0382952
C 730	19	0.6	579	9	BZ561221	BZ561221 PAC82-144	C 803	19	0.6	620	1	AM027370	AM027370 AM027370
C 731	19	0.6	580	3	B1921317	B1921317 EST541220	C 804	19	0.6	621	2	BG933813	BG933813 SK1-0085
C 732	19	0.6	580	3	BM042038	BM042038 603616036	C 805	19	0.6	622	8	DN165414	DN165414 SGP277985
C 733	19	0.6	580	9	BH447662	BH447662 BCGFP87TR	C 806	19	0.6	622	8	BB517806	BB517806 BB517806
C 734	19	0.6	581	2	BG202714	BG202714 RST22080	C 807	19	0.6	623	7	CK961454	CK961454 4102545_B
C 735	19	0.6	581	3	BP214435	BP214435 BP214435	C 808	19	0.6	623	7	A2709950	A2709950 RPCI-24-1
C 736	19	0.6	581	3	BP215536	BP215536 BP215536	C 809	19	0.6	623	9	BH168839	BH168839 VV_SBA000
C 737	19	0.6	582	3	BP214287	BP214287 BP214287	C 810	19	0.6	623	3	BH266885	BH266885 CH230-43M
C 738	19	0.6	582	3	BP222685	BP222685 BP222685	C 811	19	0.6	624	3	B0440119	B0440119 B0440119
C 739	19	0.6	582	3	BP293425	BP293425 BP293425	C 812	19	0.6	625	6	CA767825	CA767825 8aa1e1a00
C 740	19	0.6	582	3	BP294277	BP294277 BP294277	C 813	19	0.6	625	6	CA768179	CA768179 8aa1imga00
C 741	19	0.6	582	3	BP294281	BP294281 BP294281	C 814	19	0.6	626	9	BH168239	BH168239 RPCI-24-1
C 742	19	0.6	582	3	BP376655	BP376655 BP376655	C 815	19	0.6	626	9	BH168513	BH168513 VV_SBA000
C 743	19	0.6	583	1	AU262739	AU262739 AU262739	C 816	19	0.6	627	5	CA045007	CA045007 8aa1p1b05
C 744	19	0.6	583	8	BP215710	BP215710 BP215710	C 817	19	0.6	628	3	B0385399	B0385399 B0385399
C 745	19	0.6	585	8	DR545737	DR545737 WS0011.B2	C 818	19	0.6	628	3	B0440733	B0440733 B0440733
C 746	19	0.6	587	3	B0381331	B0381331 B0381331	C 819	19	0.6	628	5	BX316959	BX316959 BX316959
C 747	19	0.6	587	3	B0437182	B0437182 B0437182	C 820	19	0.6	628	5	B2126781	B2126781 CH230-309
C 748	19	0.6	588	5	B0083790	B0083790 8a1r31a03.	C 821	19	0.6	629	3	B0608089	B0608089 B0608089
C 749	19	0.6	588	5	B0355579	B0355579 B0355579	C 822	19	0.6	629	3	B0379241	B0379241 B0379241
C 750	19	0.6	588	6	CB440909	CB440909 691222_MA	C 823	19	0.6	629	3	B0625121	B0625121 B0625121
C 751	19	0.6	589	6	CF125591	CF125591 UI-HR-EL0	C 824	19	0.6	629	10	CG798678	CG798678 ZMMBBD342
C 752	19	0.6	590	11	DR13B1T	DR13B1T Danio rer	C 825	19	0.6	630	11	DE090220	DE090220 Oryzias 1

C 826	19	0.6	631	7	CV046305	CV046305 EST 8012	C 899	19	0.6	665	7	CO257262	CO257262 WS0085_B2
C 827	19	0.6	631	10	AC240743	AC240743 Lotus CCR	C 900	19	0.6	666	3	BU378796	BU378796
C 828	19	0.6	633	5	CA037935	CA037935 sea11na01	C 901	19	0.6	666	6	CD814557	CD814557 BN15_023H
C 829	19	0.6	634	2	BF296910	BF296910 044PBD08	C 902	19	0.6	666	8	CX546114	CX546114 UCRPT01_5
C 830	19	0.6	636	5	BX856958	BX856958 BX856958	C 903	19	0.6	666	11	CR232846	CR232846 Forward B
C 831	19	0.6	637	7	CK225647	CK225647 704268151	C 904	19	0.6	667	9	CE127593	CE127593 t1gr-g88-
C 832	19	0.6	638	1	AL895643	AL895643 AL895643	C 905	19	0.6	667	11	CR277407	CR277407 Forward B
C 833	19	0.6	638	2	BF297822	BF297822 056PBD10	C 906	19	0.6	668	7	CR372282	CR372282
C 834	19	0.6	639	5	BX869740	BX869740 BX869740	C 907	19	0.6	669	3	BU384573	BU384573
C 835	19	0.6	640	2	BH256749	BH256749 CH230-243	C 908	19	0.6	669	6	CD511102	CD511102 oneRTY00
C 836	19	0.6	640	9	BF296061	BF296061 030PBG01	C 909	19	0.6	669	10	CE332869	CE332869 t1gr-g88-
C 837	19	0.6	640	5	BU573145	BU573145 PA_BA000	C 910	19	0.6	670	6	CA361761	CA361761 635651 NC
C 838	19	0.6	640	6	CA363170	CA363170 637671 NC	C 911	19	0.6	670	6	CB925035	CB925035 ABA1_29_C
C 839	19	0.6	641	6	CB377311	CB377311 CmaB1_36	C 912	19	0.6	671	3	BU381149	BU381149
C 840	19	0.6	641	10	CE692050	CE692050 t1gr-g88-	C 913	19	0.6	672	5	BX867950	BX867950
C 841	19	0.6	642	1	AL641723	AL641723 AL641723	C 914	19	0.6	672	10	CL318100	CL318100 ZMBBCC000
C 842	19	0.6	642	3	BU405405	BU405405 BU405405	C 915	19	0.6	673	3	BU378456	BU378456
C 843	19	0.6	642	7	CV029287	CV029287 8011_Full1	C 916	19	0.6	673	3	BU384065	BU384065
C 844	19	0.6	643	2	BF297337	BF297337 050PBD02	C 917	19	0.6	674	8	CX282176	CX282176
C 845	19	0.6	643	3	BU441266	BU441266 BU441266	C 918	19	0.6	674	8	DR552513	DR552513
C 846	19	0.6	643	5	BX316958	BX316958 BX316958	C 919	19	0.6	674	8	EX186586	EX186586
C 847	19	0.6	645	1	AW348152	AW348152 GM210001A	C 920	19	0.6	675	5	BX863222	BX863222
C 848	19	0.6	645	3	BU911906	BU911906 BU911906	C 921	19	0.6	676	5	BU601934	BU601934
C 849	19	0.6	645	10	CM166128	CM166128 104_574_1	C 922	19	0.6	676	10	CM286496	CM286496
C 850	19	0.6	645	11	DE028101	DE028101 Branch108	C 923	19	0.6	677	7	CM675929	CM675929 A097TB02-
C 851	19	0.6	647	2	BF297165	BF297165 048PBA11	C 924	19	0.6	678	7	CK559907	CK559907 twpBD_00
C 852	19	0.6	647	3	BU437409	BU437409 BU437409	C 925	19	0.6	679	9	BH965026	BH965026 odj25901_
C 853	19	0.6	648	2	BF296658	BF296658 040PBD02	C 926	19	0.6	681	3	BU373057	BU373057
C 854	19	0.6	648	2	BF297726	BF297726 055PBD06	C 927	19	0.6	681	3	BU408091	BU408091
C 855	19	0.6	648	3	BU378497	BU378497 BU378497	C 928	19	0.6	681	8	DR429252	DR429252 nax14d03_
C 856	19	0.6	650	2	BF113497	BF113497 EST441087	C 929	19	0.6	681	10	AG276945	AG276945 Mus_muscu
C 857	19	0.6	650	6	CD595531	CD595531 RK097A2C0	C 930	19	0.6	682	3	BU528261	BU528261
C 858	19	0.6	650	6	CD595647	CD595647 RK097A4C0	C 931	19	0.6	682	6	CD510873	CD510873
C 859	19	0.6	650	7	CK243465	CK243465 EST727102	C 932	19	0.6	682	7	CR789861	CR789861 DKF2p4591
C 860	19	0.6	650	9	AQ898457	AQ898457 HS_3135_B	C 933	19	0.6	682	8	CX079050	CX079050 yda06h03_
C 861	19	0.6	650	9	CE141998	CE141998 t1gr-g88-	C 934	19	0.6	682	10	CM532704	CM532704 OP_BA003
C 862	19	0.6	650	10	BX217474	BX217474 Danilo rex	C 935	19	0.6	683	3	BU385379	BU385379
C 863	19	0.6	651	6	CB465691	CB465691 727754_MA	C 936	19	0.6	684	3	BU358242	BU358242
C 864	19	0.6	651	6	CD415012	CD415012 Gm_CK5042	C 937	19	0.6	684	7	CK225713	CK225713
C 865	19	0.6	651	8	DN091459	DN091459 JGI_CABE4	C 938	19	0.6	685	9	AQ419762	AQ419762 RPCI_11-1
C 866	19	0.6	652	6	CF808984	CF808984 PDB041X1	C 939	19	0.6	686	3	BU380603	BU380603
C 867	19	0.6	652	7	CN074357	CN074357 EC0CBA005	C 940	19	0.6	686	6	CA833984	CA833984 MCS003B05
C 868	19	0.6	653	10	CE441108	CE441108 t1gr-g88-	C 941	19	0.6	686	9	CE106835	CE106835 t1gr-g88-
C 869	19	0.6	653	1	AL868283	AL868283 AL868283	C 942	19	0.6	687	8	DR549055	DR549055
C 870	19	0.6	653	2	BE795889	BE795889 601591238	C 943	19	0.6	687	9	CE046764	CE046764 t1gr-g88-
C 871	19	0.6	655	3	BF298808	BF298808 021PBF05	C 944	19	0.6	689	2	BE794870	BE794870
C 872	19	0.6	655	3	BU373645	BU373645 BU373645	C 945	19	0.6	689	5	BU342534	BU342534
C 873	19	0.6	655	10	AC311895	AC311895 Pan_t1gr01	C 946	19	0.6	689	9	BH067015	BH067015
C 874	19	0.6	655	10	AC311895	AC311895 Pan_t1gr01	C 947	19	0.6	690	6	CA384098	CA384098
C 875	19	0.6	655	10	AC311895	AC311895 Pan_t1gr01	C 948	19	0.6	690	11	CR882501	CR882501 Sue_acroF
C 876	19	0.6	656	5	BU708132	BU708132 UI-M_FCO-	C 949	19	0.6	691	9	BZ012158	BZ012158 oel34a06_
C 877	19	0.6	656	10	CM296077	CM296077 104_777_1	C 950	19	0.6	691	9	CA408042	CA408042 PUNHP26TB
C 878	19	0.6	657	3	BU378935	BU378935 BU378935	C 951	19	0.6	693	9	AZ337730	AZ337730 IM0068G03
C 879	19	0.6	657	3	BU383584	BU383584 BU383584	C 952	19	0.6	693	3	BU383155	BU383155
C 880	19	0.6	658	7	CX690110	CX690110 ydc77h05_	C 953	19	0.6	695	3	BU385722	BU385722
C 881	19	0.6	658	7	CV278110	CV278110 WS0145_B2	C 954	19	0.6	695	3	BU385322	BU385322 603856178
C 882	19	0.6	659	5	BW725705	BW725705 BW725705	C 955	19	0.6	696	10	CE552966	CE552966 t1gr-g88-
C 883	19	0.6	660	10	BX222795	BX222795 Danilo rex	C 956	19	0.6	696	6	BX865390	BX865390
C 884	19	0.6	661	7	CO474036	CO474036 GQ0047_B3	C 957	19	0.6	696	6	CA835339	CA835339 MCS032H09
C 885	19	0.6	661	9	AZ841375	AZ841375 2M0139N14	C 958	19	0.6	697	1	AV712582	AV712582
C 886	19	0.6	662	3	BU384148	BU384148 BU384148	C 959	19	0.6	697	6	CA347899	CA347899
C 887	19	0.6	662	3	BU444846	BU444846 BU444846	C 960	19	0.6	700	3	BU444063	BU444063
C 888	19	0.6	662	10	CM844297	CM844297 GTI0860_D	C 961	19	0.6	700	8	DR181615	DR181615 RTMNT01_4
C 889	19	0.6	663	3	CC398529	CC398529 PUNHP26TB	C 962	19	0.6	700	9	CC157665	CC157665 IG25B05_9
C 890	19	0.6	664	2	BF346106	BF346106 602018652	C 963	19	0.6	701	2	BG333882	BG333882 SKI_0160
C 891	19	0.6	664	3	BU383360	BU383360 BU383360	C 964	19	0.6	701	3	BI509891	BI509891
C 892	19	0.6	664	9	AO371673	AO371673 RPCI11-15	C 965	19	0.6	701	7	CK476706	CK476706
C 893	19	0.6	664	9	CE050612	CE050612 t1gr-g88-	C 966	19	0.6	701	9	BZ779739	BZ779739 i134c07_9
C 894	19	0.6	665	2	BG323748	BG323748 602421851	C 967	19	0.6	701	9	CC408044	CC408044 PUNHP26TB
C 895	19	0.6	665	3	BU066530	BU066530 BU066530	C 968	19	0.6	702	2	BG670900	BG670900 DRNBIC12
C 896	19	0.6	665	3	BU384939	BU384939 BU384939	C 969	19	0.6	702	3	BU385920	BU385920
C 897	19	0.6	665	6	CA256109	CA256109 SCULPL418	C 970	19	0.6	702	10	CE766295	CE766295 OC_BA012
C 898	19	0.6	665	6	CA783344	CA783344 B8T22h10_	C 971	19	0.6	703	3	BU384627	BU384627

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973	19	0.6	704	6	CA078493	SCRLAM10
974	19	0.6	704	6	CA373841	648097 NC
975	19	0.6	704	9	BH365420	CH230-28G
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977	19	0.6	704	10	AG134457	AG134457 Pan t1c01
978	19	0.6	706	9	BH976476	odh67a02.
979	19	0.6	707	3	BH36135	BH36135
980	19	0.6	707	3	BH379664	BH379664
981	19	0.6	707	3	BH441241	BH441241
982	19	0.6	707	7	CR427336	CR427336
983	19	0.6	708	3	BH386122	BH386122
984	19	0.6	708	3	BH386369	BH386369
985	19	0.6	708	10	CE324682	CE324682 t1gr-g8s-
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987	19	0.6	709	8	CE65835	CE65835 HESCA 6 G
988	19	0.6	709	9	AZ960288	AZ960288 2M028T15
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992	19	0.6	710	8	DR548835	MS03213.C
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997	19	0.6	713	3	BH380398	BH380398
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## ALIGNMENTS

RESULT 1  
LOCUS CR749572 5829 bp mRNA linear HTC 19-AUG-2004  
DEFINITION Homo sapiens mRNA; cDNA DKFZp686K087 (from clone DKFZp686K087).  
ACCESSION CR749572  
VERSION CR749572.1 GI:51476810  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 5829)  
Pouetka,A., Albert,R., Moosmayer,P., Schnupp,I., Wellenreuther,R.,  
Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
Wiemann,S.  
The German CDNA Consortium  
Submitted (17-AUG-2004) MIRS, Ingolstaedter Landstr.1, D-85764  
Neuberberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFZp686K087) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp686K087  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

## FEATURES

## Source

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/issue\_type="retina"  
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DH10B; sites SfiI + SfiIb"

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LOCUS AY415971  
DEFINITION Homo sapiens IMPG1 gene, VIRIDAL TRANSCRIPT, partial sequence.  
ACCESSION AY415971  
VERSION AY415971.1 GI:39771931  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1665)  
Clark,A.G., Gianwskt,S., Nielson,R., Thomas,P., Kejarwal,A.,  
Todd,M.A., Tanendrum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Perliera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.D.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302

REFERENCE 2 (bases 1 to 1665)  
AUTHORS Clark, A.G., Glauswieski, S., Nijelso, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.O.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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Matches 1506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DKFZP686P2496.5', mRNA sequence.  
ACCESSION EXS10244  
VERSION EXS10244.1 GI:32050551  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo  
1 (Bases 1 to 690)  
Poulet, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
Mewes, H.W., Well, B., Amid, C., Oesanger, A., Fobo, G., Han, M. and  
Wiemann, S.

TITLE EST (Pouscka, A., Albert, R., Moosmayer, P., Schupp, I.,  
Wellenreuther, R., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MTPS

MTPS  
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No 5' sequence available.  
This clone (DKFZ686P2496) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

source

1. 690  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZ686P2496"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hicc3)"  
/note="Vector: pTriplEx2; Site\_1: SfiI; Site\_2: SfiIb;  
cDNA-collection"

## ORIGIN

Query Match 19.0%; Score 634; DB 5; Length 690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCAAGAGGTTATCTCTCAATCATCTGTATCATATATATATTTTTCACATTTTC 60  
DB 57 TAAACCAAGAGGTTATCTCTCAATCATCTGTATCATATATATATTTTTCACATTTTC 116  
QY 61 TGTACTTTTATATGATTTGAGGTTGTTCTGTATGTTATACAAATTTTTCCTCA 120  
DB 117 TGTACTTTTATATGATTTGAGGTTGTTCTGTATGTTATACAAATTTTTCCTCA 176  
QY 121 AAAAGCCAGATGTATTTGGAAGAGAGCTATTTTGTATTTTGGATTTTTCCTCA 180  
DB 177 AAAAGCCAGATGTATTTGGAAGAGAGCTATTTTGTATTTTGGATTTTTCCTCA 236  
QY 181 AGTTCAAGAACCAAGATATCTCATTTAATATATCAATTTTGAATTAAGACATAGA 240  
DB 237 AGTTCAAGAACCAAGATATCTCATTTAATATATCAATTTTGAATTAAGACATAGA 296  
QY 241 CAATCCCCCAAGAAATGAACTGAAAGTACTGAAATATGTAATGTAATGTAATG 300  
DB 297 CAATCCCCCAAGAAATGAACTGAAAGTACTGAAATATGTAATGTAATGTAATG 356  
QY 301 GAGACGATATTCGATTTGGCAAGATGGAACAAAGATCCGATTTTCCCAAGGG 360  
DB 357 GAGACGATATTCGATTTGGCAAGATGGAACAAAGATCCGATTTTCCCAAGGG 416  
QY 361 GGTAAAGTCTGTCCACAGAAATCATGAAACAGATTTTGAACAGTCTTCAAGCTATTA 420  
DB 417 GGTAAAGTCTGTCCACAGAAATCATGAAACAGATTTTGAACAGTCTTCAAGCTATTA 476  
QY 421 TAGATTGAGAGTGTCTCAGAGCAATATGGAAGCATATCGGATTTTCTGGATGCAAT 480  
DB 477 TAGATTGAGAGTGTCTCAGAGCAATATGGAAGCATATCGGATTTTCTGGATGCAAT 536  
QY 481 CCTGACACAGGGGATATCAGAGCTGGGTCAAGCATCTGACAGCAGAGACCTTCTGCT 540  
DB 537 CCTGACACAGGGGATATCAGAGCTGGGTCAAGCATCTGACAGCAGAGACCTTCTGCT 596  
QY 541 CTTTGACATTTGAAAAAATCTTCAGCAATTTCCAGAGCACTTGATCTTCTCCAGCAG 600  
DB 597 CTTTGACATTTGAAAAAATCTTCAGCAATTTCCAGAGCACTTGATCTTCTCCAGCAG 656

QY 601 AATTAACAGAGAGGTTCTCTGACAGAAAGAT 634  
DB 657 AATTAACAGAGAGGTTCTCTGACAGAAAGAT 690

RESULT 4  
LOCUS B0639265 626 bp mRNA 1linear EST 15-JUL-2002  
DEFINITION hd33d04.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
Homo sapiens cDNA clone hd33d04 5', mRNA sequence.  
B0639265  
ACCESSION B0639265.1 GI:21763724  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

REFERENCE  
AUTHORS Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behl, A.,  
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
TITLE Expressed sequence tag analysis of human retina for the NEIBank  
PROJECT: Retbindin, an abundant, novel retinal cDNA and alternative  
splicing of other retina-preferred gene transcripts  
Mol. Vis. 8 (4), 196-204 (2002)  
12107411

## COMMENT

Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: giseme@helix.nih.gov  
Plate: 33 row: d column: 04  
Seq primer: MJ391 reverse primer (ABI).  
Location/Qualifiers

## FEATURES

source

1. 626  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="hd33d04"  
/clone\_lib="hd33d04"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retina cDNA (Un-normalized,  
unamplified): hd/he"  
/note="Organ: Eye; Vector: pSPORT1. Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTAGTTCATGATTCGACGCGCCGCTT]5-3'. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 18.8%; Score 626; DB 5; Length 626;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 968 ACCAGAGCTGACAGAAAGTCCCACTTCAGATGCAAAAATATTAAAGAACTTCG 1027  
DB 1 ACCAGAGCTGACAGAAAGTCCCACTTCAGATGCAAAAATATTAAAGAACTTCG 60  
QY 1028 GATTCAAAAAAATCATGTGTAGATTAGCAAGAAAGAAAGAAAGTGCCTAAGCT 1087  
DB 61 GATTCAAAAAAATCATGTGTAGATTAGCAAGAAAGAAAGAAAGTGCCTAAGCT 120

QY 1088 CCACAGAGATGCACTTACGCGCATCTTTAAGAGACAGAGTGCAGAGCAAAAAGCCCTG 1147  
DB 121 CCACAGAGATGCACTTACGCGCATCTTTAAGAGACAGAGTGCAGAGCAAAAAGCCCTG 180  
QY 1148 CAGAGTACCTCTCTGCTTTTGTATCCAAACAAATTTGAAAGTGAAGTCTATCATGGA 1207  
DB 181 CAGAGTACCTCTCTGCTTTTGTATCCAAACAAATTTGAAAGTGAAGTCTATCATGGA 240  
QY 1208 CCATGAGAGAGGACAGAGCAACGAAATCTATCTGACAGCTGACAGCTCAAAAAGCTGA 1267  
DB 241 CCATGAGAGAGGACAGAGCAACGAAATCTATCTGACAGCTGACAGCTCAAAAAGCTGA 300  
QY 1268 TCAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGAGCAATTGCACTGATG 1327  
DB 301 TCAGCAAAAGCACTAAGAGAAACAATCTTTGATGTGGGAGCAATTGCACTGATG 360  
QY 1338 AAATGCTGATCACTGCGCAGCTTTGCTGACAGCCCAATCAGAGCTGCCACATCTT 1387  
DB 361 AAATGCTGATCACTGCGCAGCTTTGCTGACAGCCCAATCAGAGCTGCCACATCTT 420  
QY 1388 TTGCTGTATATACAGAGATGCTACTTTGAGTCCGAATCTTCTCTGTTGAACCCGAC 1447  
DB 421 TTGCTGTATATACAGAGATGCTACTTTGAGTCCGAATCTTCTCTGTTGAACCCGAC 480  
QY 1448 TTGAGACAGTGGACGAGAGAGAGATGCTACTGACAGCTTTGCTGCTCACTGCTA 1507  
DB 481 TTGAGACAGTGGACGAGAGAGAGATGCTACTGACAGCTTTGCTGCTCACTGCTA 540  
QY 1508 TGGCTCTACCTCCCTGTGACAGAGCTCCACCTTTCTTATGAGCATCAAGCATCTTCTG 1567  
DB 541 TGGCTCTACCTCCCTGTGACAGAGCTCCACCTTTCTTATGAGCATCAAGCATCTTCTG 600  
QY 1568 TGACTGATTAAGGACACACAGATACA 1593  
DB 601 TGACTGATTAAGGACACACAGATACA 626

RESULT 5  
BM690735 675 bp mRNA linear EST 28-FEB-2002  
LOCUS UI-E-CK0-sav-c-12-0-UI.r1 UI-E-CK0 Homo sapiens cDNA clone  
DEFINITION UI-E-CK0-sav-c-12-0-UI 5', mRNA sequence.  
ACCESSION BM690735  
VERSION BM690735.1 GI:19003993  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 675)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
PUBMED 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: benito-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.regen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..675

FEATURES  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-CK0-sav-c-12-0-UI"  
/tissue\_type="Retina Foveal and Macular"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CK0"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-CK0 is a cDNA library containing the following  
tissue(s): Retina Foveal and Macular. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is CTC.  
This library was created for the program, Gene Discovery  
in the Visual System, supported by National Eye Institute  
(NEI)."

## ORIGIN

Query Match 16.8%; Score 558; DB 3; Length 675;  
Best Local Similarity 100.0%; Pred. No. 2.0e-287;  
Matches 558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2773 AAAAAGACCTTACTTATTTAAACCCCAATGCAATGAGCAATATTTTACTA 2832  
DB 52 AAAAAGACCTTACTTATTTAAACCCCAATGCAATGAGCAATATTTTACTA 111  
QY 2833 TTTTGGATGATGATCAAAATGATCATAGCCAGGTTGCTTCCACTTCCCTGAAAT 2892  
DB 112 TTTTGGATGATGATCAAAATGATCATAGCCAGGTTGCTTCCACTTCCCTGAAAT 171  
QY 2893 TTACTCAGATCACTTTGCAACAGCATAGCTTCTTATTTGAGGACGAAACAATTT 2952  
DB 172 TTACTCAGATCACTTTGCAACAGCATAGCTTCTTATTTGAGGACGAAACAATTT 231  
QY 2953 ATTGGGAAGCAAACTCTTATATGCTAGAAAGTACATTTAAAGATGACTATTACGAG 3012  
DB 232 ATTGGGAAGCAAACTCTTATATGCTAGAAAGTACATTTAAAGATGACTATTACGAG 291  
QY 3013 GGAAGTGCAGGTCTCTTAAACGATGATATGATGTGTAGGCACTGTAGTGTG 3072  
DB 292 GGAAGTGCAGGTCTCTTAAACGATGATATGATGTGTAGGCACTGTAGTGTG 351  
QY 3073 TATATAGCTCACAATGCTGATTAACAACAACTCAGTATTCAGTTATTAGGACA 3132  
DB 352 TATATAGCTCACAATGCTGATTAACAACAACTCAGTATTCAGTTATTAGGACA 411  
QY 3133 CTAGTTTATACGCACTACTGCTTACATAGTACTGTTTGTGCGCAATATCTTTGA 3192  
DB 412 CTAGTTTATACGCACTACTGCTTACATAGTACTGTTTGTGCGCAATATCTTTGA 471  
QY 3193 ATTGTTCTTTAAAGAACTGAGTTCAGATACATACATGAAATCTTACTTTTC 3252  
DB 472 ATTGTTCTTTAAAGAACTGAGTTCAGATACATACATGAAATCTTACTTTTC 531  
QY 3253 TTGTTACTACCAAAAGCTATTTTAAAGAGATGCTATGTTGGAGAAAGGGAAGTTGTA 3312  
DB 532 TTGTTACTACCAAAAGCTATTTTAAAGAGATGCTATGTTGGAGAAAGGGAAGTTGTA 591  
QY 3313 CTATATGACATATCAAT 3330  
DB 592 CTATATGACATATCAAT 609

RESULT 6  
BM695987

LOCUS BM695987 633 bp mRNA linear EST 28-FEB-2002  
 DEFINITION UI-E-CL1-afa-m-11-0-UI-r1 UI-E-CL1 Homo sapiens cDNA clone  
 ACCESSION UI-E-CL1-afa-m-11-0-UI 5, mRNA sequence.  
 VERSION BM695987  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 633)  
 AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 PUBMED 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@iowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse  
 FEATURES  
 source  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-CL1-afa-m-11-0-UI"  
 /issue\_type="human retina"  
 /dev\_stage="adult"  
 /lab\_host="PH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_1ib="UI-E-CL1"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 UI-E-CL1 is a normalized cDNA library containing the  
 following tissue(s): retina. The library was constructed  
 according to Ronaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is CCGCG. This library was  
 created for the program, Gene Discovery in the Visual  
 System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 14.4%; Score 480; DB 3; Length 633;  
 Best Local Similarity 99.5%; Pred. No. 2,1e-245;  
 Matches 630; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2529 TGAATTACTGACCGTGAATATGAGAAATTTAAACATCAAGATTGGAGGAATTTAAA 2588  
 DB 1 TGAATTACTGACCGTGAATATGAGAAATTTAAACATCAAGATTGGAGGAATTTAAA 60  
 QY 2589 ACTGAAAAATGTACATATATCACTTAGGCTATCTCAAGAGATGATTTGCCCTTCTCAAG 2648  
 DB 61 ACTGAAAAATGTACATATATCACTTAGGCTATCTCAAGAGATGATTTGCCCTTCTCAAG 120  
 QY 2649 AAAATGAGACAGCATATTCATGGGTCAATCAAAATCCAGACATACATCAACTGAGA 2708  
 DB 121 AAAATGAGACAGCATATTCATGGGTCAATCAAAATCCAGACATACATCAACTGAGA 180

QY 2709 ATCAGCACACACCATTTTCAATATAGAAAGTCACTGACTTGGCAACCGAATAATTC 2768  
 DB 181 ATCAGCACACACCATTTTCAATATAGAAAGTCACTGACTTGGCAACCGAATAATTC 240  
 QY 2769 GAAAAAAGACATCTTATTTAAAGCCCAATGCATCCAGCGCAATATTTT 2828  
 DB 241 GAAAAAAGACATCTTATTTAAAGCCCAATGCATCCAGCGCAATATTTT 300  
 QY 2829 ACTATCTTGGATGATGATCAAAATGATCATTAAGCAGGTTGCTTCCACCTCCGTGA 2888  
 DB 301 ACTATCTTGGATGATGATCAAAATGATCATTAAGCAGGTTGCTTCCACCTCCGTGA 360  
 QY 2889 AATTTTACTCAGATCATTTGCAACAGACATGCTTACTTATTTGGAGATGAA 2948  
 DB 361 AATTTTACTCAGATCATTTGCAACAGACATGCTTACTTATTTGGAGATGAA 420  
 QY 2949 ATTTATGGGAAGCAACTTTATATGCTAGAAAGTCACTTAAAGTACTCTTAC 3008  
 DB 421 ATTTATGGGAAGCAACTTTATATGCTAGAAAGTCACTTAAAGTACTCTTAC 480  
 QY 3009 GCAGGAGATGCAAGGCTCTCTTAAAGCATGATGATGATGATGATGATGATGATG 3068  
 DB 481 GCAGGAGATGCAAGGCTCTCTTAAAGCATGATGATGATGATGATGATGATGATG 540  
 QY 3069 AGTGTATATATGCTTCAACATGCTGTGATTAACCAAACTCAGTATTCAGTTATGAG 3128  
 DB 541 AGTGTATATATGCTTCAACATGCTGTGATTAACCAAACTCAGTATTCAGTTATGAG 600  
 QY 3129 CACTAGTTTATATGCAACATGCTGCTTACT 3161  
 DB 601 CACTAGTTTATATGCAACATGCTGCTTACT 633

## RESULT 7

BX097138

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 472)  
 Ebert,U., Hell,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
 Radelof,U., Schneider,D. and Korn,B.  
 Human Unigeneset - RZPD3  
 Unpublished (2003)  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGP998N11359.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD.  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, primer sequence: TTTCACACAGGAAACAGCTATGAC.  
 Location/Qualifiers  
 1..472  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"



FEATURES	Source
<p>1. 653</p> <p>Location/Qualifiers</p> <p>1. 653</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="UI-E-CK0-aas-h-07-0-UI"</p> <p>/tissue_type="Retina Foveal and Macular"</p> <p>/dev_stage="adult"</p> <p>/lab_host="VDH10B (Life Technologies) (T1 phage resistant)"</p> <p>/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CK0 is a cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the</p>	<p>2900 CAGATCATTTGCAACAGCATAGCTACTTATTTGTTTAGGAGCAAGAAATTTTGGCA 2955</p> <p>421 CAGATCATTTGCAACAACTAGCTACTTATTTGTTTAGGAGCAAGAAATTTTGGCA 480</p> <p>2960 AGCAAACTCTTATATGCTAGAAAGTACATTTTAAAGATGACTACTTACGACGAGAGATG 3019</p> <p>481 AGCAAACTCTTATATGCTAGAAAGTACATTTTAAAGATGACTACTTACGACGAGAGATG 540</p> <p>3020 CAGGTCTCTTAAACGCATGGAATGTAAGTGTGTAGGACACTGTAGTGAATATATAT 3079</p> <p>541 CAGGTCTCTTAAACGCATGGAATGTAAGTGTGTAGGACACTGTAGTGAATATATAT 600</p> <p>3080 GCTCCACACTAGTCTGATATAA 3101</p> <p>601 GCTCCACACTAGTCTGATATAA 622</p>
<p>RESULT 9</p> <p>LOCUS</p> <p>BM685921</p> <p>DEFINITION</p> <p>UI-E-CK0-aas-h-07-0-UI r1 UI-E-CK0 Homo sapiens cDNA clone</p> <p>ACCESSION</p> <p>BM685921</p> <p>VERSION</p> <p>BM685921.1 GI:18995817</p> <p>KEYWORDS</p> <p>EST.</p> <p>SOURCE</p> <p>Homo sapiens (human)</p> <p>ORGANISM</p> <p>Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.</p> <p>1 (bases 1 to 653)</p> <p>Bonaldo M.F., Lennon G. and Soares M.B.</p> <p>Normalization and subtraction: two approaches to facilitate gene discovery</p> <p>Genome Res. 6 (9), 791-806 (1996)</p> <p>8889548</p> <p>Contact: Soares, MB</p> <p>Coordinated Laboratory for Computational Genomics</p> <p>University of Iowa</p> <p>375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA</p> <p>Tel: 319 335 8250</p> <p>Fax: 319 335 9565</p> <p>Email: bentto-soares@iowa.edu</p> <p>Tissue Procurement: Dr. Gregg Hageman</p> <p>cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa</p> <p>Clone Sequencing by: Dr. M. Bento Soares, University of Iowa</p> <p>CNA Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).</p> <p>Seq primer: M13 Reverse.</p>	<p>53 bp mRNA linear EST 27-FEB-2002</p>

**ORIGIN**

(DT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

Query Match	14.0%	Score 467	DB 3	Length 653
Best Local Similarity	99.5%	Pred. No. 2.1e-238		
Matches 6177	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy 2711	CAGCACACACCATATTTCAATATATAGAAAGTCACTGACTTGGACACAGTAATATCTGA	2770		
Db 12	CAGCACACACCATATTTCAATATATAGAAAGTCACTGACTTGGACACAGTAATATCTGA	71		
Qy 2771	AAAAAAAAGACCTTACTTATTTATTTAAACCCCAATGCAATCAGCGAAACATATTTTAC	2830		
Db 72	AGAAAAAGACCTTACTTATTTATTTAAACCCCAATGCAATCAGCGAAACATATTTTAC	131		
Qy 2831	TATCTTGGATGATAGTCAAAATGATCATTAAGCAGGTTTGTCTCCACTTCCCTGAAA	2890		
Db 132	TATCTTGGATGATAGTCAAAATGATCATTAAGCAGGTTTGTCTCCACTTCCCTGAAA	191		
Qy 2891	TTTCTACTCAGAGTCAATTTGCAACAGCATAGCTTACTTATTTGTTAGGACTGACAT	2950		
Db 192	TTTCTACTCAGAGTCAATTTGCAACAGCATAGCTTACTTATTTGTTAGGACTGACAT	251		
Qy 2951	TTATTGGGAAGCAACCTCTTTATTTGCTAGAAAGTACATTTAAAGATGACTACTTACGC	3010		
Db 252	TTATTGGGAAGCAACCTCTTTATTTGCTAGAAAGTACATTTAAAGATGACTACTTACGC	311		
Qy 3011	AGGAGATGACAGGCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATG	3070		
Db 312	AGGAGATGACAGGCTCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATG	371		
Qy 3071	TGTATATATAGTCTCCACACTAGCTGTGATTAACAACAACTCAGTATTCAGTTATTAGGCA	3130		
Db 372	TGTATATATAGTCTCCACACTAGCTGTGATTAACAACAACTCAGTATTCAGTTATTAGGCA	431		
Qy 3131	CACATAGTTTATATAGGCACTTACGTCTTACATAGTACCTGTTTGTGCGCAATATCTTT	3190		
Db 432	CACATAGTTTATATAGGCACTTACGTCTTACATAGTACCTGTTTGTGCGCAATATCTTT	491		
Qy 3191	GAATTTGTTCTTTAAAGAACTGAGTTCAGATGACATACATGAGAAATCTTACTTT	3250		
Db 492	GAATTTGTTCTTTAAAGAACTGAGTTCAGATGACATACATGAGAAATCTTACTTT	551		
Qy 3251	TCTTGTATCTACACAAAGCTATTTTAAAGAGATGCTATGTTGGAGAGGCGCAAGTTG	3310		
Db 552	TCTTGTATCTACACAAAGCTATTTTAAAGAGATGCTATGTTGGAGAGGCGCAAGTTG	611		
Qy 3311	TACTATATGACATATATCAAT 3330			
Db 612	TACTATATGACATATATCAAT 631			
RESULT 10				
LOCUS B1752112	836 bp	mRNA	linear	EST 25-SEP-2001
DEFINITION	603022336F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:519291 5',			
ACCESSION	B1752112			
VERSION	B1752112.1			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
TITLE	Hominidae; Homo.			
JOURNAL	1. (bases 1 to 836)			
COMMENT	NIH-MGC http://mgc.ncl.nih.gov/			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Straubeberg, Ph.D.			

Email: c9apbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Inqyle Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
 http://image.llnl.gov  
 Plate: ILNL1482 row: 1 column: 16  
 High quality sequence stop: 822.

## FEATURES

source

1..836  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5192991"  
 /lab\_host="DH10B"  
 /clone\_1lb="NIH\_MGC\_114"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: BclRV (destroyed); RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT  
 primed and directionally cloned (BclRV site is destroyed  
 upon cloning). Average insert size 1.5 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 019. Note:  
 this is a NIH\_MGC Library."

## ORIGIN

Query Match

Best Local Similarity 13.0%; Score 433; DB 3; Length 836;  
 Matches 533; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 2237 CTGATCAACGACATCCCTGCAAGTCTCTGGCTGGGCGCAATTTGCCCAATGTGAAGA 2296
DB 127 CTGATCAACGACATCCCTGCAAGTCTCTGGCTGGGCGCAATTTGCCCAATGTGAAGA 186
QY 2297 AGCAACGAGCTGAGAAAGCGAGTGTGCGTGCACCAACAGATATGACAGCGGAGGCC 2356
DB 187 AGCAACGAGCTGAGAAAGCGAGTGTGCGTGCACCAACAGATATGACAGCGGAGGCC 246
QY 2357 TGGACGCTGTGAAACGAGGCTCTGTGTGGCCCTGGCAAAAGAAATGCGAGTCTTCACG 2416
DB 247 TGGACGCTGTGAAACGAGGCTCTGTGTGGCCCTGGCAAAAGAAATGCGAGTCTTCACG 306
QY 2417 GAAAGGAGCTCCATGCAAGTGGCCGATCACTCTGAAAATCAAGATCAAACTAGTG 2476
DB 307 GAAAGGAGCTCCATGCAAGTGGCCGATCACTCTGAAAATCAAGATCAAACTAGTG 366
QY 2477 TTAATAAGTCCAAATCAAAATTAACAAGTAACTAGTAAGAAATTCGATTTAC 2536
DB 367 TTAATAAGTCCAAATCAAAATTAACAAGTAACTAGTAAGAAATTCGATTTAC 426
QY 2537 TGAACCTAGATATGAAGAAATTTAACCATCAAGATTTGGAGAGAAATTTAAACTGAAA 2596
DB 427 TGAACCTAGATATGAAGAAATTTAACCATCAAGATTTGGAGAGAAATTTAAACTGAAA 486
QY 2597 TGTACCAATATCACTTAGGCTATCTCAAGAGATGATTTGGCTTCTCAAGAGAAATGGA 2656
DB 487 TGTACCAATATCACTTAGGCTATCTCAAGAGATGATTTGGCTTCTCAAGAGAAATGGA 546
QY 2657 GACAGGATATTCATGGGTCACTCAAAATCAAGATCAATGCAAGTCAAGCTGAGATCAGAC 2716
DB 547 GACAGGATATTCATGGGTCACTCAAAATCAAGATCAATGCAAGTCAAGCTGAGATCAGAC 606
QY 2717 ACACCATATTTCAATATGAAGAGTCACTGTACTTGGCAACAGATTAATTTGAA 2771
DB 607 ACACCATATTTCAATATGAAGAGTCACTGTACTTGGCAACAGATTAATTTGAA 661

```

RESULT 11  
 BM726533  
 LOCUS

BM726533 422 bp mRNA linear EST 01-MAR-2002

## DEFINITION

UI-E-EJ0-ai1-e-04-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone  
 UI-E-EJ0-ai1-e-04-0-UI 5', mRNA sequence.

## ACCESSION

BM726533  
 BM726533.1 GI:19047866

## VERSION

EST.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens  
 Buiakytola; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

## REFERENCES

1 (bases 1 to 422)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.

## AUTHORS

Normalization and subtraction: two approaches to facilitate gene  
 discovery

## JOURNAL

Genome Res. 6 (9), 791-806 (1996)

## COMMENT

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

## FEATURES

source

1..422  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-EJ0-ai1-e-04-0-UI"  
 /tissue\_type="fetal eyes, lens, eye anterior segment,  
 optic nerve, retina, Retina foveal and Macular, RPS and  
 Choroid"  
 /dev\_stage="fetal and adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_1lb="UI-E-EJ0"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site 1: BclRV; Site 2: Not I;  
 UI-E-EJ0 is a subcloned cDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an BclRV adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are: fetal eyes,  
 AGATCCAGAG; lens, CGATAGCCG; eye anterior segment,  
 AATGCCGAT; optic nerve, CCGTATGAG; retina, CCGCG;  
 foveal and Macular, GTCC; RPS and Choroid, ACCCA. This  
 library was created for the program, Gene Discovery in the  
 Visual System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match

Best Local Similarity 12.3%; Score 409; DB 3; Length 422;  
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1566 TCTGACTGATCAAGGCAACCAAGATACATGAGCCACTGACCAAGCAATGCTAGTACCGG 1625
DB 1 TCTGACTGATCAAGGCAACCAAGATACATGAGCCACTGACCAAGCAATGCTAGTACCGG 60
QY 1626 GCTACCAATCCCAACCAAGTATATCTGCAATCAAGCAATGCTGAGAAATTTACA 1685
DB 61 GCTACCAATCCCAACCAAGTATATCTGCAATCAAGCAATGCTGAGAAATTTACA 120

```

QY 1686 TCACCTGATCTTTCAGATGACGCCGATCAAGTGCAGGCGAAGATATGCTCAGACA 1745  
 |||  
 DB 121 TCACCTGATCTTTCAGATGACGCCGATCAAGTGCAGGCGAAGATATGCTCAGACA 180  
 |||  
 QY 1746 CCTAGATGAATGATCTGCTGACACTCTGCGCCCATCTGAGGTACAGAGCTCAGCGA 1805  
 |||  
 DB 181 CCTAGATGAATGATCTGCTGACACTCTGCGCCCATCTGAGGTACAGAGCTCAGCGA 240  
 |||  
 QY 1806 ATATGTTTCTGCTCCGAGATCATTTCTTGAGAGATACCACTCTGCTCAGCTTTACAGTA 1865  
 |||  
 DB 241 ATATGTTTCTGCTCCGAGATCATTTCTTGAGAGATACCACTCTGCTCAGCTTTACAGTA 300  
 |||  
 QY 1866 TATCACCACATGTTCTATGACATTTGCCCCCAAGGGCCGAGACTGTGTGTTCTTCAG 1925  
 |||  
 DB 301 TATCACCACATGTTCTATGACATTTGCCCCCAAGGGCCGAGACTGTGTGTTCTTCAG 360  
 |||  
 QY 1926 TCTGCTGTTGCTATACATGAGCTTCTCACAAGCACTGTTCAACAAAGC 1974  
 |||  
 DB 361 TCTGCTGTTGCTATACATGAGCTTCTCACAAGCACTGTTCAACAAAGC 409  
 |||

RESULT 12  
 CA393958 508 bp mRNA linear EST 06-NOV-2002  
 LOCUS CA393958  
 DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs44904  
 5', mRNA sequence.  
 ACCESSION CA393958  
 VERSION CA393958.1 GI:24728064  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 508)  
 Wistow, J., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.,  
 Expressed sequence tag analysis of human RPB/choroid for the  
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 Mol. Vis. 8 (4), 205-220 (2002)  
 12107410  
 JOURNAL  
 PUBMED  
 COMMENT Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: gwaem@helix.nih.gov  
 Plate: 44 row: 9 column: 04  
 Seg primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers  
 1..508  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS44904"  
 /cstatus="RBE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPB/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the Superscript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>. The library code  
 designation was cs. For this library, cDNA inserts were

## ORIGIN

cloned into the NotI/Mlu sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

Query Match 12.1%; Score 402; DB 6; Length 508;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-203;  
 Matches 452; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1442 CCCAGCTTGAGACAGTGAAGCAGAGACATGCTTACCTGACACTTCTGATCTCCAC 1501  
 |||  
 DB 1 CCCAGCTTGAGACAGTGAAGCAGAGACATGCTTACCTGACACTTCTGATCTCCAC 60  
 |||  
 QY 1502 CTGCTATGAGCTCTTACCTCTGTCGAAAGCTTCACCTTTCTTTATGATCAAGATCT 1561  
 |||  
 DB 61 CTGCTATGAGCTCTTACCTCTGTCGAAAGCTTCACCTTTCTTTATGATCAAGATCT 120  
 |||  
 QY 1562 TCTCTCTGATGATGAAGCAGACAGATGAAATGGCCATGACCAAGATGCTATGAC 1621  
 |||  
 DB 121 TCTCTCTGATGATGAAGCAGACAGATGAAATGGCCATGACCAAGATGCTATGAC 180  
 |||  
 QY 1622 CAGGCTCAGATCCCAACCAAGTGAATTTCTGCAATCAGCACTGCTTGGAAATTT 1681  
 |||  
 DB 181 CAGGCTCAGATCCCAACCAAGTGAATTTCTGCAATCAGCACTGCTTGGAAATTT 240  
 |||  
 QY 1682 CACATCCACCTGCATCTTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGTC 1741  
 |||  
 DB 241 CACATCCACCTGCATCTTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGTC 300  
 |||  
 QY 1742 GACACCTGATGAATGATCTGCTGACACTCTGCCCCCATCTGAGTACCAAGCTCA 1801  
 |||  
 DB 301 GACACCTGATGAATGATCTGCTGACACTCTGCCCCCATCTGAGTACCAAGCTCA 360  
 |||  
 QY 1802 GGAATATGTTCTGCTCCAGATCATTTCTTGAGAGATCAGCTCTGCTCAGCTTTAC 1861  
 |||  
 DB 361 TCGAATATGTTCTGCTCCAGATCATTTCTTGAGAGATCAGCTCTGCTCAGCTTTAC 420  
 |||  
 QY 1862 AGTATATACCACTAGTCTTATGACCAATGCCC 1894  
 |||  
 DB 421 AGTATATACCACTAGTCTTATGACCAATGCCC 453  
 |||

RESULT 13  
 BG196799 801 bp mRNA linear EST 21-APR-2001  
 LOCUS BG196799  
 DEFINITION RST16026 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG196799  
 VERSION BG196799.1 GI:13718486  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 801)  
 Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,  
 Whittington, J., Lerner, L., Costanzo, D., McBilligott, K., Booser, S.,  
 Mays, R., Smith, E., Veloso, N., Kliska, A., Hess, J., Cothran, K., Lo, K.,  
 Ofendischer, J., Danzig, J. and Ducar, M.,  
 Activation of genome-wide protein expression libraries using random  
 Nat. Biotechnol. 19 (5), 440-445 (2001)  
 11329013  
 JOURNAL  
 PUBMED  
 COMMENT Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scai@athersys.com  
 High quality sequence atp: 474.  
 Location/Qualifiers  
 1..801  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS44904"  
 /cstatus="RBE/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH10B"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPB/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the Superscript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>. The library code  
 designation was cs. For this library, cDNA inserts were

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HT1080"
/note="See 'Atherlys RAGE Library'
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

```

## ORIGIN

```

Query Match      11.9%; Score 395; DB 2; Length 801;
Best Local Similarity 99.5%; Pred. No. 1.1e-199;
Matches 545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2558 TTACCATCAAGATTGGAGAGAAATTTAAATCTGAAATGTACATTATTCATTAGGCT 2617
    |||||
DB 131 TTACCATCAAGATTGGAGAGAAATTTAAATCTGAAATGTACATTATTCATTAGGCT 190
    |||||
QY 2618 ATCTCAAGAGATGATTTGGCTTCTCAAGAGAAATGAGACAGCATTTTCATGGGTCA 2677
    |||||
DB 191 ATCTCAAGAGATGATTTGGCTTCTCAAGAGAAATGAGACAGCATTTTCATGGGTCA 250
    |||||
QY 2678 TCAAAATCCAGACATACAGTCAACAGTCAAGATCAGACACACATTTTCAATATAGA 2737
    |||||
DB 251 TCAAAATCCAGACATACAGTCAACAGTCAAGATCAGACACACATTTTCAATATAGA 310
    |||||
QY 2738 AGAGTCATGTACTTGGCAACAGTAATTTCTGAAAAAAGACACTTACTTATTTAA 2797
    |||||
DB 311 AGAGTCATGTACTTGGCAACAGTAATTTCTGAAAAAAGACACTTACTTATTTAA 370
    |||||
QY 2798 ACCCCAAATGCAATCGCAAAATTTTCTATCTTGTGATGATTAAGTCAAAATGATC 2857
    |||||
DB 371 ACCCCAAATGCAATCGCAAAATTTTCTATCTTGTGATGATTAAGTCAAAATGATC 430
    |||||
QY 2858 ATTAAGCCAGTTTGTTCACACCTTCCCTGAAAAATTTTACTCAAGATCATTGCAACAG 2917
    |||||
DB 431 ATTAAGCCAGTTTGTTCACACCTTCCCTGAAAAATTTTACTCAAGATCATTGCAACAG 490
    |||||
QY 2918 CATAGCTTACTTATTTAGGAGCTGAACAAATTTATTTGGAGAACAACTTTATATGC 2977
    |||||
DB 491 CATAGCTTACTTATTTAGGAGCTGAACAAATTTATTTGGAGAACAACTTTATATGC 550
    |||||
QY 2978 TAGAAAGTACATTTAAAGATGACTTACGACAGGAGATGCAAGTCTCTTAAACGCA 3037
    |||||
DB 551 TAGAAAGTACATTTAAAGATGACTTACGACAGGAGATGCAAGTCTCTTAAACGCA 610
    |||||
QY 3038 TGAATGTATGTAGTGTAGGACCTGTAGAGTGTATATATGCTCCACATACGCTGA 3097
    |||||
DB 611 TGAATGTATGTAGTGTAGGACCTGTAGAGTGTATATATGCTCCACATACGCTGA 670
    |||||
QY 3098 TAAACACA 3105
    |||||
DB 671 TAAACACA 678
    |||||

```

```

RESULT 14
BO636596      598 bp      mRNA      linear      EST 15-JUL-2002
LOCUS        hd11h02.v1 Human Retina cDNA (Un-normalized, unamblyfied): hd/he
DEFINITION   Homo sapiens cDNA clone hd11h02 5', mRNA sequence.
ACCESSION    BO636596
VERSION      BO636596.1 GI:21761055
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE    1 (bases 1 to 598)
AUTHORS     Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,

```

```

TITLE
JOURNAL
PUBMED
COMMENT
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: g.wistow@nei.nih.gov
Plate: 11 row: h column: 02
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers

```

## FEATURES

source

```

1..598
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd11h02"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMD10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ng of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the Superscript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTGCTTCAGATGCGGCGGCGCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
```

## ORIGIN

```

Query Match      11.4%; Score 380; DB 5; Length 598;
Best Local Similarity 99.3%; Pred. No. 1.2e-191;
Matches 580; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

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QY 1490 CTGGTCTCCACCTGTATGAGCTCTTACCTCCCTGTGAGAAAGCTTCACCTTTTATAG 1549
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DB 15 CTGGTCTCCACCTGTATGAGCTCTTACCTCCCTGTGAGAAAGCTTCACCTTTTATAG 74
    |||||
QY 1550 CATCAAGATCTTCTCTCTGACTGATCAAGGACACAGATCAATGGCCACTGACCA 1609
    |||||
DB 75 CATCAAGATCTTCTCTCTGACTGATCAAGGACACAGATCAATGGCCACTGACCA 134
    |||||
QY 1610 CAATGCTAGTACAGAGGCTCAACATCCGACAGATGATTTATTTGCAATCAAGCACTGG 1669
    |||||
DB 135 CAATGCTAGTACAGAGGCGGACATCCGACAGATGATTTATTTGCAATCAAGCACTGG 194
    |||||
QY 1670 CTGTGGAAATTTACATCCACTGTGATCTTATGATGACAGCCGATCAAGTGAAGTGG 1729
    |||||
DB 195 CTGTGGAAATTTACATCCACTGTGATCTTATGATGACAGCCGATCAAGTGAAGTGG 254
    |||||
QY 1730 AAGATATGTGACACCTAGATGAAGATCTGTCTGACATCCCTGCCCCCATGTAGG 1789
    |||||
DB 255 AAGATATGTGACACCTAGATGAAGATCTGTCTGACATCCCTGCCCCCATGTAGG 314
    |||||
QY 1790 TACAGAGCTCAGCAATATGTTTCTGTCCAGATCATTTCTTGGAGATACCACTCTG 1849
    |||||
DB 315 TACAGAGCTCAGCAATATGTTTCTGTCCAGATCATTTCTTGGAGATACCACTCTG 374
    |||||
QY 1850 TCTCAGCTTTACAGTATATCAACCACTAGTTCTATGACCATTTGCCCAAGGCGGAGAGC 1909
    |||||
DB 375 TCTCAGCTTTACAGTATATCAACCACTAGTTCTATGACCATTTGCCCAAGGCGGAGAGC 434
    |||||

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QY 1910 TGGTAGTGTCTTCAGTCTGCGTGTGCTTAACATGGCTTTCACAGACCTTTCAACA 1969  
DB 435 TGGTAGTGTCTTCAGTCTGCGTGTGCTTAACATGGCTTTCACAGACCTTTCAACA 494  
QY 1970 AGAGCTCTCTGAGTACCGAGCTCTGAGACAACTTACACAGCTGTGCTTCATATC 2029  
DB 495 AGAGCTCTCTGAGTACCGAGCTCTGAGACAACTTACACAGCTGTGCTTCATATC 554  
QY 2030 TACGATCCAACTTTACAGATTTAAGCACTTGAATTAATTAC 2073  
DB 555 TACGATCCAACTTTACAGATTTAAGCACTTGAATTAATTAC 598

RESULT 15  
BU732814/c 683 bp mRNA linear EST 09-OCT-2002  
LOCUS BU732814  
DEFINITION UI-E-COI-afz-1-04-0-UI-81 UI-E-COI Homo sapiens cDNA clone  
UI-E-COI-afz-1-04-0-UI 3', mRNA sequence.  
BU732814  
VERSION BU732814  
KEYWORDS GI:23659091  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 683)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 FORWARD  
POLYA=yes.

## FEATURES

source

Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-COI-afz-1-04-0-UI"  
/tissue\_type="optic nerve"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-E-COI is a normalized cDNA library containing the  
following tissue(s): optic nerve. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
CCATTAAGTC. This library was created for the program, Gene  
Discovery in the Visual System, supported by National Eye

Institute (NEI).  
TAG\_TISSUE=human optic nerve  
TAG\_LIB=UI-E-COI  
TAG\_SEQ=CCATTAAGTC"

ORIGIN  
Query Match 11.2%; Score 373; DB 5; Length 683;  
Best Local Similarity 100.0%; Pred. No. 7e-188;  
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 620 GAAGCAAACTTTTATAGCTAGAAAGTACATTTAAAGATGACTACTTACGAGGAGA 561  
QY 3018 TCGAGGTCTCTTAAACGATGATATGATGTAGTGAAGCACTGTAGTATAT 3077  
DB 560 TCGAGGTCTCTTAAACGATGATATGATGTAGTGAAGCACTGTAGTATAT 501  
QY 3078 ATGCTTCACATGACGTCTGATTAACACAACTCAGTATTCAGTTTAAAGCACTAGT 3137  
DB 500 ATGCTTCACATGACGTCTGATTAACACAACTCAGTATTCAGTTTAAAGCACTAGT 441  
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DB 440 TTTATACGCACTACTGCTTACATATGATGACTGTTTGTGCAATTAATCTTGAATTGT 381  
QY 3198 TCTTTAAAGAACTGAGGTTGATGATACATACATGCAAAATCTTCTTGT 3257  
DB 380 TCTTTAAAGAACTGAGGTTGATGATACATACATGCAAAATCTTCTTGT 321  
QY 3258 ACTACAAAGCTATTTTAAAGATGCTATGTTGGAGAGGCGAAGTTGTACTATA 3317  
DB 320 ACTACAAAGCTATTTTAAAGATGCTATGTTGGAGAGGCGAAGTTGTACTATA 261  
QY 3318 TGACATTAATCAAT 3330  
DB 260 TGACATTAATCAAT 248

Search completed: January 13, 2006, 23:42:51  
Job time : 12744 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2006, 23:42:54 ; Search time 526 Seconds  
(without alignments)  
5123.821 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 603814 seqs, 404674181 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 1000 summaries

Database : Published Applications NA.New.\*

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Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	25	0.8	25	7	US-11-121-849-177181
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7	25	0.8	25	7	US-11-121-849-177183
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15	24	0.7	24	6	US-10-310-914A-213670
16	24	0.7	24	6	US-10-310-914A-213680
17	23	0.7	23	6	US-10-310-914A-213683
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19	23	0.7	23	6	US-10-310-914A-213671
20	23	0.7	23	6	US-10-310-914A-213679
21	23	0.7	23	6	US-10-310-914A-213691
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292	18	0.5	2768	7	US-11-136-527-2378	Sequence 2378, Ap
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307	18	0.5	166339	7	US-11-121-086-52	Sequence 87, Appl
308	18	0.5	172311	7	US-11-121-086-28	Sequence 28, Appl
309	18	0.5	172781	7	US-11-112-908-25	Sequence 25, Appl
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312	18	0.5	1080000	6	US-10-928-446A-181	Sequence 181, App
313	18	0.5	1080000	6	US-10-928-446A-183	Sequence 183, App
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392	17	0.5	1492	6	US-10-750-623-47603	Sequence 47603, A	C 465	17	0.5	4552	6	US-10-750-185-33133	Sequence 33133, A
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409	17	0.5	1699	6	US-10-750-185-59477	Sequence 59477, A	C 482	17	0.5	110847	7	US-11-121-086-11	Sequence 11, App1
410	17	0.5	1699	6	US-10-750-623-59477	Sequence 59477, A	C 483	17	0.5	114801	7	US-11-121-086-22	Sequence 22, App1
411	17	0.5	1792	6	US-10-750-185-40231	Sequence 40231, A	C 484	17	0.5	118996	7	US-11-121-086-84	Sequence 84, App1
412	17	0.5	1792	6	US-10-750-623-40231	Sequence 40231, A	C 485	17	0.5	128021	7	US-11-117-187-202	Sequence 202, App
413	17	0.5	1809	6	US-10-750-185-38041	Sequence 38041, A	C 486	17	0.5	134072	6	US-10-995-561-13312	Sequence 13312, A
414	17	0.5	1809	6	US-10-750-623-38041	Sequence 38041, A	C 487	17	0.5	139054	7	US-11-121-086-46	Sequence 46, App1
415	17	0.5	1831	6	US-10-750-185-43691	Sequence 43691, A	C 488	17	0.5	146054	7	US-11-121-086-68	Sequence 68, App1
416	17	0.5	1831	6	US-10-750-623-43691	Sequence 43691, A	C 489	17	0.5	158410	7	US-11-121-086-46	Sequence 46, App1
417	17	0.5	1856	6	US-10-750-185-60696	Sequence 60696, A	C 490	17	0.5	155786	7	US-11-121-086-92	Sequence 92, App1
418	17	0.5	1856	6	US-10-750-623-60696	Sequence 60696, A	C 491	17	0.5	160262	7	US-11-121-086-29	Sequence 29, App1
419	17	0.5	1874	7	US-11-150-533-13	Sequence 13, App1	C 492	17	0.5	165331	7	US-11-117-187-212	Sequence 212, App
420	17	0.5	1922	6	US-10-750-185-25924	Sequence 25924, A	C 493	17	0.5	176503	7	US-11-121-086-53	Sequence 53, App1
421	17	0.5	1922	6	US-10-750-623-25924	Sequence 25924, A	C 494	17	0.5	178877	7	US-11-121-086-17	Sequence 17, App1
422	17	0.5	1951	6	US-10-750-185-32751	Sequence 32751, A	C 495	17	0.5	181172	7	US-11-121-086-41	Sequence 41, App1
423	17	0.5	1951	6	US-10-750-623-32751	Sequence 32751, A	C 496	17	0.5	181172	7	US-11-121-086-41	Sequence 41, App1
424	17	0.5	2030	6	US-10-750-185-31356	Sequence 31356, A	C 497	17	0.5	190276	6	US-10-661-966-1	Sequence 1, App1
425	17	0.5	2030	6	US-10-750-623-31356	Sequence 31356, A	C 498	17	0.5	192980	7	US-11-112-908-20	Sequence 20, App1
426	17	0.5	2116	6	US-10-750-185-55368	Sequence 55368, A	C 499	17	0.5	324009	6	US-10-995-561-13204	Sequence 13204, A
427	17	0.5	2116	6	US-10-750-623-55368	Sequence 55368, A	C 500	17	0.5	394468	6	US-11-102-978-3	Sequence 3, App1
428	17	0.5	2120	6	US-10-750-185-58147	Sequence 58147, A	C 501	17	0.5	464370	6	US-10-995-561-13473	Sequence 13473, A
429	17	0.5	2120	6	US-10-750-623-58147	Sequence 58147, A	C 502	17	0.5	1145000	6	US-10-995-561-13292	Sequence 13292, A
430	17	0.5	2203	6	US-10-750-185-64144	Sequence 64144, A	C 503	17	0.5	18	6	US-10-310-914A-697614	Sequence 697614, A
431	17	0.5	2203	6	US-10-750-623-64144	Sequence 64144, A	C 504	17	0.5	19	8	US-11-101-244-108221	Sequence 108221, A
432	17	0.5	2264	6	US-10-750-185-51613	Sequence 51613, A	C 505	17	0.5	19	8	US-11-101-244-108317	Sequence 108317, A
433	17	0.5	2264	6	US-10-750-623-51613	Sequence 51613, A	C 506	17	0.5	340009	7	US-11-101-244-108317	Sequence 108317, A
434	17	0.5	2424	6	US-10-750-185-34345	Sequence 34345, A	C 507	17	0.5	394468	6	US-10-995-561-13473	Sequence 13473, A
435	17	0.5	2424	6	US-10-750-623-34345	Sequence 34345, A	C 508	17	0.5	643170	6	US-10-995-561-13292	Sequence 13292, A
436	17	0.5	2453	6	US-10-750-185-46634	Sequence 46634, A	C 509	17	0.5	1145000	6	US-10-995-561-13292	Sequence 13292, A
437	17	0.5	2453	6	US-10-750-623-46634	Sequence 46634, A	C 510	17	0.5	18	6	US-10-310-914A-697614	Sequence 697614, A
438	17	0.5	2453	6	US-10-750-185-57978	Sequence 57978, A	C 511	17	0.5	19	8	US-11-101-244-108317	Sequence 108317, A
439	17	0.5	2453	6	US-10-750-623-57978	Sequence 57978, A	C 512	17	0.5	19	8	US-11-101-244-108420	Sequence 108420, A
440	17	0.5	2453	6	US-10-750-185-43843	Sequence 43843, A	C 513	17	0.5	19	8	US-11-101-244-108520	Sequence 108520, A
441	17	0.5	2645	6	US-10-750-623-43843	Sequence 43843, A	C 514	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
442	17	0.5	2645	6	US-10-750-185-25629	Sequence 25629, A	C 515	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
443	17	0.5	2675	6	US-10-750-623-25629	Sequence 25629, A	C 516	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
444	17	0.5	2797	6	US-10-750-185-59963	Sequence 59963, A	C 517	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
445	17	0.5	2797	6	US-10-750-623-59963	Sequence 59963, A	C 518	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
446	17	0.5	3012	6	US-10-750-185-31651	Sequence 31651, A	C 519	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
447	17	0.5	3012	6	US-10-750-623-31651	Sequence 31651, A	C 520	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
448	17	0.5	3236	6	US-10-750-185-38585	Sequence 38585, A	C 521	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
449	17	0.5	3236	6	US-10-750-623-38585	Sequence 38585, A	C 522	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
450	17	0.5	3249	7	US-11-128-061-3446	Sequence 3446, App	C 523	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
451	17	0.5	3301	6	US-10-750-185-35555	Sequence 35555, A	C 524	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
452	17	0.5	3301	6	US-10-750-623-35555	Sequence 35555, A	C 525	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
453	17	0.5	3607	6	US-10-750-185-41921	Sequence 41921, A	C 526	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
454	17	0.5	3607	6	US-10-750-623-41921	Sequence 41921, A	C 527	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
455	17	0.5	3741	7	US-11-044-899-1	Sequence 1, App1	C 528	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
456	17	0.5	3874	6	US-10-750-185-34427	Sequence 34427, A	C 529	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
457	17	0.5	3874	6	US-10-750-623-34427	Sequence 34427, A	C 530	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
458	17	0.5	4049	6	US-10-750-185-46291	Sequence 46291, A	C 531	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
459	17	0.5	4049	6	US-10-750-623-46291	Sequence 46291, A	C 532	17	0.5	19	8	US-11-101-244-108619	Sequence 108619, A
460	17	0.5	4162	6	US-10-750-185-63977	Sequence 63977, A	C 533	17	0.5	19	9	US-11-083-784-108221	Sequence 108221, A
461	17	0.5	4162	6	US-10-750-623-63977	Sequence 63977, A	C 534	17	0.5	19	9	US-11-083-784-108317	Sequence 108317, A

C 535	16	0.5	19	9	US-11-083-784-108420	Sequence 108420,	608	16	0.5	201	6	US-10-995-561-33529	Sequence 33529, A
C 536	16	0.5	19	9	US-11-083-784-108520	Sequence 108520,	609	16	0.5	201	6	US-10-995-561-33802	Sequence 33802, A
C 537	16	0.5	19	9	US-11-083-784-108619	Sequence 108619,	610	16	0.5	201	6	US-10-995-561-33803	Sequence 33803, A
C 538	16	0.5	19	9	US-11-083-784-240695	Sequence 240695,	611	16	0.5	201	6	US-10-995-561-34281	Sequence 34281, A
C 539	16	0.5	19	9	US-11-083-784-461118	Sequence 461118,	612	16	0.5	201	6	US-10-995-561-36308	Sequence 36308, A
C 540	16	0.5	19	9	US-11-083-784-508525	Sequence 508525,	613	16	0.5	201	6	US-10-995-561-36365	Sequence 36365, A
C 541	16	0.5	19	9	US-11-083-784-545859	Sequence 545859,	614	16	0.5	201	6	US-10-995-561-36372	Sequence 36372, A
C 542	16	0.5	19	9	US-11-083-784-661892	Sequence 661892,	615	16	0.5	201	6	US-10-995-561-50943	Sequence 50943, A
C 543	16	0.5	19	9	US-11-083-784-859507	Sequence 859507,	616	16	0.5	201	6	US-10-995-561-51569	Sequence 51569, A
C 544	16	0.5	19	9	US-11-083-784-1069137	Sequence 1069137,	617	16	0.5	201	6	US-10-995-561-63600	Sequence 63600, A
C 545	16	0.5	19	9	US-11-083-784-1173681	Sequence 1173681,	618	16	0.5	201	6	US-10-995-561-63601	Sequence 63601, A
C 546	16	0.5	19	9	US-11-083-784-1271654	Sequence 1271654,	619	16	0.5	201	6	US-10-995-561-65783	Sequence 65783, A
C 547	16	0.5	19	9	US-11-083-784-1271701	Sequence 1271701,	620	16	0.5	201	6	US-10-995-561-74357	Sequence 74357, A
C 548	16	0.5	19	9	US-11-083-784-1466025	Sequence 1466025,	621	16	0.5	201	6	US-10-995-561-74366	Sequence 74366, A
C 549	16	0.5	19	9	US-11-083-784-1468839	Sequence 1468839,	622	16	0.5	201	6	US-10-995-561-74370	Sequence 74370, A
C 550	16	0.5	19	9	US-11-083-784-1489779	Sequence 1489779,	623	16	0.5	201	6	US-10-995-561-74384	Sequence 74384, A
C 551	16	0.5	19	9	US-11-083-784-1489789	Sequence 1489789,	624	16	0.5	201	6	US-10-995-561-74388	Sequence 74388, A
C 552	16	0.5	19	9	US-11-083-784-1489806	Sequence 1489806,	625	16	0.5	201	6	US-10-995-561-74391	Sequence 74391, A
C 553	16	0.5	19	9	US-11-083-784-1503894	Sequence 1503894,	626	16	0.5	201	6	US-10-995-561-76321	Sequence 76321, A
C 554	16	0.5	19	9	US-11-083-784-1503931	Sequence 1503931,	627	16	0.5	201	6	US-10-995-561-76654	Sequence 76654, A
C 555	16	0.5	19	9	US-11-083-784-1527897	Sequence 1527897,	628	16	0.5	201	6	US-10-995-561-77268	Sequence 77268, A
C 556	16	0.5	20	6	US-10-310-914A-50695	Sequence 50695, A	629	16	0.5	201	6	US-10-995-561-79646	Sequence 79646, A
C 557	16	0.5	20	6	US-10-750-185-11868	Sequence 11868, A	630	16	0.5	201	6	US-10-995-561-79683	Sequence 79683, A
C 558	16	0.5	21	6	US-10-750-623-11868	Sequence 11868, A	631	16	0.5	201	6	US-10-995-561-79684	Sequence 79684, A
C 559	16	0.5	21	6	US-10-310-914A-227799	Sequence 227799,	632	16	0.5	201	6	US-10-995-561-79685	Sequence 79685, A
C 560	16	0.5	21	6	US-10-310-914A-455789	Sequence 455789,	633	16	0.5	201	6	US-10-995-561-79686	Sequence 79686, A
C 561	16	0.5	21	6	US-10-310-914A-807809	Sequence 807809,	634	16	0.5	201	6	US-10-995-561-79688	Sequence 79688, A
C 562	16	0.5	22	6	US-10-310-914A-108185	Sequence 108185,	635	16	0.5	201	6	US-10-995-561-79690	Sequence 79690, A
C 563	16	0.5	22	6	US-10-310-914A-108221	Sequence 108221,	636	16	0.5	201	6	US-10-995-561-79706	Sequence 79706, A
C 564	16	0.5	22	6	US-10-310-914A-197401	Sequence 197401,	637	16	0.5	201	6	US-10-995-561-81898	Sequence 81898, A
C 565	16	0.5	22	6	US-10-310-914A-521990	Sequence 521990,	638	16	0.5	201	7	US-11-124-368A-5162	Sequence 5162, A
C 566	16	0.5	22	6	US-10-310-914A-777100	Sequence 777100,	639	16	0.5	201	7	US-11-124-368A-5261	Sequence 5261, A
C 567	16	0.5	22	6	US-10-310-914A-1017241	Sequence 1017241,	640	16	0.5	201	7	US-11-124-368A-12561	Sequence 12561, A
C 568	16	0.5	23	6	US-10-310-914A-108186	Sequence 108186,	641	16	0.5	201	7	US-11-124-368A-15455	Sequence 15455, A
C 569	16	0.5	23	6	US-10-310-914A-108198	Sequence 108198,	642	16	0.5	201	7	US-11-124-368A-17217	Sequence 17217, A
C 570	16	0.5	23	6	US-10-310-914A-134576	Sequence 134576,	643	16	0.5	201	7	US-11-124-368A-16388	Sequence 16388, A
C 571	16	0.5	23	6	US-10-310-914A-971908	Sequence 971908,	644	16	0.5	201	7	US-11-124-368A-16388	Sequence 16388, A
C 572	16	0.5	24	6	US-10-310-914A-149192	Sequence 149192,	645	16	0.5	201	7	US-11-124-368A-16951	Sequence 16951, A
C 573	16	0.5	24	6	US-10-310-914A-153952	Sequence 153952,	646	16	0.5	201	7	US-11-124-368A-20716	Sequence 20716, A
C 574	16	0.5	24	6	US-10-310-914A-227800	Sequence 227800,	647	16	0.5	342	7	US-11-102-743-6	Sequence 6
C 575	16	0.5	24	6	US-10-310-914A-353979	Sequence 353979,	648	16	0.5	396	7	US-10-750-621-465	Sequence 465, A
C 576	16	0.5	24	6	US-10-310-914A-384676	Sequence 384676,	649	16	0.5	422	7	US-11-000-688-127-289	Sequence 289, A
C 577	16	0.5	25	6	US-10-310-914A-971792	Sequence 971792,	650	16	0.5	493	6	US-10-750-185-11871	Sequence 11871, A
C 578	16	0.5	25	6	US-10-310-914A-743739	Sequence 743739,	651	16	0.5	493	6	US-10-750-185-11871	Sequence 11871, A
C 579	16	0.5	25	7	US-11-121-849-149242	Sequence 149242,	652	16	0.5	554	6	US-10-750-621-30481	Sequence 30481, A
C 580	16	0.5	25	7	US-11-121-849-593215	Sequence 593215,	653	16	0.5	554	6	US-10-750-621-30481	Sequence 30481, A
C 581	16	0.5	25	7	US-11-121-849-593215	Sequence 593215,	654	16	0.5	554	6	US-10-750-621-30481	Sequence 30481, A
C 582	16	0.5	25	7	US-11-121-849-593215	Sequence 593215,	655	16	0.5	578	7	US-11-000-688-1296	Sequence 1296, A
C 583	16	0.5	25	7	US-11-121-849-606117	Sequence 606117,	656	16	0.5	598	6	US-10-750-185-11813	Sequence 11813, A
C 584	16	0.5	25	7	US-11-136-527-314800	Sequence 314800,	657	16	0.5	598	6	US-10-750-185-11850	Sequence 11850, A
C 585	16	0.5	25	7	US-11-136-527-314813	Sequence 314813,	658	16	0.5	598	6	US-10-750-185-11894	Sequence 11894, A
C 586	16	0.5	25	7	US-11-136-527-350709	Sequence 350709,	659	16	0.5	598	6	US-10-750-621-4113	Sequence 4113, A
C 587	16	0.5	27	6	US-10-310-914A-153960	Sequence 153960,	660	16	0.5	598	6	US-10-750-621-19850	Sequence 19850, A
C 588	16	0.5	30	6	US-10-857-780-174	Sequence 174, App	661	16	0.5	598	6	US-10-750-621-19994	Sequence 19994, A
C 589	16	0.5	51	7	US-11-102-743-14	Sequence 14, App	662	16	0.5	600	6	US-10-750-185-1188	Sequence 1188, A
C 590	16	0.5	63	6	US-10-310-914A-7452	Sequence 7452, App	663	16	0.5	600	6	US-10-750-185-1188	Sequence 1188, A
C 591	16	0.5	63	6	US-10-310-914A-577	Sequence 577, App	664	16	0.5	600	6	US-10-750-185-2132	Sequence 2132, A
C 592	16	0.5	164	6	US-10-995-561-6005	Sequence 6005, App	665	16	0.5	600	6	US-10-750-621-2224	Sequence 2224, A
C 593	16	0.5	201	6	US-10-995-561-3188	Sequence 3188, App	666	16	0.5	600	6	US-10-750-185-11952	Sequence 11952, A
C 594	16	0.5	201	6	US-10-995-561-5170	Sequence 5170, App	667	16	0.5	600	6	US-10-750-185-20862	Sequence 20862, A
C 595	16	0.5	201	6	US-10-995-561-14580	Sequence 14580, A	668	16	0.5	600	6	US-10-750-185-21279	Sequence 21279, A
C 596	16	0.5	201	6	US-10-995-561-15584	Sequence 15584, A	669	16	0.5	600	6	US-10-750-621-2108	Sequence 2108, A
C 597	16	0.5	201	6	US-10-995-561-16055	Sequence 16055, A	670	16	0.5	600	6	US-10-750-621-2132	Sequence 2132, App
C 598	16	0.5	201	6	US-10-995-561-16305	Sequence 16305, A	671	16	0.5	600	6	US-10-750-621-2132	Sequence 2132, App
C 599	16	0.5	201	6	US-10-995-561-16323	Sequence 16323, A	672	16	0.5	600	6	US-10-750-621-2224	Sequence 2224, App
C 600	16	0.5	201	6	US-10-995-561-19694	Sequence 19694, A	673	16	0.5	600	6	US-10-750-621-22952	Sequence 22952, A
C 601	16	0.5	201	6	US-10-995-561-23382	Sequence 23382, A	674	16	0.5	600	6	US-10-750-621-20862	Sequence 20862, A
C 602	16	0.5	201	6	US-10-995-561-23138	Sequence 23138, A	675	16	0.5	600	7	US-11-136-527-21279	Sequence 21279, A
C 603	16	0.5	201	6	US-10-995-561-26334	Sequence 26334, A	676	16	0.5	600	7	US-11-136-527-6674	Sequence 6674, App
C 604	16	0.5	201	6	US-10-995-561-27814	Sequence 27814, A	677	16	0.5	600	7	US-11-136-527-7766	Sequence 7766, App
C 605	16	0.5	201	6	US-10-995-561-30979	Sequence 30979, A	678	16	0.5	636	6	US-10-131-826A-507	Sequence 507, App
C 606	16	0.5	201	6	US-10-995-561-30993	Sequence 30993, A	679	16	0.5	653	6	US-10-750-185-60513	Sequence 60513, A
C 607	16	0.5	201	6	US-10-995-561-33529	Sequence 33529, A	680	16	0.5	653	6	US-10-750-185-60513	Sequence 60513, A

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C 682	16	0.5	682	6	US-10-750-185-33129	Sequence 33129, A	755	16	0.5	1036	6	US-10-750-185-35248	Sequence 25248, A
C 683	16	0.5	682	6	US-10-750-623-33129	Sequence 33129, A	756	16	0.5	1036	6	US-10-750-623-35248	Sequence 25248, A
C 684	16	0.5	701	6	US-10-750-185-37301	Sequence 37301, A	757	16	0.5	1048	6	US-10-750-185-50231	Sequence 30231, A
C 685	16	0.5	701	6	US-10-750-623-37301	Sequence 37301, A	758	16	0.5	1048	6	US-10-750-623-30231	Sequence 30231, A
C 686	16	0.5	710	6	US-10-750-185-44241	Sequence 44241, A	759	16	0.5	1052	6	US-10-750-185-49803	Sequence 49803, A
C 687	16	0.5	710	6	US-10-750-623-44241	Sequence 44241, A	760	16	0.5	1052	6	US-10-750-623-35983	Sequence 35983, A
C 688	16	0.5	713	6	US-10-750-185-25895	Sequence 25895, A	761	16	0.5	1061	6	US-10-750-185-46949	Sequence 46949, A
C 689	16	0.5	713	6	US-10-750-623-25895	Sequence 25895, A	762	16	0.5	1061	6	US-10-750-623-46949	Sequence 46949, A
C 690	16	0.5	720	6	US-10-750-185-38540	Sequence 38540, A	763	16	0.5	1085	6	US-10-750-185-30543	Sequence 30543, A
C 691	16	0.5	720	6	US-10-750-623-38540	Sequence 38540, A	764	16	0.5	1085	6	US-10-750-185-30543	Sequence 30543, A
C 692	16	0.5	733	6	US-10-750-185-38689	Sequence 38689, A	765	16	0.5	1085	6	US-10-750-623-30543	Sequence 30543, A
C 693	16	0.5	733	6	US-10-750-623-38689	Sequence 38689, A	766	16	0.5	1085	6	US-10-750-623-31776	Sequence 31776, A
C 694	16	0.5	743	6	US-10-750-185-31219	Sequence 31219, A	C 767	16	0.5	1101	7	US-11-136-527-3670	Sequence 3670, Ap
C 695	16	0.5	743	6	US-10-750-623-31219	Sequence 31219, A	768	16	0.5	1101	6	US-10-750-185-39476	Sequence 39476, A
C 696	16	0.5	744	6	US-10-512-184-11	Sequence 11, Appl	769	16	0.5	1103	6	US-10-750-623-39476	Sequence 39476, A
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C 698	16	0.5	753	6	US-10-750-185-55019	Sequence 55019, A	C 771	16	0.5	1115	6	US-10-750-623-34091	Sequence 34091, A
C 699	16	0.5	753	6	US-10-750-623-55019	Sequence 55019, A	772	16	0.5	1125	7	US-11-136-527-4994	Sequence 4994, App
C 700	16	0.5	759	6	US-10-750-185-63783	Sequence 63783, A	773	16	0.5	1132	6	US-10-750-185-27461	Sequence 27461, A
C 701	16	0.5	759	6	US-10-750-623-63783	Sequence 63783, A	774	16	0.5	1132	6	US-10-750-623-27461	Sequence 27461, A
C 702	16	0.5	769	6	US-10-750-623-41177	Sequence 41177, A	775	16	0.5	1141	6	US-10-750-185-59835	Sequence 59835, A
C 703	16	0.5	769	6	US-10-750-185-41177	Sequence 41177, A	776	16	0.5	1141	6	US-10-750-623-59835	Sequence 59835, A
C 704	16	0.5	771	6	US-10-467-657-175	Sequence 175, App	C 777	16	0.5	1149	6	US-10-750-185-59099	Sequence 59099, A
C 705	16	0.5	771	6	US-10-467-657-175	Sequence 175, App	C 778	16	0.5	1149	6	US-10-750-623-59099	Sequence 59099, A
C 706	16	0.5	772	6	US-10-750-185-26624	Sequence 26624, A	C 779	16	0.5	1151	6	US-10-750-185-45225	Sequence 45225, A
C 707	16	0.5	772	6	US-10-750-623-26624	Sequence 26624, A	780	16	0.5	1151	6	US-10-750-623-45225	Sequence 45225, A
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C 712	16	0.5	795	6	US-10-750-185-59336	Sequence 59336, A	C 785	16	0.5	1157	6	US-10-750-185-59375	Sequence 59375, A
C 713	16	0.5	795	6	US-10-750-623-59336	Sequence 59336, A	786	16	0.5	1157	6	US-10-750-623-45746	Sequence 45746, A
C 714	16	0.5	795	7	US-11-188-743-14	Sequence 14, Appl	C 787	16	0.5	1157	6	US-10-750-623-45746	Sequence 45746, A
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C 719	16	0.5	821	6	US-10-750-185-52327	Sequence 52327, A	C 792	16	0.5	1187	6	US-10-750-185-37975	Sequence 37975, A
C 720	16	0.5	821	6	US-10-750-623-52327	Sequence 52327, A	C 793	16	0.5	1187	6	US-10-750-623-37975	Sequence 37975, A
C 721	16	0.5	832	6	US-10-750-185-37014	Sequence 37014, A	C 794	16	0.5	1199	6	US-10-750-185-51619	Sequence 51619, A
C 722	16	0.5	832	6	US-10-750-623-37014	Sequence 37014, A	C 795	16	0.5	1199	6	US-10-750-623-51619	Sequence 51619, A
C 723	16	0.5	860	6	US-10-750-185-45542	Sequence 45542, A	C 796	16	0.5	1210	6	US-10-750-185-51932	Sequence 51932, A
C 724	16	0.5	860	6	US-10-750-623-45542	Sequence 45542, A	C 797	16	0.5	1210	6	US-10-750-623-51932	Sequence 51932, A
C 725	16	0.5	867	6	US-10-750-185-28541	Sequence 28541, A	C 798	16	0.5	1224	6	US-10-750-185-32034	Sequence 32034, A
C 726	16	0.5	867	6	US-10-750-623-28541	Sequence 28541, A	799	16	0.5	1224	6	US-10-750-623-32034	Sequence 32034, A
C 727	16	0.5	884	6	US-10-750-185-43902	Sequence 43902, A	C 800	16	0.5	1225	6	US-10-750-185-60731	Sequence 60731, A
C 728	16	0.5	884	6	US-10-750-623-43902	Sequence 43902, A	C 801	16	0.5	1225	6	US-10-750-623-60731	Sequence 60731, A
C 729	16	0.5	897	7	US-11-128-061-270	Sequence 270, App	C 802	16	0.5	1235	6	US-10-750-185-28369	Sequence 28369, A
C 730	16	0.5	913	6	US-10-750-185-62985	Sequence 62985, A	C 803	16	0.5	1235	6	US-10-750-623-28369	Sequence 28369, A
C 731	16	0.5	913	6	US-10-750-623-62985	Sequence 62985, A	C 804	16	0.5	1247	6	US-10-118-590-15	Sequence 15, Appl
C 732	16	0.5	938	6	US-10-750-185-58777	Sequence 58777, A	C 805	16	0.5	1254	6	US-10-821-224-64	Sequence 64, App
C 733	16	0.5	938	6	US-10-750-623-58777	Sequence 58777, A	C 806	16	0.5	1263	6	US-10-750-185-33787	Sequence 33787, A
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C 735	16	0.5	939	6	US-10-750-185-33635	Sequence 33635, A	C 808	16	0.5	1267	6	US-10-750-185-50045	Sequence 50045, A
C 736	16	0.5	939	6	US-10-750-623-33635	Sequence 33635, A	C 809	16	0.5	1267	6	US-10-750-623-50045	Sequence 50045, A
C 737	16	0.5	958	6	US-10-750-185-57703	Sequence 57703, A	C 810	16	0.5	1312	6	US-10-750-185-27465	Sequence 27465, A
C 738	16	0.5	958	6	US-10-750-623-57703	Sequence 57703, A	C 811	16	0.5	1312	6	US-10-750-623-27465	Sequence 27465, A
C 739	16	0.5	958	6	US-10-750-185-57703	Sequence 57703, A	C 812	16	0.5	1334	7	US-11-136-527-3397	Sequence 3397, Ap
C 740	16	0.5	958	6	US-10-750-623-31017	Sequence 31017, A	C 813	16	0.5	1334	7	US-11-136-527-8093	Sequence 8093, Ap
C 741	16	0.5	960	7	US-11-150-883-20	Sequence 20, Appl	C 814	16	0.5	1336	6	US-10-750-185-57569	Sequence 57569, A
C 742	16	0.5	961	6	US-10-750-185-38959	Sequence 38959, A	C 815	16	0.5	1336	6	US-10-750-623-57569	Sequence 57569, A
C 743	16	0.5	961	6	US-10-750-623-38959	Sequence 38959, A	C 816	16	0.5	1342	6	US-10-750-185-57274	Sequence 57274, A
C 744	16	0.5	968	6	US-10-750-185-32656	Sequence 32656, A	C 817	16	0.5	1342	6	US-10-750-623-57274	Sequence 57274, A
C 745	16	0.5	968	6	US-10-750-623-32656	Sequence 32656, A	C 818	16	0.5	1349	7	US-11-136-527-2578	Sequence 2578, Ap
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C 748	16	0.5	991	6	US-10-944-272-82	Sequence 82, Appl	C 821	16	0.5	1361	6	US-10-750-185-35593	Sequence 35593, A
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C 751	16	0.5	996	6	US-10-750-623-48337	Sequence 48337, A	C 824	16	0.5	1362	6	US-10-750-623-41591	Sequence 41591, A
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C 828	16	0.5	1376	6	US-10-750-185-55168	Sequence 55168, A	C 901	16	0.5	1693	6	US-10-750-623-30216	Sequence 30216, A
C 829	16	0.5	1376	6	US-10-750-623-55168	Sequence 55168, A	C 902	16	0.5	1707	6	US-10-750-185-60686	Sequence 60686, A
C 830	16	0.5	1380	6	US-10-750-185-35064	Sequence 35064, A	C 903	16	0.5	1707	6	US-10-750-623-60686	Sequence 60686, A
C 831	16	0.5	1380	6	US-10-750-623-35064	Sequence 35064, A	C 904	16	0.5	1716	6	US-10-750-185-26455	Sequence 26455, A
C 832	16	0.5	1397	6	US-10-750-185-37725	Sequence 37725, A	C 905	16	0.5	1716	6	US-10-750-623-26455	Sequence 26455, A
C 833	16	0.5	1397	6	US-10-750-623-37725	Sequence 37725, A	C 906	16	0.5	1718	6	US-10-750-185-32514	Sequence 32514, A
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C 835	16	0.5	1400	7	US-11-136-527-7622	Sequence 7622, Ap	C 908	16	0.5	1733	6	US-10-750-185-30627	Sequence 30627, A
C 836	16	0.5	1400	7	US-11-136-527-7959	Sequence 7959, Ap	C 909	16	0.5	1733	6	US-10-750-623-30627	Sequence 30627, A
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C 840	16	0.5	1406	6	US-10-750-623-41344	Sequence 41344, A	C 913	16	0.5	1741	6	US-10-750-623-39483	Sequence 39483, A
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C 844	16	0.5	1411	6	US-10-750-623-59086	Sequence 59086, A	C 917	16	0.5	1755	6	US-10-750-623-60604	Sequence 60604, A
C 845	16	0.5	1418	6	US-10-750-185-53328	Sequence 53328, A	C 918	16	0.5	1759	6	US-10-750-185-57531	Sequence 57531, A
C 846	16	0.5	1418	6	US-10-750-623-53328	Sequence 53328, A	C 919	16	0.5	1759	6	US-10-750-623-57531	Sequence 57531, A
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C 848	16	0.5	1420	6	US-10-750-623-58111	Sequence 58111, A	C 921	16	0.5	1766	6	US-10-750-623-58111	Sequence 58111, A
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C 854	16	0.5	1466	6	US-10-750-623-37048	Sequence 37048, A	C 927	16	0.5	1784	6	US-10-750-623-34508	Sequence 34508, A
C 855	16	0.5	1473	6	US-10-750-185-45340	Sequence 45340, A	C 928	16	0.5	1785	7	US-11-188-743-13	Sequence 13, Appl1
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C 874	16	0.5	1526	6	US-10-750-623-24606	Sequence 24606, A	C 947	16	0.5	1865	6	US-10-750-623-52204	Sequence 52204, A
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C 880	16	0.5	1571	6	US-10-750-623-59692	Sequence 59692, A	C 953	16	0.5	1896	6	US-10-750-623-29524	Sequence 29524, A
C 881	16	0.5	1581	6	US-10-750-185-40863	Sequence 40863, A	C 954	16	0.5	1903	6	US-10-750-185-37484	Sequence 37484, A
C 882	16	0.5	1581	6	US-10-750-623-51037	Sequence 51037, A	C 955	16	0.5	1903	6	US-10-750-623-37484	Sequence 37484, A
C 883	16	0.5	1581	6	US-10-750-185-40863	Sequence 40863, A	C 956	16	0.5	1904	6	US-10-118-590-29	Sequence 29, Appl1
C 884	16	0.5	1581	6	US-10-750-623-51037	Sequence 51037, A	C 957	16	0.5	1905	6	US-10-750-185-46690	Sequence 46690, A
C 885	16	0.5	1593	6	US-10-750-185-50074	Sequence 50074, A	C 958	16	0.5	1905	6	US-10-750-623-46690	Sequence 46690, A
C 886	16	0.5	1593	6	US-10-750-623-50074	Sequence 50074, A	C 959	16	0.5	1910	7	US-11-136-527-8	Sequence 8, Appl1
C 887	16	0.5	1596	6	US-10-750-185-53539	Sequence 53539, A	C 960	16	0.5	1911	7	US-11-136-527-395	Sequence 395, Ap
C 888	16	0.5	1596	6	US-10-750-623-53539	Sequence 53539, A	C 961	16	0.5	1923	6	US-10-750-185-28658	Sequence 28658, A
C 889	16	0.5	1610	6	US-10-750-185-62791	Sequence 62791, A	C 962	16	0.5	1923	6	US-10-750-623-28658	Sequence 28658, A
C 890	16	0.5	1613	6	US-10-750-623-62791	Sequence 62791, A	C 963	16	0.5	1954	6	US-10-750-185-33352	Sequence 33352, A
C 891	16	0.5	1638	6	US-10-750-623-43499	Sequence 43499, A	C 964	16	0.5	1972	6	US-10-750-623-33352	Sequence 33352, A
C 892	16	0.5	1638	6	US-10-750-185-43499	Sequence 43499, A	C 965	16	0.5	1972	6	US-10-750-185-59457	Sequence 59457, A
C 893	16	0.5	1654	7	US-11-122-144-3	Sequence 3, Appl1	C 966	16	0.5	1972	6	US-10-750-623-59457	Sequence 59457, A
C 894	16	0.5	1670	6	US-10-750-185-57206	Sequence 57206, A	C 967	16	0.5	1990	6	US-10-750-185-64598	Sequence 64598, A
C 895	16	0.5	1670	6	US-10-750-623-57206	Sequence 57206, A	C 968	16	0.5	2000	7	US-11-194-246-380	Sequence 380, App
C 896	16	0.5	1682	6	US-10-750-185-39703	Sequence 39703, A	C 969	16	0.5	2002	6	US-10-750-185-52154	Sequence 52154, A
C 897	16	0.5	1682	6	US-10-750-623-39703	Sequence 39703, A	C 970	16	0.5	2002	6	US-10-750-623-52154	Sequence 52154, A
C 898	16	0.5	1688	6	US-10-750-185-29497	Sequence 29497, A	C 971	16	0.5	2022	6	US-10-750-185-47864	Sequence 47864, A
C 899	16	0.5	1688	6	US-10-750-623-29497	Sequence 29497, A	C 972	16	0.5	2022	6	US-10-750-623-47864	Sequence 47864, A

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973      16      0.5      2025      7      US-11-167-048-2      Sequence 2, Appl1
C 974      16      0.5      2030      6      US-10-750-185-35998      Sequence 35998, A
C 975      16      0.5      2030      6      US-10-750-623-35998      Sequence 35998, A
C 976      16      0.5      2038      6      US-10-750-185-40987      Sequence 40987, A
C 977      16      0.5      2038      6      US-10-750-623-40987      Sequence 40987, A
C 978      16      0.5      2045      6      US-10-750-185-47809      Sequence 47809, A
C 979      16      0.5      2045      6      US-10-750-623-47809      Sequence 47809, A
C 980      16      0.5      2057      6      US-10-118-590-27      Sequence 27, Appl
C 981      16      0.5      2085      6      US-10-750-185-53162      Sequence 53162, A
C 982      16      0.5      2085      6      US-10-750-623-53162      Sequence 53162, A
C 983      16      0.5      2100      6      US-10-750-185-54849      Sequence 54849, A
C 984      16      0.5      2100      6      US-10-750-623-54849      Sequence 54849, A
C 985      16      0.5      2126      7      US-11-136-527-3324      Sequence 3324, Ap
C 986      16      0.5      2139      6      US-10-453-372-47      Sequence 47, Appl
C 987      16      0.5      2145      6      US-10-750-185-30137      Sequence 30137, A
C 988      16      0.5      2161      6      US-10-750-623-30137      Sequence 30137, A
C 989      16      0.5      2161      6      US-10-750-185-37376      Sequence 37376, A
C 990      16      0.5      2170      6      US-10-750-623-37376      Sequence 37376, A
C 991      16      0.5      2170      6      US-10-750-185-53966      Sequence 53966, A
C 992      16      0.5      2179      6      US-10-750-623-53966      Sequence 53966, A
C 993      16      0.5      2179      6      US-10-750-185-46423      Sequence 46423, A
C 994      16      0.5      2179      6      US-10-750-623-46423      Sequence 46423, A
C 995      16      0.5      2184      6      US-10-467-657-1441      Sequence 1441, Ap
C 996      16      0.5      2194      6      US-10-775-163-245      Sequence 245, App
C 997      16      0.5      2196      6      US-10-750-185-30957      Sequence 30957, A
C 998      16      0.5      2196      6      US-10-750-623-30957      Sequence 30957, A
C 999      16      0.5      2209      6      US-10-750-185-62656      Sequence 62656, A
C1000     16      0.5      2209      6      US-10-750-623-62656      Sequence 62656, A
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## ALIGNMENTS

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RESULT 1
US-10-750-185-30474
/ Sequence 30474, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFIELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30474
/ LENGTH: 1219
/ TYPE: DNA
/ ORGANISM: Bovine 19866880607526
US-10-750-185-30474

Query Match      1.0%; Score 34; DB 6; Length 1219;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      516      TCTGCCAGCAGAGACCTTCTGCTCTTTGACAT      549
DB      1161      TCTGCCAGCAGAGACCTTCTGCTCTTTGACAT      1194

RESULT 2
US-10-750-623-30474
/ Sequence 30474, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
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/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFIELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30474
/ LENGTH: 1219
/ TYPE: DNA
/ ORGANISM: Bovine 19866880607526
US-10-750-623-30474

Query Match      1.0%; Score 34; DB 6; Length 1219;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      516      TCTGCCAGCAGAGACCTTCTGCTCTTTGACAT      549
DB      1161      TCTGCCAGCAGAGACCTTCTGCTCTTTGACAT      1194
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RESULT 3
US-10-310-914A-213685/c
/ Sequence 213685, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shiller, Kyuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087,0200,CEUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 1388402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 213685
/ LENGTH: 25
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-213685

Query Match      0.8%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3239      AAATCTACTTTCTTCTGTTACTACA      3263
DB      25      AAATCTACTTTCTTCTGTTACTACA      1

RESULT 4
US-11-121-849-177180
/ Sequence 177180, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177180

Query Match
Best Local Similarity 100.0%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3009 GCAGGAGATGCAGTCTCTCTTAA 3033
DB 1 GCAGGAGATGCAGTCTCTCTTAA 25

RESULT 5
US-11-121-849-177181
; Sequence 177181, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177181

Query Match
Best Local Similarity 100.0%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3019 GCAGGTCTCTTAACGATGATG 3043
DB 1 GCAGGTCTCTTAACGATGATG 25

RESULT 6
US-11-121-849-177182
; Sequence 177182, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177182

Query Match
Best Local Similarity 100.0%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3071 TGTATATGCTCCACACTACGCT 3095
DB 1 TGTATATGCTCCACACTACGCT 3095

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177183
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177183

Query Match
Best Local Similarity 100.0%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3079 TGTCCACACTACGCTGATTAACA 3103
DB 1 TGTCCACACTACGCTGATTAACA 25

RESULT 8
US-11-121-849-177184
; Sequence 177184, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 177184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-177184

Query Match
Best Local Similarity 100.0%; Score 25; DB 7; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3096 GATAACACAACCTCAGATTACAG 3120
DB 1 GATAACACAACCTCAGATTACAG 25

RESULT 9
US-11-121-849-177185
; Sequence 177185, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
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/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 177185
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-177185

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3109 CTCAGTATTCACTATTATAGGCACAC 3133
DB      1 CTCAGTATTCACTATTATAGGCACAC 25

RESULT 10
US-11-121-849-177186
/ Sequence 177186, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 177186
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-177186

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3124 TTAGGCACACTAGTTTATACGCA 3148
DB      1 TTAGGCACACTAGTTTATACGCA 25

RESULT 11
US-11-121-849-177187
/ Sequence 177187, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 177187
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-177187

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3140 TATACGCACTACTGCTTACTACT 3164
DB      1 TATACGCACTACTGCTTACTACT 25

RESULT 12
US-11-121-849-177188
/ Sequence 177188, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 177188
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-177188

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3166 GACTGTTTGTGGCAATATCTTT 3190
DB      1 GACTGTTTGTGGCAATATCTTT 25

RESULT 13
US-11-121-849-177189
/ Sequence 177189, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 177189
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-177189

Query Match      0.8%; Score 25; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3213 GAGGTTCAATACATACATCGA 3237
DB      1 GAGGTTCAATACATACATCGA 25

RESULT 14
US-11-121-849-177190
/ Sequence 177190, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
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; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 177190  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-177190

Query Match 0.8%; Score 25; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3245 TACTTTCTGTTACTACACAAAGC 3269  
DB 1 TACTTTCTGTTACTACACAAAGC 25

RESULT 15  
US-10-310-914A-213670/c  
; Sequence 213670, Application US/10310914A  
; Publication No.: US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 213670  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-213670

Query Match 0.7%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2907 TTGCAACAAGCATAGCTTACTTA 2930  
DB 24 TTGCAACAAGCATAGCTTACTTA 1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3330	100.0	3330	5 US-10-007-270-1	Sequence 1, Appl1
2	2476	74.4	2887	5 US-10-007-270-1	Sequence 3, Appl1
3	2094	62.9	3261	5 US-10-007-270-27	Sequence 27, Appl1
4	1503	45.1	2244	5 US-10-007-270-5	Sequence 5, Appl1
5	197	5.9	596	5 US-10-027-633-286848	Sequence 286848, Appl1
6	197	5.9	596	5 US-10-027-633-286848	Sequence 286848, Appl1
7	197	5.9	596	5 US-10-007-270-7	Sequence 7, Appl1
8	112	3.4	555	5 US-10-007-270-14	Sequence 14, Appl1
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10	67	2.0	536	4 US-09-925-065A-462444	Sequence 462444, Appl1
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18	22	0.7	14829	9 US-10-863-116-49	Sequence 49, Appl1
19	22	0.7	39239	9 US-10-863-116-48	Sequence 48, Appl1
20	22	0.7	40431	9 US-10-863-116-46	Sequence 46, Appl1
21	21	0.6	907	7 US-10-424-599-132463	Sequence 132463, A
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c 96	20	0.6	3673778	6	US-10-312-841-1	Sequence 1, Appl1













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C 978	17	0.5	160	6	US-09-864-761-30728	Sequence 30728, A
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## ALIGNMENTS

## RESULT 1

US-10-007-270-1  
Sequence 1, Application US/10007270  
Publication No. US20020160954A1  
GENERAL INFORMATION:  
APPLICANT: Hageman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
APPLICANT: University of Iowa Research Foundation  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
FILE REFERENCE: 020618-000120US  
CURRENT APPLICATION NUMBER: US/10/007,270  
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PRIOR APPLICATION NUMBER: US 09/430,195  
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PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 3330  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA, isoform A  
US-10-007-270-1

Query Match 100.0%; Score 3330; DB 5; Length 3330;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
US-10-007-270-3  
; Sequence 3. Application us/10007270  
; Publication No. US20020160954A1

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/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ APPLICANT: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-00012005
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ PRIOR FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 2887
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform B
US-10-007-270-3
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Query Match      74.4%; Score 2476; DB 5; Length 2887;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 4  
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Sequence 5, Application US/10007270  
Publication No. US20020160954A1  
GENERAL INFORMATION:  
APPLICANT: Hageman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
TITLE OF INVENTION: University of Iowa Research Foundation  
FILE REFERENCE: 020618-000120US  
CURRENT APPLICATION NUMBER: US/10/007,270  
CURRENT FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US 09/430,195  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 09/183,972  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 2244  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
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RESULT 5
US-10-027-632-286848/c
; Sequence 286848, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
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; LENGTH: 596
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US-10-027-632-286848

Query Match
Best Local Similarity 100.0%; Score 197; DB 5; Length 596;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 60
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OY 61 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTCACATGCAC 120
DB 465 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTCACATGCAC 406
OY 121 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 180
DB 405 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 346
OY 181 AGTTCAAGAACCAAG 197
DB 345 AGTTCAAGAACCAAG 329

RESULT 6
US-10-027-632-286848/c
; Sequence 286848, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
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; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 286848
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-286848

Query Match
Best Local Similarity 100.0%; Score 197; DB 6; Length 596;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 60
DB 525 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 466
OY 61 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTCACATGCAC 120
DB 465 TGTACTTTTAAATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTCACATGCAC 406
OY 121 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 180
DB 405 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 346
OY 181 AGTTCAAGAACCAAG 197
DB 345 AGTTCAAGAACCAAG 329

RESULT 7
US-10-007-270-7
; Sequence 7, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 7
; LENGTH: 1858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human IMPG1 gene, regulatory region
; NAME/KEY: mlec feature
; LOCATION: (1)-(1858)
; OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-7

Query Match
Best Local Similarity 100.0%; Score 197; DB 5; Length 1858;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TAAACCAAGAGGTTATCTCATCATCTGGTATCATATATATATATTTTTCACATTTTC 60
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US-09-908-975-16399  
; Sequence 16399, Application US/09908975/  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Av1  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli

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/ APPLICANT: MINTZ, Liat
/ APPLICANT: FAIGER, Simchon
/ TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
/ TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
/ FILE REFERENCE: 36688-0005
/ CURRENT APPLICATION NUMBER: US 09/908,975
/ PRIOR FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 16399
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-908-975-16399

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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3009 GCAGGAGATGACGAGTCTCTCTTAACGATGATGTAGTGTAGGACCTGTAGTG 3068
Db      1 GCAGGAGATGACGAGTCTCTCTTAACGATGATGTAGTGTAGGACCTGTAGTG 60

RESULT 12
US-09-925-065A-127697
/ Sequence 127697, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCES: 108827.135
/ CURRENT APPLICATION NUMBER: US 09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 127697
/ LENGTH: 586
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-127697

Query Match      1.0%; Score 33; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US 09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 127698
/ LENGTH: 586
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-127698

Query Match      1.0%; Score 33; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      595 GCAGGATTAACGAGAGATTCCCTGACG 627
Db      221 GCAGGATTAACGAGAGATTCCCTGACG 253

RESULT 14
US-10-007-270-10
/ Sequence 10, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ TITLE OF INVENTION: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-000120US
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ CURRENT FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ PRIOR FILING DATE: 1998-10-29
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10
/ LENGTH: 1726
/ TYPE: DNA
/ ORGANISM: Mus sp.
/ OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D
US-10-007-270-10

Query Match      1.0%; Score 32; DB 5; Length 1726;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1001 TGCAAAAGATATTTTAAAGAACTTCAGGATTC 1032
Db      726 TGCAAAAGATATTTTAAAGAACTTCAGGATTC 757

RESULT 15
US-10-007-270-8
/ Sequence 8, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
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; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3668
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, Isoform A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3668)
; OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-8

Query Match      1.0%; Score 32; DB 5; Length 3668;
Best Local Similarity 100.0%; Pred.No.3.9e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1001 TGCAGAGATATTAGAACTTCAGATTC 1032
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Db      1013 TGCAGAGATATTAGAACTTCAGATTC 1044
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Search completed: January 14, 2006, 05:21:28  
Job time : 2587 secs

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c 999      16      0.5      601      3      US-09-949-016-46745      Sequence 46745, A
c 1000     16      0.5      601      3      US-09-949-016-47140      Sequence 47140, A
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## ALIGNMENTS

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RESULT 1
US-09-949-016-16073/c
; Sequence 16073, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16073
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(385136)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16073
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Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 35113, Application US/09949016
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35113
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35113
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Best Local Similarity 100.0%; Pred. No. 30;
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Db      387 AAGAGCTATTTTGTGTTTTT 406
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US-09-949-016-35114
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35114
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35114
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Query Match      0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-949-016-35115
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35115
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35115

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 559 AAGACTATTTTGTGTTTTT 578

RESULT 5
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; Sequence 142318, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142318
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142318

Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 148 AAGACTATTTTGTGTTTTT 167
Db 387 AAGACTATTTTGTGTTTTT 406

RESULT 6
US-09-949-016-142319
; Sequence 142319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142319
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142319

Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 148 AAGACTATTTTGTGTTTTT 167
Db 392 AAGACTATTTTGTGTTTTT 411

RESULT 7
US-09-949-016-142320
; Sequence 142320, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142320
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142320

Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 148 AAGACTATTTTGTGTTTTT 167
Db 559 AAGACTATTTTGTGTTTTT 578

RESULT 8
US-09-949-016-161496
; Sequence 161496, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
```

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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 161496
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-161496
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Query Match          0.6%; Score 20; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      36 AATATATATATATTTTTCAC 55
      |||
DB      138 AATATATATATATTTTTCAC 157
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RESULT 9
US-08-617-785-5
/ Sequence 5, Application US/08617785E
/ Patent No. 6228610
/ GENERAL INFORMATION:
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```
/ APPLICANT: Flor, Peter J.
/ APPLICANT: Kuhn, Rainer
/ APPLICANT: Lindaur, Kristen
/ APPLICANT: Puttner, Irene
/ APPLICANT: Knopfel, Thomas
/ TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
/ FILE REFERENCE: 4-19679/A/PCT
/ CURRENT APPLICATION NUMBER: US/08/617,785E
/ EARLIER FILING DATE: 1996-03-19
/ EARLIER APPLICATION NUMBER: PCT/EP94/02991
/ EARLIER FILING DATE: 1994-09-07
/ EARLIER APPLICATION NUMBER: EPO 9416553.7
/ EARLIER FILING DATE: 1994-08-19
/ EARLIER APPLICATION NUMBER: EPO 93810663.0
/ EARLIER FILING DATE: 1993-09-20
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.0
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/ SEQ ID NO 5
/ LENGTH: 1399
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(270)
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (920)..(1090)
/ OTHER INFORMATION: Nucleotides designated as n could be a or g or c
/ OTHER INFORMATION: or t/u
US-08-617-785-5
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Query Match          0.6%; Score 20; DB 3; Length 1399;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1201 CATGAACCATGAGAGAGA 1220
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DB      283 CATGAACCATGAGAGAGA 302
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RESULT 10
US-09-817-464-5
/ Sequence 5, Application US/09817464
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/ Patent No. 6515107
/ GENERAL INFORMATION:
/ APPLICANT: Flor, Peter J.
/ APPLICANT: Kuhn, Rainer
/ APPLICANT: Lindaur, Kristen
/ APPLICANT: Puttner, Irene
/ APPLICANT: Knopfel, Thomas
/ TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
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/ TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
/ FILE REFERENCE: 4-19679/A/PCT
/ CURRENT APPLICATION NUMBER: US/09/817,464
/ CURRENT FILING DATE: 2001-03-26
/ EARLIER APPLICATION NUMBER: US/08/617,785
/ EARLIER FILING DATE: 1996-03-19
/ EARLIER APPLICATION NUMBER: EPO 9416553.7
/ EARLIER FILING DATE: 1994-08-19
/ EARLIER APPLICATION NUMBER: EPO 93810663.0
/ EARLIER FILING DATE: 1993-09-20
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 1399
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(270)
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (920)..(1090)
/ OTHER INFORMATION: Nucleotides designated as n could be a or g or c
/ OTHER INFORMATION: or t/u
US-09-817-464-5
```

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Query Match          0.6%; Score 20; DB 3; Length 1399;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1201 CATGAACCATGAGAGAGA 1220
      |||
DB      283 CATGAACCATGAGAGAGA 302
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RESULT 11
US-07-977-434-11/c
/ Sequence 11, Application US/07977434
/ Patent No. 5466591
/ GENERAL INFORMATION:
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/ APPLICANT: Geland, David H.
/ APPLICANT: Abramson, Richard D.
/ TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
/ TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
/ NUMBER OF SEQUENCES: 38
/ CORRESPONDENCE ADDRESS:
```

```
/ ADDRESS: Hoffmann-La Roche Inc.
/ STREET: 340 Kingsland Street
/ CITY: Nutley
/ STATE: New Jersey
/ ZIP: 07110-1199
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: Macintosh
/ OPERATING SYSTEM: 7
/ SOFTWARE: WordPerfect 2.1
/ CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/07/977,434
/ FILING DATE:
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/ CLASSIFICATION: 435
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/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 590,490
/ FILING DATE: 28-SEP-1990
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/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 590,466
/ FILING DATE: 28-SEP-1990
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/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 523,394
/ FILING DATE: 15-MAY-1990
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/ PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Luann Caeer  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: Case No. 5465591 8753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2972  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2679 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Thermosiphon africanus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2676  
US-07-977-434-11

Query Match 0.6%; Score 20; DB 2; Length 2679;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3181 AATAATCTTGAATGTTCT 3200  
DB 550 AATAATCTTGAATGTTCT 531

RESULT 12  
US-08-458-819-11/c  
Sequence 11, Application US/08458819  
Patent No. 5795762  
GENERAL INFORMATION:  
APPLICANT: Gelfand, David H.  
APPLICANT: Abramson, Richard D.  
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASIS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
ZIP: 07110-1199

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7  
SOFTWARE: WordPerfect 2.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,819  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/977,434  
FILING DATE: 23-FEB-1993  
APPLICATION NUMBER: US 590,490  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,466  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,213  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 523,394  
FILING DATE: 15-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Luann Caeer  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: Case No. 5795762 8753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2972  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2679 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Thermosiphon africanus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2676  
US-08-458-819-11

Query Match 0.6%; Score 20; DB 2; Length 2679;

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3181 AATACTTGAATTGTTCT 3200  
Db 550 AATACTTGAATTGTTCT 531

## RESULT 13

PCT-US91-07035-11/c

; Sequence 11, Application PC/TUS9107035  
; GENERAL INFORMATION:  
; APPLICANT: Gelfand, David H.  
; APPLICANT: Adrason, Richard D.  
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cetus Corporation  
; STREET: 1400 Fifty-third Street  
; CITY: Emeryville  
; STATE: California  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/07035  
; FILING DATE: 19910930  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 590,490  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 590,466  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 590,213  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 523,394  
; FILING DATE: 15-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 143,441  
; FILING DATE: 12-JAN-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 063,509  
; FILING DATE: 17-JUN-1987  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,241  
; FILING DATE: 22-AUG-1986  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 746,121  
; FILING DATE: 15-AUG-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US90/07641  
; FILING DATE: 21-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 585,471  
; FILING DATE: 20-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 455,611  
; FILING DATE: 22-DEC-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 609,157  
; FILING DATE: 02-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 557,517  
; FILING DATE: 24-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sias Ph.D, Stacey R.

; REGISTRATION NUMBER: 32,630  
; REFERENCE/DOCKET NUMBER: Case No. 2580  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-420-3300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2679 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Thermophilus africanus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2676  
; PCT-US91-07035-11

Query Match 0.6%; Score 20; DB 6; Length 2679;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3181 AATACTTGAATTGTTCT 3200  
Db 550 AATACTTGAATTGTTCT 531

## RESULT 14

US-09-016-434-1118

; Sequence 118, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREMITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEPHONE: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1118:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3021 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:

LIBRARY: GENBANK  
CLONE: 91370110  
US-09-016-434-1118

Query Match 0.6%; Score 20; DB 3; Length 3021;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1201 CATGGAACCATGAGAGGA 1220  
|||  
Db 2999 CATGGAACCATGAGAGGA 3018

## RESULT 15

US-08-617-785-3  
Sequence 3, Application US/08617785E  
Patent No. 6228610

## GENERAL INFORMATION:

APPLICANT: Flor, Peter J.  
APPLICANT: Kuhn, Ranier  
APPLICANT: Lindaur, Kristen  
APPLICANT: Puttner, Irene  
APPLICANT: Knopfel, Thomas  
TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,  
TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds  
FILE REFERENCE: 4-19679/A/PCT  
CURRENT APPLICATION NUMBER: US/08/617,785E

EARLIER FILING DATE: 1996-03-19  
EARLIER APPLICATION NUMBER: PCT/EP94/02991  
EARLIER FILING DATE: 1994-09-07  
EARLIER APPLICATION NUMBER: EPO 9416553.7  
EARLIER FILING DATE: 1994-08-19  
EARLIER APPLICATION NUMBER: EPO 93810663.0  
EARLIER FILING DATE: 1993-09-20  
NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 3804

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(2604)

FEATURE:

NAME/KEY: unsure

LOCATION: (3325)..(3495)

OTHER INFORMATION: nucleotides designated as n could be a or g or c

OTHER INFORMATION: or t/u

US-08-617-785-3

Query Match 0.6%; Score 20; DB 3; Length 3804;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1201 CATGGAACCATGAGAGGA 1220  
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Db 2688 CATGGAACCATGAGAGGA 2707

Search completed: January 14, 2006, 04:38:47  
Job time : 601 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2006, 11:43:25 : Search time 1892 Seconds  
(without alignments)  
11730.141 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaccacaagaagctatcct.....tactatatagcataatcaat 3330

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 333246308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 1000 summaries

Database :

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1: geneseqn1990s:\*  
2: geneseqn2000s:\*  
3: geneseqn2001as:\*  
4: geneseqn2001bs:\*  
5: geneseqn2002as:\*  
6: geneseqn2002bs:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2003ds:\*  
11: geneseqn2004as:\*  
12: geneseqn2004bs:\*  
13: geneseqn2004cs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3330	100.0	3330	10	ADA14840 Human int
3	2476	74.4	2887	9	ACCS7947 Human int
4	2476	74.4	2887	10	ADA14842 Human int
5	2095	62.9	3263	3	AAA46205 Human int
6	2094	62.9	3261	9	ACCS7948 Human int
7	2094	62.9	3261	10	ADA14866 Human int
8	1992	59.8	2966	3	AAA46328 Human int
9	1503	45.1	2244	3	AAA46329 Human int
10	1503	45.1	2244	9	ACCS7949 Human int
11	1503	45.1	2244	10	ADA14844 Human int
12	1937	5.9	1858	3	AAA46327 Human int
13	1937	5.9	1858	9	ACCS7949 Human int
14	1937	5.9	1858	10	ADA14846 Human int
15	112	3.4	555	3	AAA46204 Human int
16	112	3.4	555	9	ACCS7953 Human int
17	112	3.4	555	10	ADA14853 Human int
18	60	1.8	60	6	ABN43651 Human int
19	32	1.0	1726	9	ACCS7951 Human int

20	32	1.0	1726	10	ADA14849	ADA14849 Mouse int
21	32	1.0	3206	9	AAA46309	AAA46309 CDNA enco
22	32	1.0	3668	9	ACCS7950	ACCS7950 Mouse int
23	32	1.0	3668	10	ADA14847	ADA14847 Mouse int
24	27	0.8	27	3	AAA46239	AAA46239 Primer IP
25	24	0.7	1321	9	ACCS7952	ACCS7952 Mouse int
26	24	0.7	1321	10	ADA14851	ADA14851 Mouse int
27	23	0.7	19127	10	ADH13786	ADH13786 Prostate
28	22	0.7	22	3	AAA46219	AAA46219 Primer IP
29	22	0.7	22	3	AAA46229	AAA46229 Primer IP
30	22	0.7	22	3	AAA46237	AAA46237 Primer IP
31	22	0.7	22	3	AAA46236	AAA46236 Primer IP
32	22	0.7	22	3	AAA46209	AAA46209 Primer IP
33	22	0.7	22	3	AAA46221	AAA46221 Primer IP
34	22	0.7	22	3	AAA46227	AAA46227 Primer IP
35	22	0.7	22	13	ADR74360	ADR74360 Allele sp
36	22	0.7	636	3	ACCS4136	ACCS4136 Arabidops
37	22	0.7	3760	12	ADG63322	ADG63322 Novel hum
38	22	0.7	56330	14	ADZ13264	ADZ13264 Murine ca
39	21	0.6	21	3	AAA46212	AAA46212 Primer IP
40	21	0.6	21	3	AAA46224	AAA46224 Primer IP
41	21	0.6	21	3	AAA46230	AAA46230 Primer IP
42	21	0.6	21	3	AAA46238	AAA46238 Primer IP
43	21	0.6	21	3	AAA46242	AAA46242 Primer IP
44	21	0.6	22	13	ADR74359	ADR74359 Allele sp
45	20	0.6	20	3	AAA46213	AAA46213 Primer IP
46	20	0.6	20	3	AAA46218	AAA46218 Primer IP
47	20	0.6	20	3	AAA46240	AAA46240 Primer IP
48	20	0.6	20	3	AAA46241	AAA46241 Primer IP
49	20	0.6	20	3	AAA46216	AAA46216 Primer IP
50	20	0.6	20	3	AAA46222	AAA46222 Primer IP
51	20	0.6	20	3	AAA46220	AAA46220 Primer IP
52	20	0.6	20	3	AAA46232	AAA46232 Primer IP
53	20	0.6	20	3	AAA46211	AAA46211 Primer IP
54	20	0.6	20	3	AAA46225	AAA46225 Primer IP
55	20	0.6	20	3	AAA46226	AAA46226 Primer IP
56	20	0.6	20	3	AAA46215	AAA46215 Primer IP
57	20	0.6	20	3	AAA46234	AAA46234 Primer IP
58	20	0.6	20	3	AAA46210	AAA46210 Primer IP
59	20	0.6	20	3	AAA46233	AAA46233 Primer IP
60	20	0.6	20	3	AAA46228	AAA46228 Primer IP
61	20	0.6	181	12	ACH94178	ACH94178 Human gen
62	20	0.6	320	5	AD176679	AD176679 Human ova
63	20	0.6	320	5	AD177053	AD177053 Human ova
64	20	0.6	466	5	AD141915	AD141915 Human ova
65	20	0.6	484	4	AAK78636	AAK78636 Human imm
66	20	0.6	486	4	AA12761	AA12761 Human bre
67	20	0.6	529	5	AD141887	AD141887 Human ova
68	20	0.6	541	12	ACH80478	ACH80478 Human gen
69	20	0.6	550	4	AA12760	AA12760 Human bre
70	20	0.6	560	5	AD176651	AD176651 Human ova
71	20	0.6	560	5	AD170323	AD170323 Human ova
72	20	0.6	678	4	AA121632	AA121632 Human bre
73	20	0.6	759	4	AA121631	AA121631 Human bre
74	20	0.6	819	6	ABN98966	ABN98966 Arabidops
75	20	0.6	822	11	ACN82898	ACN82898 Breast ca
76	20	0.6	878	11	ACN82899	ACN82899 Breast ca
77	20	0.6	887	5	AD162470	AD162470 Human ova
78	20	0.6	887	11	ACN90927	ACN90927 Breast ca
79	20	0.6	1206	9	ADB09676	ADB09676 Altiolococ
80	20	0.6	1206	9	ADB09676	ADB09676 Altiolococ
81	20	0.6	1290	6	ABQ41841	ABQ41841 Oligonuci
82	20	0.6	1290	6	ABQ41840	ABQ41840 Oligonuci
83	20	0.6	1291	6	ABQ41862	ABQ41862 Oligonuci
84	20	0.6	1291	6	ABQ41863	ABQ41863 Oligonuci
85	20	0.6	1399	6	ABQ89344	ABQ89344 Human mgl
86	20	0.6	1716	8	ADA68600	ADA68600 Arabidops
87	20	0.6	2000	8	ADY71441	ADY71441 Rice gene
88	20	0.6	2000	12	ADY41616	ADY41616 Plant CDN
89	20	0.6	2265	2	AAQ24332	AAQ24332 Mutant th
90	20	0.6	2403	2	AAQ24331	AAQ24331 Mutant th
91	20	0.6	2568	2	AAQ28937	AAQ28937 Encodes T
92	20	0.6	2571	2	AAQ24330	AAQ24330 Mutant th













C 969	17	0.5	636	13	ACN52158	ACN52158	Cotton	at
C 970	17	0.5	639	5	AA657088	AA667088	DNA	encod
C 971	17	0.5	641	2	AAQ94409	AAQ94409	Aspergill	
C 972	17	0.5	644	6	ABT07946	ABT07946	Human lun	
C 973	17	0.5	649	5	AA571858	AA571858	DNA	encod
C 974	17	0.5	649	5	AA582936	AA582936	DNA	encod
C 975	17	0.5	657	10	ADPF5987	ADPF5987	Human	pcD
C 976	17	0.5	661	12	ADU42624	ADU42624	Plant	cdN
C 977	17	0.5	662	4	AA535606	AA535606	Human car	
C 978	17	0.5	662	10	ADDE45685	ADDE45685	Human car	
C 979	17	0.5	662	13	ADJ07103	ADJ07103	Human car	
C 980	17	0.5	667	5	AA664922	AA664922	Human	sec
C 981	17	0.5	675	13	ADSG61532	ADSG61532	Bacterial	
C 982	17	0.5	683	11	ADT94846	ADT94846	Human can	
C 983	17	0.5	683	11	ADX41328	ADX41328	Human	cdN
C 984	17	0.5	692	4	AA015478	AA015478	Human NOV	
C 985	17	0.5	693	10	ADK65610	ADK65610	Murine del	
C 986	17	0.5	696	14	ADZ00155	ADZ00155	Salmonell	
C 987	17	0.5	708	4	AA104289	AA104289	Human rep	
C 988	17	0.5	714	2	AA661769	AA661769	B. burgdo	
C 989	17	0.5	714	3	AAA47328	AAA47328	Fte2 homo	
C 990	17	0.5	717	4	ABE11189	ABE11189	Drosophi	
C 991	17	0.5	719	12	ADJ42622	ADJ42622	Plant	cdN
C 992	17	0.5	722	4	AA162826	AA162826	Human	gen
C 993	17	0.5	722	4	AA162825	AA162825	Human	gen
C 994	17	0.5	722	5	ABA15137	ABA15137	Human ner	
C 995	17	0.5	722	5	ABA15136	ABA15136	Human ner	
C 996	17	0.5	723	14	ACT60365	ACT60365	Human col	
C 997	17	0.5	730	2	AA337499	AA337499	Human	sec
C 998	17	0.5	730	10	ADD37551	ADD37551	Human	sec
C 999	17	0.5	730	10	ADAS5885	ADAS5885	Gene	enc
C1000	17	0.5	732	4	ABE09017	ABE09017	Drosophi	

## ALIGNMENTS

RESULT 1	ID	ACCS7946	standard; cDNA; 3330 BP.
XX	AC	ACCS7946;	
XX	DT	11-AUG-2003	(first entry)
XX	DE	Human Interphotoreceptor matrix IPM 150, isoform A, cDNA.	
XX	KM	Human; Interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC	
XX	KM	receptor; ophthalmological; gene therapy; gene; ss.	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
XX	FT	CDS	131..2586
XX	FT	/*tag= a	
XX	FT	/product= "IPM 150"	
XX	FT	/transl_except= (pos:668..756,aa:Thr-Asp)	
XX	FT	sig_peptide	131..150
XX	FT	/*tag= b	
XX	PN	W02003039346-A2.	
XX	PD	15-MAY-2003.	
XX	PF	08-NOV-2002; 2002W0-US036090.	
XX	PR	08-NOV-2001; 2001US-00077270.	
XX	PA	(IOWA ) UNIV IOWA RES FOUND.	
XX	PI	Hageman GS, Kuehn MH;	
XX	DR	WPI; 2003-441440/41.	

XX	P-PSDB:ABR42342.
XX	New interphotoreceptor matrix proteins and polynucleotides, useful for
XX	treating or preventing photoreceptor death or retinal detachment, or for
XX	treating ocular disorders.
PS	Claim 1, Page 77, 105pp; English.
XX	
CC	The present sequence is that of cDNA encoding isoform A of novel human
CC	interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
CC	interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
CC	is located on chromosome 6p13-q15, a region that also contains loci for
CC	progressive bifocal chorioretinal atrophy, autosomal dominant Stargardt's
CC	-like macular dystrophy, North Carolina macular dystrophy and Salla
CC	disease. Members of the IPMC gene family have been identified in humans,
CC	monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
CC	Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
CC	invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
CC	antibodies that specifically bind the polypeptides, and vectors
CC	comprising the polynucleotides. A claimed method of treating or
CC	preventing photoreceptor death or retinal detachment involves
CC	administering an IPMC polynucleotide, polypeptide or antibody. Also
CC	claimed is a method for identifying a compound capable of modulating IPMC
CC	gene expression
XX	
SQ	Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;
	Query Match 100.0%; Score 3330; DB 9; Length 3330;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 TAAACCAAGAGATTATCTTCATCATCTGGTATCATATATATATATTTTTCACATTTTC
DB	1 TAAACCAAGAGATTATCTTCATCATCTGGTATCATATATATATATATTTTTCACATTTTC
QY	61 TGTATCTTTTAAAGAGATTGAGAGTTGTCGTATGTTATGAGAAATTTACCAATGAC
DB	61 TGTATCTTTTAAAGAGATTGAGAGTTGTCGTATGTTATGAGAAATTTACCAATGAC
QY	121 AAAAGCCAGAAATGATTTGGAAACATGAAAGACATATTTTGTTTTGGATTTTCTCCA
DB	121 AAAAGCCAGAAATGATTTGGAAACATGAAAGACATATTTTGTTTTGGATTTTCTCCA
QY	121 AAAAGCCAGAAATGATTTGGAAACATGAAAGACATATTTTGTTTTGGATTTTCTCCA
DB	121 AAAAGCCAGAAATGATTTGGAAACATGAAAGACATATTTTGTTTTGGATTTTCTCCA
QY	181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATTTCTGAAACTTAAGACATAGA
DB	181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATTTCTGAAACTTAAGACATAGA
QY	181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATTTCTGAAACTTAAGACATAGA
DB	181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATTTCTGAAACTTAAGACATAGA
QY	241 CAATCCCCCAAGAAATGAAACATGAAAGTCTGAAAAAATGTACAAAATGTCAACTAT
DB	241 CAATCCCCCAAGAAATGAAACATGAAAGTCTGAAAAAATGTACAAAATGTCAACTAT
QY	241 CAATCCCCCAAGAAATGAAACATGAAAGTCTGAAAAAATGTACAAAATGTCAACTAT
DB	241 CAATCCCCCAAGAAATGAAACATGAAAGTCTGAAAAAATGTACAAAATGTCAACTAT
QY	301 GAGACGAATATTCGATTTGGCAAGACATCGAACAAAAAAGATCCGATTTTCCCAAGGG
DB	301 GAGACGAATATTCGATTTGGCAAGACATCGAACAAAAAAGATCCGATTTTCCCAAGGG
QY	301 GAGACGAATATTCGATTTGGCAAGACATCGAACAAAAAAGATCCGATTTTCCCAAGGG
DB	301 GAGACGAATATTCGATTTGGCAAGACATCGAACAAAAAAGATCCGATTTTCCCAAGGG
QY	361 GGTAAAGTCTGTCCACAGGAATCATGAAACAGATTTTGAACAGTCTTCAAGCTTATTA
DB	361 GGTAAAGTCTGTCCACAGGAATCATGAAACAGATTTTGAACAGTCTTCAAGCTTATTA
QY	361 GGTAAAGTCTGTCCACAGGAATCATGAAACAGATTTTGAACAGTCTTCAAGCTTATTA
DB	361 GGTAAAGTCTGTCCACAGGAATCATGAAACAGATTTTGAACAGTCTTCAAGCTTATTA
QY	421 TAGATTGAGAGTGTCTCAGAAAGCATGATGGAGACATATCGGATCTTTCTGGATCGAT
DB	421 TAGATTGAGAGTGTCTCAGAAAGCATGATGGAGACATATCGGATCTTTCTGGATCGAT
QY	421 TAGATTGAGAGTGTCTCAGAAAGCATGATGGAGACATATCGGATCTTTCTGGATCGAT
DB	421 TAGATTGAGAGTGTCTCAGAAAGCATGATGGAGACATATCGGATCTTTCTGGATCGAT
QY	481 CCTTGACACAGGGGAATATCAGGAATCTGGGTACGATCTGCCACAGAGAGACCTTCTGGCT
DB	481 CCTTGACACAGGGGAATATCAGGAATCTGGGTACGATCTGCCACAGAGAGACCTTCTGGCT
QY	481 CCTTGACACAGGGGAATATCAGGAATCTGGGTACGATCTGCCACAGAGAGACCTTCTGGCT
DB	481 CCTTGACACAGGGGAATATCAGGAATCTGGGTACGATCTGCCACAGAGAGACCTTCTGGCT
QY	541 CTTTGACATTTGGAAAAAATCTCAGCAATTTCCAGAGACCTTGATCTTCTCAGAGAG
DB	541 CTTTGACATTTGGAAAAAATCTCAGCAATTTCCAGAGACCTTGATCTTCTCAGAGAG
QY	541 CTTTGACATTTGGAAAAAATCTCAGCAATTTCCAGAGACCTTGATCTTCTCAGAGAG
DB	541 CTTTGACATTTGGAAAAAATCTCAGCAATTTCCAGAGACCTTGATCTTCTCAGAGAG
QY	601 AATAAAACAGAAAGTTTCCCTGACAGAAAAGATGAAATATTTGACAGAGACATTTGGG
DB	601 AATAAAACAGAAAGTTTCCCTGACAGAAAAGATGAAATATTTGACAGAGACATTTGGG

Db 601 AATTAACAGAGAAATTCCCTGACAGAAAAGTGAATATCTGCAGAGAACATTGGG 660  
Qy 661 AGAGCCTGGTGAACCAATTGTCTTCAACAGCAATCTAATTTCAAAAGCTTGGCACT 720  
Db 661 AGAGCCTGGTGAACCAATTGTCTTCAACAGCAATCTAATTTCAAAAGCTTGGCACT 720  
Qy 721 ATTCTAAGAAAACCTCAGAGAAGCAAAATTCAAGATGTGGCCAGCTCTCACTTGGGCGT 780  
Db 721 ATTCTAAGAAAACCTCAGAGAAGCAAAATTCAAGATGTGGCCAGCTCTCACTTGGGCGT 780  
Qy 781 TTCCCTCTCACTCTGTATGACACCCCTCTCTCAATGAATTTCTGTATTAACACTCAACGAC 840  
Db 781 TTCCCTCTCACTCTGTATGACACCCCTCTCTCAATGAATTTCTGTATTAACACTCAACGAC 840  
Qy 841 ACCAAGATGCCCTACACAGAAAAGAAAACGAATTTGGCTGTGTGGAGGACAGAGGGTG 900  
Db 841 ACCAAGATGCCCTACACAGAAAAGAAAACGAATTTGGCTGTGTGGAGGACAGAGGGTG 900  
Qy 901 GAGCTCAGGCTCTCTGTGGTAAACAGAAAGTTCAAGGACAGGCTGGTGACTCCAGTCC 960  
Db 901 GAGCTCAGGCTCTCTGTGGTAAACAGAAAGTTCAAGGACAGGCTGGTGACTCCAGTCC 960  
Qy 961 CCATATTTACAGAGAGCTAGCAGAGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAA 1020  
Db 961 CCATATTTACAGAGAGCTAGCAGAGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAA 1020  
Qy 1021 CTTTCCAGGATTCAAAATAATCCATGTGTAGATTTTGAACCAAGAAAAGATGGC 1080  
Db 1021 CTTTCCAGGATTCAAAATAATCCATGTGTAGATTTTGAACCAAGAAAAGATGGC 1080  
Qy 1081 TCAAGCTCCACAGAGATGCAACTTACGGCATCTTTAAGAGACACAGTGCAGAAAGCAAA 1140  
Db 1081 TCAAGCTCCACAGAGATGCAACTTACGGCATCTTTAAGAGACACAGTGCAGAAAGCAAA 1140  
Qy 1141 AGCCCTGCAAGTGAAGCTCTGTCTTTTGAATCCAAAGAAATTTGAAGAGAGATCTAT 1200  
Db 1141 AGCCCTGCAAGTGAAGCTCTGTCTTTTGAATCCAAAGAAATTTGAAGAGAGATCTAT 1200  
Qy 1201 CATGGAAACATGGAGAGAGACAAAGCAACCAAGAAATATATCTACAGCTACAGACTCAAA 1260  
Db 1201 CATGGAAACATGGAGAGAGACAAAGCAACCAAGAAATATATCTACAGCTACAGACTCAAA 1260  
Qy 1261 AGGCTGATCAGAAAGCACTAAGAGAAACAATCTTTGATGTGGGCAATTCAGTTC 1320  
Db 1261 AGGCTGATCAGAAAGCACTAAGAGAAACAATCTTTGATGTGGGCAATTCAGTTC 1320  
Qy 1321 ACTGATGAATTTGCTGATCACTGCGAGCTTGTGCTGACACCAATCAGAGCTGCC 1380  
Db 1321 ACTGATGAATTTGCTGATCACTGCGAGCTTGTGCTGACACCAATCAGAGCTGCC 1380  
Qy 1381 ACATCTTTTGTCTGTATTAACAGAGAGTCTACTTTGATGTCAGAACTTCTCTGTGAA 1440  
Db 1381 ACATCTTTTGTCTGTATTAACAGAGAGTCTACTTTGATGTCAGAACTTCTCTGTGAA 1440  
Qy 1441 CCCGAGCTTGAAGAGTGAACGAGAGAGAGCAATGCTTCACTGACACTTCTGTGCTCCA 1500  
Db 1441 CCCGAGCTTGAAGAGTGAACGAGAGAGAGCAATGCTTCACTGACACTTCTGTGCTCCA 1500  
Qy 1501 CCTGTATGAGCTTCACTCTCTGTCAAGAGCTCACTTCTTTATGAGCATCAAGCATC 1560  
Db 1501 CCTGTATGAGCTTCACTCTCTGTCAAGAGCTCACTTCTTTATGAGCATCAAGCATC 1560  
Qy 1561 TTCTCTCTGACTGATCAAGAGCAACAGATACATGGCCATGACCAAGCAATGCTAGTA 1620  
Db 1561 TTCTCTCTGACTGATCAAGAGCAACAGATACATGGCCATGACCAAGCAATGCTAGTA 1620  
Qy 1621 CCAGGAGCTCAACATCCCAACAGTGAATTTGTGCAATGAGCAATGGCTCTGGGGAAT 1680  
Db 1621 CCAGGAGCTCAACATCCCAACAGTGAATTTGTGCAATGAGCAATGGCTCTGGGGAAT 1680  
Qy 1681 TCACATTCACCTGATCTTCAAGTACAGCCGATCAAGTGAAGGTGGGAAATATGTGC 1740  
Db 1681 TCACATTCACCTGATCTTCAAGTACAGCCGATCAAGTGAAGGTGGGAAATATGTGC 1740

Qy 1741 AGACACCTAGATGAATGGAATCTGTCTGACACTCCCGCCCAATCTGAGTACAGAGCTC 1800  
Db 1741 AGACACCTAGATGAATGGAATGGAATCTGTCTGACACTCCCGCCCAATCTGAGTACAGAGCTC 1800  
Qy 1801 AGCGAATATGTTCTGTCCAGATCATTTCTTGGAGATACCACTCTCTCAAGCTTAA 1860  
Db 1801 AGCGAATATGTTCTGTCCAGATCATTTCTTGGAGATACCACTCTCTCTCAAGCTTAA 1860  
Qy 1861 CAGTATATCAACAATGATTCTATGACCAATGGCCCCCAAGAGGCTGGATGTTTC 1920  
Db 1861 CAGTATATCAACAATGATTCTATGACCAATGGCCCCCAAGAGGCTGGATGTTTC 1920  
Qy 1921 TTCACTGTCCGTGTGCTTAACTATGAGCTTCTCCAAAGACCTGTTCAAAGAGCTCTCG 1980  
Db 1921 TTCACTGTCCGTGTGCTTAACTATGAGCTTCTCCAAAGACCTGTTCAAAGAGCTCTCTCG 1980  
Qy 1981 GAGTACCGAGCTCTGGAGCAAAATTCACAGAGCTGTGGTTCCATATCTACGATCCAA 2040  
Db 1981 GAGTACCGAGCTCTGGAGCAAAATTCACAGAGCTGTGGTTCCATATCTACGATCCAA 2040  
Qy 2041 CTTACAGGATTTTAAAGCACTTGAAATACCTTAACCTTCAAGAACGGAGTGTATGTAAT 2100  
Db 2041 CTTACAGGATTTTAAAGCACTTGAAATACCTTAACCTTCAAGAACGGAGTGTATGTAAT 2100  
Qy 2101 AGCAAAATGAAGTTGCTTAACTGTGTGCTGTATTAACCTCAACAGAGCTGTGACGGGGTC 2160  
Db 2101 AGCAAAATGAAGTTGCTTAACTGTGTGCTGTATTAACCTCAACAGAGCTGTGACGGGGTC 2160  
Qy 2161 TTGAGAGATTTTGTCTGTGCTGACAGCCCAACCACTCTGGAATATGACAGCTACTCT 2220  
Db 2161 TTGAGAGATTTTGTCTGTGCTGACAGCCCAACCACTCTGGAATATGACAGCTACTCT 2220  
Qy 2221 CTCAACATTGAACAGCTGATCAAGCAGATCCCTGCAAGTTCTGGCTCGGCGCAATTT 2280  
Db 2221 CTCAACATTGAACAGCTGATCAAGCAGATCCCTGCAAGTTCTGGCTCGGCGCAATTT 2280  
Qy 2281 GCCCAATGTGTAAAGAAAGGAACGGACTGAGAGAGGGAGTGTGCTGTCAAAACAGATAT 2340  
Db 2281 GCCCAATGTGTAAAGAAAGGAACGGACTGAGAGAGGGAGTGTGCTGTCAAAACAGATAT 2340  
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Qy 2401 TGGAGGTCCTTCAAGGAAAGGAGCTCATTGCAAGGTTGCGAGATCACTCTGAAATCA 2460  
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Qy 2521 AGAAATTCGAAATTAACGAGTGAATTAAGAAATTAACCAAGAAATGGGAAGGA 2580  
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Qy 2581 AATTAAAACTGAATATGACATTAATCACTTGGCTATCTCAAGAGAGATGATTGGCT 2640  
Db 2581 AATTAAAACTGAATATGACATTAATCACTTGGCTATCTCAAGAGAGATGATTGGCT 2640  
Qy 2641 TCTCAAGGAAATGAGACAGGCAATATTCATGAGTCAATCAAAATCAGACATACAGTCA 2700  
Db 2641 TCTCAAGGAAATGAGACAGGCAATATTCATGAGTCAATCAAAATCAGACATACAGTCA 2700  
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Qy 2761 TAAATTCGAAAAAAGACATTAATTAATTAATAAACCACCAATGCAATCAGGAAAC 2820  
Db 2761 TAAATTCGAAAAAAGACATTAATTAATTAATAAACCACCAATGCAATCAGGAAAC 2820

Chr	Start (kb)	End (kb)	Gene	Transcript	Accession	Length (nt)	GC (%)	GC3 (%)	GC4 (%)	GC5 (%)	GC6 (%)	GC7 (%)	GC8 (%)	GC9 (%)	GC10 (%)	GC11 (%)	GC12 (%)	GC13 (%)	GC14 (%)	GC15 (%)	GC16 (%)	GC17 (%)	GC18 (%)	GC19 (%)	GC20 (%)	GC21 (%)	GC22 (%)	GC23 (%)	GC24 (%)	GC25 (%)	GC26 (%)	GC27 (%)	GC28 (%)	GC29 (%)	GC30 (%)	GC31 (%)	GC32 (%)	GC33 (%)	GC34 (%)	GC35 (%)	GC36 (%)	GC37 (%)	GC38 (%)	GC39 (%)	GC40 (%)	GC41 (%)	GC42 (%)	GC43 (%)	GC44 (%)	GC45 (%)	GC46 (%)	GC47 (%)	GC48 (%)	GC49 (%)	GC50 (%)	GC51 (%)	GC52 (%)	GC53 (%)	GC54 (%)	GC55 (%)	GC56 (%)	GC57 (%)	GC58 (%)	GC59 (%)	GC60 (%)	GC61 (%)	GC62 (%)	GC63 (%)	GC64 (%)	GC65 (%)	GC66 (%)	GC67 (%)	GC68 (%)	GC69 (%)	GC70 (%)	GC71 (%)	GC72 (%)	GC73 (%)	GC74 (%)	GC75 (%)	GC76 (%)	GC77 (%)	GC78 (%)	GC79 (%)	GC80 (%)	GC81 (%)	GC82 (%)	GC83 (%)	GC84 (%)	GC85 (%)	GC86 (%)	GC87 (%)	GC88 (%)	GC89 (%)	GC90 (%)	GC91 (%)	GC92 (%)	GC93 (%)	GC94 (%)	GC95 (%)	GC96 (%)	GC97 (%)	GC98 (%)	GC99 (%)	GC100 (%)	GC101 (%)	GC102 (%)	GC103 (%)	GC104 (%)	GC105 (%)	GC106 (%)	GC107 (%)	GC108 (%)	GC109 (%)	GC110 (%)	GC111 (%)	GC112 (%)	GC113 (%)	GC114 (%)	GC115 (%)	GC116 (%)	GC117 (%)	GC118 (%)	GC119 (%)	GC120 (%)	GC121 (%)	GC122 (%)	GC123 (%)	GC124 (%)	GC125 (%)	GC126 (%)	GC127 (%)	GC128 (%)	GC129 (%)	GC130 (%)	GC131 (%)	GC132 (%)	GC133 (%)	GC134 (%)	GC135 (%)	GC136 (%)	GC137 (%)	GC138 (%)	GC139 (%)	GC140 (%)	GC141 (%)	GC142 (%)	GC143 (%)	GC144 (%)	GC145 (%)	GC146 (%)	GC147 (%)	GC148 (%)	GC149 (%)	GC150 (%)	GC151 (%)	GC152 (%)	GC153 (%)	GC154 (%)	GC155 (%)	GC156 (%)	GC157 (%)	GC158 (%)	GC159 (%)	GC160 (%)	GC161 (%)	GC162 (%)	GC163 (%)	GC164 (%)	GC165 (%)	GC166 (%)	GC167 (%)	GC168 (%)	GC169 (%)	GC170 (%)	GC171 (%)	GC172 (%)	GC173 (%)	GC174 (%)	GC175 (%)	GC176 (%)	GC177 (%)	GC178 (%)	GC179 (%)	GC180 (%)	GC181 (%)	GC182 (%)	GC183 (%)	GC184 (%)	GC185 (%)	GC186 (%)	GC187 (%)	GC188 (%)	GC189 (%)	GC190 (%)	GC191 (%)	GC192 (%)	GC193 (%)	GC194 (%)	GC195 (%)	GC196 (%)	GC197 (%)	GC198 (%)	GC199 (%)	GC200 (%)	GC201 (%)	GC202 (%)	GC203 (%)	GC204 (%)	GC205 (%)	GC206 (%)	GC207 (%)	GC208 (%)	GC209 (%)	GC210 (%)	GC211 (%)	GC212 (%)	GC213 (%)	GC214 (%)	GC215 (%)	GC216 (%)	GC217 (%)	GC218 (%)	GC219 (%)	GC220 (%)	GC221 (%)	GC222 (%)	GC223 (%)	GC224 (%)	GC225 (%)	GC226 (%)	GC227 (%)	GC228 (%)	GC229 (%)	GC230 (%)	GC231 (%)	GC232 (%)	GC233 (%)	GC234 (%)	GC235 (%)	GC236 (%)	GC237 (%)	GC238 (%)	GC239 (%)	GC240 (%)	GC241 (%)	GC242 (%)	GC243 (%)	GC244 (%)	GC245 (%)	GC246 (%)	GC247 (%)	GC248 (%)	GC249 (%)	GC250 (%)	GC251 (%)	GC252 (%)	GC253 (%)	GC254 (%)	GC255 (%)	GC256 (%)	GC257 (%)	GC258 (%)	GC259 (%)	GC260 (%)	GC261 (%)	GC262 (%)	GC263 (%)	GC264 (%)	GC265 (%)	GC266 (%)	GC267 (%)	GC268 (%)	GC269 (%)	GC270 (%)	GC271 (%)	GC272 (%)	GC273 (%)	GC274 (%)	GC275 (%)	GC276 (%)	GC277 (%)	GC278 (%)	GC279 (%)	GC280 (%)	GC281 (%)	GC282 (%)	GC283 (%)	GC284 (%)	GC285 (%)	GC286 (%)	GC287 (%)	GC288 (%)	GC289 (%)	GC290 (%)	GC291 (%)	GC292 (%)	GC293 (%)	GC294 (%)	GC295 (%)	GC296 (%)	GC297 (%)	GC298 (%)	GC299 (%)	GC300 (%)	GC301 (%)	GC302 (%)	GC303 (%)	GC304 (%)	GC305 (%)	GC306 (%)	GC307 (%)	GC308 (%)	GC309 (%)	GC310 (%)	GC311 (%)	GC312 (%)	GC313 (%)	GC314 (%)	GC315 (%)	GC316 (%)	GC317 (%)	GC318 (%)	GC319 (%)	GC320 (%)	GC321 (%)	GC322 (%)	GC323 (%)	GC324 (%)	GC325 (%)	GC326 (%)	GC327 (%)	GC328 (%)	GC329 (%)	GC330 (%)	GC331 (%)	GC332 (%)	GC333 (%)	GC334 (%)	GC335 (%)	GC336 (%)	GC337 (%)	GC338 (%)	GC339 (%)	GC340 (%)	GC341 (%)	GC342 (%)	GC343 (%)	GC344 (%)	GC345 (%)	GC346 (%)	GC347 (%)	GC348 (%)	GC349 (%)	GC350 (%)	GC351 (%)	GC352 (%)	GC353 (%)	GC354 (%)	GC355 (%)	GC356 (%)	GC357 (%)	GC358 (%)	GC359 (%)	GC360 (%)	GC361 (%)	GC362 (%)	GC363 (%)	GC364 (%)	GC365 (%)	GC366 (%)	GC367 (%)	GC368 (%)	GC369 (%)	GC370 (%)	GC371 (%)	GC372 (%)	GC373 (%)	GC374 (%)	GC375 (%)	GC376 (%)	GC377 (%)	GC378 (%)	GC379 (%)	GC380 (%)	GC381 (%)	GC382 (%)	GC383 (%)	GC384 (%)	GC385 (%)	GC386 (%)	GC387 (%)	GC388 (%)	GC389 (%)	GC390 (%)	GC391 (%)	GC392 (%)	GC393 (%)	GC394 (%)	GC395 (%)	GC396 (%)	GC397 (%)	GC398 (%)	GC399 (%)	GC400 (%)	GC401 (%)	GC402 (%)	GC403 (%)	GC404 (%)	GC405 (%)	GC406 (%)	GC407 (%)	GC408 (%)	GC409 (%)	GC410 (%)	GC411 (%)	GC412 (%)	GC413 (%)	GC414 (%)	GC415 (%)
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Pf	08-NOV-2001; 2001US-00007270.
Xx	
Pr	29-OCT-1998; 98US-00183972.
Pr	29-OCT-1999; 99US-00430195.
Xx	
Pa	(IOWA ) UNIV IOWA RES FOUND.
Xx	
Xx	Hageman GS, Kuehn MH;
Dr	WPI, 2003-238235/23.
Dr	P-PsDB; ADA14841.
Pt	New isolated or recombinant interphotoreceptor matrix component
Pt	polynucleotide and polypeptide, useful for diagnosing, preventing,
Pt	treating or prognosticating ocular disorders, e.g. macular degeneration
Pt	or retinal detachment.
Xx	
Ps	Claim 3; Page 29-30; 76pp; English.
Xx	
Cc	The invention relates to an isolated or recombinant interphotoreceptor
Cc	matrix component (IPMC) polynucleotide. Also disclosed is a vector
Cc	comprising a promoter of an interphotoreceptor matrix component (IPMC)
Cc	gene operatively linked to the IPMC polynucleotide. The IPMC
Cc	polynucleotides, polypeptides and antibodies are useful for diagnosing,
Cc	preventing, treating or prognosticating ocular disorders, e.g. macular
Cc	degeneration, photoreceptor death or retinal detachment. They are also
Cc	useful for identifying a compound capable of modulating IPMC gene
Cc	expression in a cell. The present sequence represents cDNA encoding human
Cc	interphotoreceptor matrix component, IPMC, 150 isoform A.
Xx	
SQ	Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;
	Query Match 100.0%; Score 3330; DB 10; Length 3330;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 TAAACCAAGAAAGTTATCTTCATCATCTGGTATCATATATTAATTATTTGCATTTC 60
Dd	1 TAAACCAAGAAAGTTATCTTCATCATCTGGTATCATATATTAATTATTTGCATTTC 60
Oy	61 TGTTACTTTTAAAGAGTTGAGGTGTCGCGATGTTATTCGAATTACCAATGCAC 120
Dd	61 TGTTACTTTTAAAGAGTTGAGGTGTCGCGATGTTATTCGAATTACCAATGCAC 120
Oy	121 AAAAGCCAGAATNGTATTTGGAAAACATAGAAAGCATATTTTGTTTTTGGAATTTTCTCCA 180
Dd	121 AAAAGCCAGAATNGTATTTGGAAAACATAGAAAGCATATTTTGTTTTTGGAATTTTCTCCA 180
Oy	181 AGTTCAAGGAACCAAAGATATCTCCATTACAATATACCATCTGTGAACTTAAAGACATAGA 240
Dd	181 AGTTCAAGGAACCAAAGATATCTCCATTACAATATACCATCTGTGAACTTAAAGACATAGA 240
Oy	241 CAATCCCCCAAGAAATGAAACAATCGAAGATCTGAAAAAATGTAACAAAATGTCACATAT 300
Dd	241 CAATCCCCCAAGAAATGAAACAATCGAAGATCTGAAAAAATGTAACAAAATGTCACATAT 300
Oy	301 GAGACGAATATTCGATTTGGCGAAAGCATCGAACAAAAGATCCGCATTTTCCCAACGGG 360
Dd	301 GAGACGAATATTCGATTTGGCGAAAGCATCGAACAAAAGATCCGCATTTTCCCAACGGG 360
Oy	361 GGTTAAAGTCTGTGCCAGGAATCCATGAACAGATTTTAGACAGTCTTCAAGCTTATTA 420
Dd	361 GGTTAAAGTCTGTGCCAGGAATCCATGAACAGATTTTAGACAGTCTTCAAGCTTATTA 420
Oy	421 TAGATTGAGAGTGTCTCAGAAAGCATGATGGGAACATATCGGATCTTTCTGGATTCGCA 480
Dd	421 TAGATTGAGAGTGTCTCAGAAAGCATGATGGGAACATATCGGATCTTTCTGGATTCGCA 480
Oy	481 CCTGACACAGGGGAATATCAGGACTGGGTCAGATCTGCCAGCAGAGAGACCTTCTGCT 540
Dd	481 CCTGACACAGGGGAATATCAGGACTGGGTCAGATCTGCCAGCAGAGAGACCTTCTGCT 540
Oy	541 CTTTGACATGGAAAAAATTCAGCAATTCACAGAGACCTGATCTTCTCAGACAGAG 600

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Db 541 CTTTGCATTTGAAAAAATTGAGCAATTCAGAGGCACTGSGACTTCTCCAGAGAG 600
Qy 601 AATTAACAGAGAGATTTCCTCGACAGAAAAGTGAATATCTGCAGAGAGACATTGG 660
Db 601 AATTAACAGAGAGATTTCCTCGACAGAAAAGTGAATATCTGCAGAGAGACATTGG 660
Qy 661 AGAGCTGGTGAACCAATGTGCAATTTCAACAGAACTCAATTTCAAGAATTGGGCAAT 720
Db 661 AGAGCTGGTGAACCAATGTGCAATTTCAACAGAACTCAATTTCAAGAATTGGGCAAT 720
Qy 721 ATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTTGCCAAGCTCTCACTTGGGCT 780
Db 721 ATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGATGTTGCCAAGCTCTCACTTGGGCT 780
Qy 781 TTCCCTCTCACTCTGATGACACCTCTCTCATAGAAATTCGTGATATATCACTCAAGAC 840
Db 781 TTCCCTCTCACTCTGATGACACCTCTCTCATAGAAATTCGTGATATATCACTCAAGAC 840
Qy 841 ACCAAGATGCTTACACAGAAAGAGAAACGAAATTCGCTGTGTGAGGAGCAGAGGCT 900
Db 841 ACCAAGATGCTTACACAGAAAGAGAAACGAAATTCGCTGTGTGAGGAGCAGAGGCT 900
Qy 901 GAGCTCAGGCTCTCTGTGTAACAGAAATTCAAGCAGAGCTCGCTGACTCCAGTCC 960
Db 901 GAGCTCAGGCTCTCTGTGTAACAGAAATTCAAGCAGAGCTCGCTGACTCCAGTCC 960
Qy 961 CCAATATTACAGAGAGCTAGCAGAGAAAGTCCAACTTCAGATGCAAAAGATTTAAGAA 1020
Db 961 CCAATATTACAGAGAGCTAGCAGAGAAAGTCCAACTTCAGATGCAAAAGATTTAAGAA 1020
Qy 1021 CTTCCAGGATTTCAAAAAATCCATGTGTTAGATTAGACCAAAAGAAAAGATGGC 1080
Db 1021 CTTCCAGGATTTCAAAAAATCCATGTGTTAGATTAGACCAAAAGAAAAGATGGC 1080
Qy 1081 TCAAGCTCCACAGAGATGCACTTACGGGCATCTTTAAGAGACAGTCAAGAGCAAA 1140
Db 1081 TCAAGCTCCACAGAGATGCACTTACGGGCATCTTTAAGAGACAGTCAAGAGCAAA 1140
Qy 1141 AGCCCTGCAAGTGAACCTCTGTCTTTGATTCCAACAAAATTGAAGTGAAGTCTAT 1200
Db 1141 AGCCCTGCAAGTGAACCTCTGTCTTTGATTCCAACAAAATTGAAGTGAAGTCTAT 1200
Qy 1201 CATGGAACCATGAGAGAGACAGCAACAGAAATCTATCTCAACAGCTACAGACTCAAA 1260
Db 1201 CATGGAACCATGAGAGAGACAGCAACAGAAATCTATCTCAACAGCTACAGACTCAAA 1260
Qy 1261 AGGCTGATCAGAAAGCACTAAGAGAAACAATCTTGGATGTGGGACAAATTCAGTTC 1320
Db 1261 AGGCTGATCAGAAAGCACTAAGAGAAACAATCTTGGATGTGGGACAAATTCAGTTC 1320
Qy 1321 ACTGATGAATATGCTGGATCACTGCCAGCCTTGTGCTGACACCCAAATCAGAGTGC 1380
Db 1321 ACTGATGAATATGCTGGATCACTGCCAGCCTTGTGCTGACACCCAAATCAGAGTGC 1380
Qy 1381 AATCTTTTGTCTGTATTAACAGAGATGCTAATTTGAGTCCAGAACTTCTCTGTGAA 1440
Db 1381 AATCTTTTGTCTGTATTAACAGAGATGCTAATTTGAGTCCAGAACTTCTCTGTGAA 1440
Qy 1441 CCCCAAGCTTGAAGAGTGAAGAGAGAGAGAGAGAGTGTACGTGACACTTCTTGGTCTCA 1500
Db 1441 CCCCAAGCTTGAAGAGTGAAGAGAGAGAGAGAGTGTACGTGACACTTCTTGGTCTCA 1500
Qy 1501 CCTGTATAGGCTTACCTCTCTCAGAGTCCACTTTCTTTATGSCATCAAGCATC 1560
Db 1501 CCTGTATAGGCTTACCTCTCTCAGAGTCCACTTTCTTTATGSCATCAAGCATC 1560
Qy 1561 TTTCTCTGATGATGATCAAGGACCAAGATACATATGAGCCATGACAGACATGCTAGTA 1620
Db 1561 TTTCTCTGATGATGATCAAGGACCAAGATACATATGAGCCATGACAGACATGCTAGTA 1620
Qy 1621 CCAAGGCTCAACATCCCAAGATGATTTATCTGCAATCAGGCAACTGGCTCTGGGAAT 1680
Db 1621 CCAAGGCTCAACATCCCAAGATGATTTATCTGCAATCAGGCAACTGGCTCTGGGAAT 1680

Db 1621 CCAAGGCTCAACATCCCAAGATGATTTATCTGCAATCAGGCAACTGGCTCTGGGAAT 1680
Qy 1681 TCAATTCACCTGCACTTTCAATGATACAGCCGATCAAGTGCAGGTGGCAAGATATGTC 1740
Db 1681 TCAATTCACCTGCACTTTCAATGATACAGCCGATCAAGTGCAGGTGGCAAGATATGTC 1740
Qy 1741 AGACACTAGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 AGACACTAGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Qy 1801 AGCAGATATGTTCTGTCCAGATATCTTGTGAGATACCACTCTCTCAGCTTAA 1860
Db 1801 AGCAGATATGTTCTGTCCAGATATCTTGTGAGATACCACTCTCTCAGCTTAA 1860
Qy 1861 CAGTATATCACTAGTCTATGACATGTCCTCCCAAGGCGAGAGCTGTAGTTC 1920
Db 1861 CAGTATATCACTAGTCTATGACATGTCCTCCCAAGGCGAGAGCTGTAGTTC 1920
Qy 1921 TTCACTGCGGTGTGTGATGATGAGCTTCTCCAAAGACCTGTGCAAGAGCTCTCG 1980
Db 1921 TTCACTGCGGTGTGTGATGATGAGCTTCTCCAAAGACCTGTGCAAGAGCTCTCG 1980
Qy 1981 GAGTACCGAGCTCTGAGCAACAATTCACACAGCTGTGTTCATATCTAGATCAAT 2040
Db 1981 GAGTACCGAGCTCTGAGCAACAATTCACACAGCTGTGTTCATATCTAGATCAAT 2040
Qy 2041 CTTACAGATTTTAAAGCACTTGAATCTTAACTTCAAGAAAGGAGTGTATGTAAT 2100
Db 2041 CTTACAGATTTTAAAGCACTTGAATCTTAACTTCAAGAAAGGAGTGTATGTAAT 2100
Qy 2101 AGCAAAATGAATTTGCTAAGTCTGTGCGCTAATCTTCAAGAGCTGTGACGGGCT 2160
Db 2101 AGCAAAATGAATTTGCTAAGTCTGTGCGCTAATCTTCAAGAGCTGTGACGGGCT 2160
Qy 2161 TTGAGGATTTTGTGTTCTGTGTCAGCCCAACAATCTCACTGGAATGACAGTACT 2220
Db 2161 TTGAGGATTTTGTGTTCTGTGTCAGCCCAACAATCTCACTGGAATGACAGTACT 2220
Qy 2221 CTCAACATTGAACAGCTGATCAAGCAGATCCCTGCAAGTTCCTGCGCGCAATTT 2280
Db 2221 CTCAACATTGAACAGCTGATCAAGCAGATCCCTGCAAGTTCCTGCGCGCAATTT 2280
Qy 2281 GCCCAATGTGTAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2340
Db 2281 GCCCAATGTGTAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2340
Qy 2341 GACAGCGAGGAGAGCTGAGAGCTGTGGAACAGGCTCTGTGGCTGTGGCAAGAGAA 2400
Db 2341 GACAGCGAGGAGAGCTGAGAGCTGTGGAACAGGCTCTGTGGCTGTGGCAAGAGAA 2400
Qy 2401 TCGAGGCTCTTCAGAGAAAGGAGCTCATGCAAGTTCAGAGATCACTTGAATCA 2460
Db 2401 TCGAGGCTCTTCAGAGAAAGGAGCTCATGCAAGTTCAGAGATCACTTGAATCA 2460
Qy 2461 GCATCAAAATCTAGTGTAAAAAGTTCCAAAATCAACAAAATACAGATATCGTAA 2520
Db 2461 GCATCAAAATCTAGTGTAAAAAGTTCCAAAATCAACAAAATACAGATATCGTAA 2520
Qy 2521 AGAAATTCGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2580
Db 2521 AGAAATTCGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2580
Qy 2581 AATTAACAACTGAATATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2640
Db 2581 AATTAACAACTGAATATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2640
Qy 2641 TCTCAAGAAATATGAGACAGGATATTAAGGCTGATCAAAATCAAGATCAAGTCA 2700
Db 2641 TCTCAAGAAATATGAGACAGGATATTAAGGCTGATCAAAATCAAGATCAAGTCA 2700
Qy 2701 CACTGAGATCAGCACAACCATATTTCAAAATTAAGAGATCATGTATCTTGGCAACAG 2760
Db 2701 CACTGAGATCAGCACAACCATATTTCAAAATTAAGAGATCATGTATCTTGGCAACAG 2760
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OY 2761 TAAATTCGAAAAAGACCTTATTATTATTAACCCCAATGCAATCAGGGAAC 2820
XX |||||||
DB 2761 TAAATTCGAAAAAGACCTTATTATTATTAACCCCAATGCAATCAGGGAAC 2820
OY 2821 ATATTTTATGATTTCTTGATGATAGTCAAAAATGATCATTAAGCAGGTTGGCTTACCT 2880
XX |||||||
DB 2821 ATATTTTATGATTTCTTGATGATAGTCAAAAATGATCATTAAGCAGGTTGGCTTACCT 2880
OY 2881 TCCCGAAAAATTTTCTCAAGATCATTTGGCAAGCCTAGCTTACTTATTTGTTTAAAGG 2940
XX |||||||
DB 2881 TCCCGAAAAATTTTCTCAAGATCATTTGGCAAGCCTAGCTTACTTATTTGTTTAAAGG 2940
OY 2941 ACTGAAACAATTTATTTGGGAAGAACTCTTTATATGCTAGAAAGTACATTTTAAAGATGA 3000
XX |||||||
DB 2941 ACTGAAACAATTTATTTGGGAAGAACTCTTTATATGCTAGAAAGTACATTTTAAAGATGA 3000
OY 3001 CTACTTACGCAAGGAGATGCAAGGCTCTCTTAAACGATGATATGATGTGTAGGCA 3060
XX |||||||
DB 3001 CTACTTACGCAAGGAGATGCAAGGCTCTCTTAAACGATGATATGATGTGTAGGCA 3060
OY 3061 CTGTAGTGTGTATATATGCTCCACACTAGCTGTGATTAACAACAACCTCAGTATTCAG 3120
XX |||||||
DB 3061 CTGTAGTGTGTATATATGCTCCACACTAGCTGTGATTAACAACAACCTCAGTATTCAG 3120
OY 3121 TTATTAGGCACTAGTTTATACGCACTAGCTTACATAGTGAAGTGTGTTGTTGCC 3180
XX |||||||
DB 3121 TTATTAGGCACTAGTTTATACGCACTAGCTTACATAGTGAAGTGTGTTGTTGCC 3180
OY 3181 AATTAATCTTGAATTTGTTTAAAGAACTGAGGTTCAATATACATATCAGTGAAGAA 3240
XX |||||||
DB 3181 AATTAATCTTGAATTTGTTTAAAGAACTGAGGTTCAATATACATATCAGTGAAGAA 3240
OY 3241 ATCTTAATCTTGTGTTTACTTACACAAAGCTATTTTAAAGAATGTAATGTTGGAGAG 3300
XX |||||||
DB 3241 ATCTTAATCTTGTGTTTACTTACACAAAGCTATTTTAAAGAATGTAATGTTGGAGAG 3300
OY 3301 GCGGAAGTTGTACTATATGACATTAATCAAT 3330
XX |||||||
DB 3301 GCGGAAGTTGTACTATATGACATTAATCAAT 3330
RESULT 3
ACCS7947
ID ACCS7947 standard; cDNA; 2887 BP.
AC
ACCS7947;
DT 11-AUG-2003 (first entry)
XX
DE Human Interphotoreceptor matrix IPM 150, isoform B, cDNA.
XX
KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX receptor; ophthalmological; gene therapy; gene; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 2..2143
XX FT /*tag= a
XX FT /product= "IPM 150"
XX FT /partial
XX FT /note= "No start codon"
XX
XX WO2003039346-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002MO-US036090.
XX
XX 08-NOV-2001; 2001US-00077270.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
PA
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XX
PI Hageman GS, Kuehn MH;
XX
XX WPI, 2003-441440/41.
DR
XX
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
PS Claim 1; Page 78-79; 105pp; English.
XX
XX The present sequence is that of cDNA encoding isoform B of novel human
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 6q13-q15, a region that also contains loci for
XX progressive bilateral chorioretinal atrophy, autosomal dominant Stargardt's
XX -like macular dystrophy, North Carolina macular dystrophy and Sallé
XX disease. Members of the IPMC gene family have been identified in humans,
XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
XX Subfamilies are designated IPM 150 (or IPMg1) and IPM 200 (or IPMg2). The
XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
XX antibodies that specifically bind the polypeptides, and vectors
XX comprising the polynucleotides. A claimed method of treating or
XX preventing photoreceptor death or retinal detachment involves
XX administering an IPMC polynucleotide, polypeptide or antibody. Also
XX claimed is a method for identifying a compound capable of modulating IPMC
XX gene expression
SQ
Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;
Query Match 74.4%; Score 2476; DB 9; Length 2887;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 753 AGATGTTGCCAAGCTCTTACCTTGGGCTTTCCTCTCACTCTGTATGACACCTTCCTAA 812
DB 310 AGATGTTGCCAAGCTCTTACCTTGGGCTTTCCTCTCACTCTGTATGACACCTTCCTAA 369
OY 813 TGAATTTCTGATTAATCACTCAACGACACCAAGTGTCTCAACAGAAAGAAACAGA 872
DB 370 TGAATTTCTGATTAATCACTCAACGACACCAAGTGTCTCAACAGAAAGAAACAGA 429
OY 873 ATTGCTGTGTTGAGAGAGACAGAGGTGAGACTGAGCTCTCTGTGTTAAACAGAAATT 932
DB 430 ATTGCTGTGTTGAGAGAGACAGAGGTGAGACTGAGCTCTCTGTGTTAAACAGAAATT 489
OY 933 CAAGCAGAGCTCGCTGACCTCCAGTCCCATATTACAGAGAGCTTACAGAGAAAGTCCCA 992
DB 490 CAAGCAGAGCTCGCTGACCTCCAGTCCCATATTACAGAGAGCTTACAGAGAAAGTCCCA 549
OY 993 ACTTCAGATGCAAAAGATTAATTAAGAACTTCCAGGATTCAAAAAATCCATGTTTAAAG 1052
DB 550 ACTTCAGATGCAAAAGATTAATTAAGAACTTCCAGGATTCAAAAAATCCATGTTTAAAG 609
OY 1053 ATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCAACTTACGGCCAT 1112
DB 610 ATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCAACTTACGGCCAT 669
OY 1113 CTTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGTGAATGACTCTGTCTTTGATTTC 1172
DB 670 CTTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGTGAATGACTCTGTCTTTGATTTC 729
OY 1173 CAACAAATTTGAAGTGAAGAGTCTATCATGGAACCATGAGAGGACCAAGCAACGAGA 1232
DB 730 CAACAAATTTGAAGTGAAGAGTCTATCATGGAACCATGAGAGGACCAAGCAACGAGA 789
OY 1233 AATCTATCTCAGCTACAGACCTCAAAAGGCTGTATCAGCAAAAGCATAGAGAGAAAGACA 1292
DB 790 AATCTATCTCAGCTACAGACCTCAAAAGGCTGTATCAGCAAAAGCATAGAGAGAAAGACA 849
OY 1293 ATCTTTGATGTGGGAGCAATTCAGTTCATGATGAATTTGCTGTGATCATCTGCCAGCTT 1352
DB 850 ATCTTTGATGTGGGAGCAATTCAGTTCATGATGAATTTGCTGTGATCATCTGCCAGCTT 909
```

QY 1353 TGGTCTGACACCCCAATCAGAGCTGCACATCTTTTGTGTTATTAACAGAGATGCTAC 1412  
DB 910 TGGTCTGACACCCCAATCAGAGCTGCACATCTTTTGTGTTATTAACAGAGATGCTAC 969  
QY 1413 TTTGAGTCCAGAACTTCTCTCTGTGTAACCCAGCTTGAGACAGTGAACGAGCAGACGA 1472  
DB 970 TTTGAGTCCAGAACTTCTCTCTGTGTAACCCAGCTTGAGACAGTGAACGAGCAGACGA 1029  
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DB 1090 TCCACCTTTCTTATGAGCATCAAGCATCTTCTCTGATCAAGGACCAAGATAC 1149  
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DB 1210 TGGCATCAGCCAACTGGCTCTGGGAAATTTCAATCCACTGACCTTCAAGATGACAGCCG 1269  
QY 1713 ATCAAGTGAAGTGGGAGATATGTTGTCAGACACCTAGATGAAATGGAATCTGTCTGACAC 1772  
DB 1270 ATCAAGTGAAGTGGGAGATATGTTGTCAGACACCTAGATGAAATGGAATCTGTCTGACAC 1329  
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QY 1893 CCCCAAGGCGGAGCTGGTATGTTCTTCAAGTCTGCGGTGCTCAATGCGCTTCTTC 1952  
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DB 1570 GCTGCTGTTCAATCTACGATCCAATCTTACAGGATTTAAGCACTTGAATATCTTA 1629  
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DB 1750 ACTCCACTGAAATGACAGCTACTCTCAACATTGAACAGCTGATCAAGCAGATCC 1809  
QY 2253 CTGCAAGTTCTGCGCTGCGGGAATTTGCCAATGTGTAAGAAACGAACGACCTGAGGA 2312  
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DB 1930 AGGCTCTGTGGCCCTGGACAAAGGAATGCGAGGTCTCTCAAGGAAAGGAGCTCCATG 1989

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QY 2553 AGAATTTAAACATCAAGATTTGGAGAGAAATTTAAACCTGAAATGTACATTTATCACT 2612  
DB 2110 AGAATTTAAACATCAAGATTTGGAGAGAAATTTAAACCTGAAATGTACATTTATCACT 2169  
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DB 2170 AGGCTATCTCAAGAGATGATTTGCTCTCAAGGAAATGAGACAGGCATATTCAG 2229  
QY 2673 GGTCAATCAAAATCCAGACATACAGTCAACACTGAGATGACACACCATATTTCAAT 2732  
DB 2230 GGTCAATCAAAATCCAGACATACAGTCAACACTGAGATGACACACCATATTTCAAT 2289  
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DB 2290 ATGAAAGATCATGTACTTGGCAACAGTAAATCTGAAAAAAGACACTTATTTA 2349  
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QY 2913 ACAAGCATAGCTTACTTATGTTTAAAGGACGTAACAATTTATGGAGCAAACTCTTTA 2972  
DB 2470 ACAAGCATAGCTTACTTATGTTTAAAGGACGTAACAATTTATGGAGCAAACTCTTTA 2529  
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QY 3033 AGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3092  
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QY 3093 TCTGATTAACACAAACCTCAGATTCAGTTATTTAGGACACATGTTTATAGCACTAC 3152  
DB 2650 TCTGATTAACACAAACCTCAGATTCAGTTATTTAGGACACATGTTTATAGCACTAC 2709  
QY 3153 TGGTCAATAGTGAAGCTGTTTGTGCGCAATATCTTGAATGTTGTTTAAAGAACT 3212  
DB 2710 TGGTCAATAGTGAAGCTGTTTGTGCGCAATATCTTGAATGTTGTTTAAAGAACT 2769  
QY 3213 GAGGTTGAGATCAATCAATGGAATAATCTTCTTCTGTTACTACACAAAGCTAT 3272  
DB 2770 GAGGTTGAGATCAATCAATGGAATAATCTTCTTCTGTTACTACACAAAGCTAT 2829  
QY 3273 TTTAAAGAAAGATGCTATGTTGGAGAGGCGAAGTTGACTATATGACATATCAAT 3330  
DB 2830 TTTAAAGAAAGATGCTATGTTGGAGAGGCGAAGTTGACTATATGACATATCAAT 2887

RESULT 4  
ADAI4842  
ID ADAI4842 standard; cDNA; 2887 BP.  
XX ADAI4842;  
AC  
XX  
DT 06-NOV-2003 (first entry)  
XX  
XX Human Interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.  
DE ss: gene; human; IPMC 150 isoform B; gene therapy;  
XX  
XX  
KM Interphotoreceptor matrix component; IPMC; ocular disorder;

KW macular degeneration; photoreceptor death; retinal detachment.  
XX OS Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 5..2143  
FT /\*tag= a  
FT /partial  
FT /product= "IPMC 150 isoform B"  
FT /note= "No start codon given. Encodes residues 8-719 of  
FT {seqid:4}"  
XX US2002160954-A1.  
XX 31-OCT-2002.  
XX 08-NOV-2001; 2001US-00007270.  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX (IOWA ) UNTV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
XX MPI; 2003-238235/23.  
XX P-PsDB; ADA14843.  
XX New isolated or recombinant interphotoreceptor matrix component  
XX polynucleotide and polypeptide, useful for diagnosing, preventing,  
XX treating or prognosticating ocular disorders, e.g. macular degeneration  
XX or retinal detachment.  
XX Claim 3; Page 33-34; 76pp; English.  
XX The invention relates to an isolated or recombinant interphotoreceptor  
XX matrix component (IPMC) polynucleotide. Also disclosed is a vector  
XX comprising a promoter of an interphotoreceptor matrix component (IPMC)  
XX gene operatively linked to the IPMC polynucleotide. The IPMC  
XX polynucleotides, polypeptides and antibodies are useful for diagnosing,  
XX preventing, treating or prognosticating ocular disorders, e.g. macular  
XX degeneration, photoreceptor death or retinal detachment. They are also  
XX useful for identifying a compound capable of modulating IPMC gene  
XX expression in a cell. The present sequence represents cDNA encoding human  
XX interphotoreceptor matrix component, IPMC, 150 isoform B.  
SQ Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;  
Query Match 74.4%; Score 2476; DB 10; Length 2887;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2576; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 753 AGATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTCACTCTGTATGACACCTCTCTAA 812  
DB 310 AGATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTCACTCTGTATGACACCTCTCTAA 369  
QY 813 TGAATTCCTCGAATTAACAACAACAACAACAACAACAACAACAACAACAACAACAACA 872  
DB 370 TGAATTCCTCGAATTAACAACAACAACAACAACAACAACAACAACAACAACAACA 429  
QY 873 ATTGCTGTGTGAGAGACAGAGGTGAGCTCAGCGTCTCTGTGTAAACCAAGTT 932  
DB 430 ATTGCTGTGTGAGAGACAGAGGTGAGCTCAGCGTCTCTGTGTAAACCAAGTT 489  
QY 933 CAAGCAGAGCTGCTGACTCCCAAGTCCCATATTAACAAGAGCTAGCAGAAAGTCCA 992  
DB 490 CAAGCAGAGCTGCTGACTCCCAAGTCCCATATTAACAAGAGCTAGCAGAAAGTCCA 549  
QY 993 ACTTCAGATGCAAAAGATATTTAAAGAACTTCCAGATTCAAAATAATCAAGTGTAG 1052  
DB 550 ACTTCAGATGCAAAAGATATTTAAAGAACTTCCAGATTCAAAATAATCAAGTGTAG 609  
QY 1053 ATTAGACCAAGAAAGAAAGATGCTCAAGCTTCACAGAGATGCACTTACGGCCAT 1112

DB 610 ATTTAGACAAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCACTTACGGCCAT 669  
QY 1113 CTTTAAAGAGACAGCTGACAGAGCAAAAGCCCTGCAAGTACCTCTGTCTTTGATTC 1172  
DB 670 CTTTAAAGAGACAGCTGACAGAGCAAAAGCCCTGCAAGTACCTCTGTCTTTGATTC 729  
QY 1173 CAACAAATTGAAGTGAAGAGAGTCTATCATGAAACCATGAGAGGACAAGCAACAGA 1232  
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DB 790 AATCTATCTCAGACTACAGACTCAAAAGGCTGATCAGCAAGCACTAGAGAAAGCA 849  
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DB 850 ATCTTTGATGTGGGAGCAATTCAGTTCACTGATGAAATTCCTGATACCTGCCAGCTT 909  
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DB 910 TGGTCTGAGACCCCAATCAGAGCTGCCCAATCTTTGCTGTTTAAACAGAGATGCTAC 969  
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DB 1150 AATGGCCTAGCAGACCAATGCTAGTACAGAGGCTCCACATCCCAAGTATATTC 1209  
QY 1653 TGCATACGCCAAGCTGCTGTGGGAATTTCAATCCACTGCTATTCATGATGACAGCG 1712  
DB 1210 TGCATACGCCAAGCTGCTGTGGGAATTTCAATCCACTGCTATTCATGATGACAGCG 1269  
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QY 1833 GAGAGATACCACTCTGTGTCTCAGCTTTACAGTATATCACCACTAGTTCTTAGACCATTC 1892  
DB 1390 GAGAGATACCACTCTGTGTCTCAGCTTTACAGTATATCACCACTAGTTCTTAGACCATTC 1449  
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DB 1450 CCCCAAGGCGGAGAGCTGTAGTGTCTTCAAGTGTGCTGTGCTAATGAGCTTCTC 1509  
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DB 1510 CAACGACCTGTTCACAAGAGCTCTTGAAGTACCGAGCTCTGAGCAACAATTGACA 1569  
QY 2013 GCTGCTGTTTCATATCTACAGATCCAACTTACAGAGTTTAAAGCACTTGAATCTTAA 2072  
DB 1570 GCTGCTGTTTCATATCTACAGATCCAACTTACAGAGTTTAAAGCACTTGAATCTTAA 1629  
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QY 2133 TAACTTCACAAAGGCTGTGACAGGAGCTTGGAGAGATTTGTGCTGACGCCAACA 2192

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Db 2050 TCACAAATTAACAAGTATCATGTAAGAAATTCGAAATTAAGTACCGGTGAATATGA 2109  
Qy 2553 AGAATTTAACATCAAGATTGGAGAAATTTAAAACTGAAATGTACATTTATCATCTT 2612  
Db 2110 AGAATTTAACATCAAGATTGGAGAAATTTAAAACTGAAATGTACATTTATCATCTT 2169  
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Db 2230 GGTCAATCAAAATCCAGACATACAGTCAACATGAGATGAGACACACCATATTTCAAAT 2289  
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Db 2410 TGATCATTAAGCAGGTTGCTTCCACCTCCCTGAAAAATTTTACTCAGACGATCATTTGCA 2469  
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Qy 3273 TTTAAAGAGATGCTATGTTGGAGAGGCGCAAGTTGACTATATGACATATCAT 3330  
Db 2830 TTTAAAGAGATGCTATGTTGGAGAGGCGCAAGTTGACTATATGACATATCAT 2887  
RESULT 5  
AAA46205  
ID AAA46205 standard; cDNA, 3263 BP.  
XX  
AC AAA46205;  
XX  
DT 04-SBP-2000 (first entry)  
XX  
DE cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).  
XX  
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
KW chromosome 6q13-q15; ocular disease; retinal detachment;  
KW choriorretinal degeneration; retinal degeneration; cone degeneration;  
KW age related macular degeneration; photoreceptor degeneration;  
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
KW rod-cone dystrophy; cone-rod dystrophy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 128..244  
FT /tag=a  
FT /trans\_except= (pos: 2411..2414, aa: Lys)  
FT /product="Interphotoreceptor matrix proteoglycan IPM150"  
XX  
PN WO200026367-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99WO-US025440.  
XX  
PR 29-OCT-1998; 98US-00183972.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Hageman GS, Kuehn MH;  
XX WPI; 2000-365616/31.  
XX P-PSDB; AAY93336.  
XX  
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
PT preventing, diagnosing and treating ocular disorders such as retinal  
PT detachment and Choriorretinal degeneration.  
XX  
PS Claim 2; Fig 3; 183pp; English.  
XX  
CC The present sequence encodes an interphotoreceptor matrix (IPM)  
CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).  
CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
CC is located on chromosome 6q13-q15, between markers CHC.GATA1P10 and  
CC D6S284. The IPM proteins may be used to supplement a patient's own  
CC production of the protein or to rectify alterations in their nucleic  
CC acids that result in expression of an inactive protein. The IPM nucleic  
CC acids may be used in this way to treat ocular diseases such as retinal  
CC detachment, choriorretinal degeneration, retinal degeneration, age related  
CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment  
CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
CC also be used to assay for other modulators of IPM proteoglycan expression  
CC and activity that may be used to treat ocular diseases. The nucleic acids  
CC and proteins may also be used as diagnostic reagents to detect the  
CC presence of IPM nucleic acids and their products in samples from patients  
CC according to standard methodologies  
XX  
SQ Sequence 3263 BP; 1040 A; 721 C; 663 G; 838 T; 0 U; 1 Other;  
Query Match 62.9%; Score 2095; DB 3; Length 3263;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2575; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

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Db |||||||
QY 688 AGATGTCGCAACGCTCTCACTTGGGCTTCCCTCTCACTCCCTGATGACACCTCTCTCA 747
Db |||||||
QY 813 TGAATAATCTCGAATAATACACTCAACGACACCAAGATGCTTACAAACGAAAGAAACAGA 872
Db 748 TGAATAATCTCGAATAATACACTCAACGACACCAAGATGCTTACAAACGAAAGAAACAGA 807
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Db 868 CAAGGCAAGCTCGGCTGACTCCAGTCCCATATTACAGAGACTAGAGGAAAGTCCCA 927
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Db 928 ACTTCAGATGCAAAAAGATATTTAAGAACTTCAGAGATTCAAAAAATCCATGTGTAG 987
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Db 1168 AATCTATCTCAGCTACAGACTCTCAAAAGCTGATCAGCAAGCACTAGAGAAAGACA 1227
QY 1293 ATCTTGGATGGGGGCAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCCT 1352
Db 1228 ATCTTGGATGGGGGCAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCCT 1287
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QY 1473 TGGTCACTGACACTTCTTGGTCTGCACTGCTATGAGCTGTAACCTCCCTGTCAGAAC 1532
Db 1408 TGGTCACTGACACTTCTTGGTCTGCACTGCTATGAGCTGTAACCTCCCTGTCAGAAC 1467
QY 1533 TCCAACCTTCTTATGAGCATCAAGCATCTTCTCTGACTGATCAAGGACCAAGATAC 1592
Db 1468 TCCAACCTTCTTATGAGCATCAAGCATCTTCTCTGACTGATCAAGGACCAAGATAC 1527
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Db 1528 AATGGCACTGACCAAGCATGCTAGTACAGAGGCTCACATCCCAAGTGAATTATTC 1587
QY 1653 TGGAAATCAGCCCAATGGCTCTGGGAATTTCAATCCACTGCACTTTCAGATGACGCG 1712
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Db 1648 ATCAAGTGAAGTGGGGAAGATATGCTCAGACACTAGATGAAATGATCTGTCTGACAC 1707
QY 1773 TCTGCCCCATCTGAGGTACAGAGTCAAGCGAATATGTTTCTGTCCAGATCATTTCT 1832
Db |||||||
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Db 1708 TCTGCCCCATCTGAGGTACAGAGCTCAGGGAATATGTTCTGTCCAGATCATTTCT 1767
QY 1833 GGAGGATACCACTCCGCTCAGGCTTACAGATATACCACTAGTCTATAGCAATTC 1892
Db |||||||
QY 1768 GGAGGATACCACTCCGCTCAGGCTTACAGATATACCACTAGTCTATAGCAATTC 1827
Db |||||||
QY 1893 CCCCAAGGGGCGAGAGCTGTAGTGTCTTCAAGTCTGCGTGTGTAAACATGGCTCTGC 1952
Db 1828 CCCCAAGGGGCGAGAGCTGTAGTGTCTTCAAGTCTGCGTGTGTAAACATGGCTCTGC 1887
QY 1953 CAACGACTGTTCAACAAAGACTCTCTGGAAGTACCGAGCTTGAGCAACATTTACACA 2012
Db 1888 CAACGACTGTTCAACAAAGACTCTCTGGAAGTACCGAGCTTGAGCAACATTTACACA 1947
QY 2013 GCTGCTGATTCATATCTACGATCCAACTTACAGATTTTAAAGCACTTGAAATACTTAA 2072
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QY 2073 CTTCAAGAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTTGTAAATGTCGCGTA 2132
Db 2008 CTTCAAGAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTTGTAAATGTCGCGTA 2067
QY 2133 TAACTTCAACAAAGCTGTGACAGGGCTTTGAGAGATTTTGTTCTCTGCAACCCCAACA 2192
Db 2068 TAACTTCAACAAAGCTGTGACAGGGCTTTGAGAGATTTTGTTCTCTGCAACCCCAACA 2127
QY 2193 ACTCATCTGGAATAATAGACAGTACTCTCTCAACTTGAACAGCTGATCAAGCAGATCC 2252
Db 2128 ACTCATCTGGAATAATAGACAGTACTCTCTCAACTTGAACAGCTGATCAAGCAGATCC 2187
QY 2253 CTGCAAGTTCTCTGCGCTCGCGAATTTTGCCCAATGTGTAAAGAACGACCTGAGGA 2312
Db 2188 CTGCAAGTTCTCTGCGCTCGCGAATTTTGCCCAATGTGTAAAGAACGACCTGAGGA 2247
QY 2313 AGCGAGTGTGCTGCAACCAAGATATGACACGCCAGGGAGCTGTGACGCTGTGGAACC 2372
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Db 2308 AGGCTCTGTGGG-CTTGCAACAAAGAAATGAGAGTCTCCCAAGGAAAGGAGCTCAATG 2366
QY 2433 CAGGTTGCAAGTCACTCTGAAATCAAGCATACAAAATAGTGTAAAAAGTTCAAAA 2492
Db 2367 C-GGTT-CGAGTCACTCTGAAATCAAGCATACAAAATAGTGTAAAAAGTTCAAAA 2424
QY 2493 TCAACAAATTAACAAAGTATCAAGTAAAGAAATTTCTGAATTA-CTGACCGTGAATATG 2551
Db 2425 TCAACAAATTAACAAAGTATCAAGTAAAGAAATTTCTGAATTAATCTGACCGTGAATATG 2484
QY 2552 AAGATTTTACCATCAAGATTTGGGAAGAAATTTAAATCTGAAATATGTAATTAATCACT 2611
Db 2485 AAGATTTTACCATCAAGATTTGGGAAGAAATTTAAATCTGAAATATGTAATTAATCACT 2544
QY 2612 TAGGCTATCTCAAGAGATGATTTTGCTTCAAGGAAATGAGACAGGATATTCAT 2671
Db 2545 TAGGCTATCTCAAGAGATGATTTTGCTTCAAGGAAATGAGACAGGATATTCAT 2604
QY 2672 GGGTATCAAAAATCCAGACATACAGTCAACACTGGAATGACGACACACATATTTCAA 2731
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QY 2732 TATTAAGAGTCATGTAATCTGCAACAGTAAATCTGAAATTAAGACACTTACTTAT 2791
Db 2665 TATTAAGAGTCATGTAATCTGCAACAGTAAATCTGAAATTAAGACACTTACTTAT 2724
QY 2792 ATTTAAACCCCAATATGACGAAACATATTTTATCTATCTTGTGATGATGCAAA 2851
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OY	2912	AACAAGCACTACCTTA	CTTAATGTTTAGGGA	CTGAACAATTATTTAGGGAAGAA	ACTCTT	2971
Db	2845	AACAGCACTACCTTA	CTTAATGTTTAGGGA	CTGAACAATTATTTAGGGAAGAA	ACTCTT	2904
OY	2972	ATATGCTAGAAAGTA	CACTTTAAAGANTGA	CTACTACGAGGAGANTCAGGTC	CTCTTA	3031
Db	2905	ATATGCTAGAAAGTA	CACTTTAAAGANTGA	CTACTACGAGGAGANTCAGGTC	CTCTTA	2966
OY	3032	AACGATTAATGTATGT	ATGTGTGTATGGCA	CTGTACTGATGTATATATGCTCCACA	CTAC	3091
Db	2965	AACGATTAATGTATGT	ATGTGTGTATGGCA	CTGTACTGATGTATATATGCTCCACA	CTAC	3024
OY	3092	GTCGTATTAACACAA	ACCTCAGTATTCAGTTA	ATTAGGACA	CTGTTTATATACGA	CACTA 3154
Db	3025	GTCGTATTAACACAA	ACCTCAGTATTCAGTTA	ATTAGGACA	CTGTTTATATACGA	CACTA 3084
OY	3152	CTGCTTACATAGTAGA	CTGTTTTGTGTGCCAAT	TAATCTTTGAATGTTCTTTAAAA	GAAC	3211
Db	3085	CTGCTTACATAGTAGA	CTGTTTTGTGTGCCAAT	TAATCTTTGAATGTTCTTTAAAA	GAAC	3144
OY	3212	TGAGGTCAGATACACAT	ACATGGAATAATCTTA	CTTTCTGTACTACACAA	AGCTA	3271
Db	3145	TGAGGTCAGATACACAT	ACATGGAATAATCTTA	CTTTCTGTACTACACAA	AGCTA	3204
OY	3272	TTTTTAAACAATGCTAT	GTTGGGAGAAAGGCGAAG	TGTACTATATAGCACTAAT	CAAT 3330	
Db	3205	TTTTTAAACAATGCTAT	GTTGGGAGAAAGGCGAAG	TGTACTATATAGCACTAAT	CAAT 3263	

RESULT 6  
ACC57960  
ID ACC57960 standard; cDNA; 3261 BP

DT 11-AUG-2003 (first entry)

Human Interphotoreceptor matrix IPM 150, isoform A variant, cDNA.

KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15, IPMC;  
KW receptor; ophthalmological; gene therapy; gene; ss.

**Homo sapiens.**

FH	Key	Location/Qualifiers
FT	CDS	128. .2443
FT		/*tag= a
FT		/product= "IPM 150"

PN WO2003039346-A2.

PD 15-MAY-2003.

PF 08-NOV-2002; 2002WO-US036090

PR 08-NOV-2001; 2001US-00077270

PA (IOWA ) UNIV IOWA RES FOUND.

PI Hageman GS, Kuehn MH;

DR WPI; 2003-441440/41.

XX  
XX

PT New interphotoreceptor matrix proteins and polynucleotides, useful for  
PT treating or preventing photoreceptor death or retinal detachment, or for  
PT creating ocular disorders.

PS Claim 1; Page 91-94; 105pp; English.

CC The present sequence is that of cDNA encoding a variant of isoform A of  
CC novel human interphotoreceptor matrix 150 (IPM 150), a member of the

CC newly identified invertebrate receptor matrix component (IPMC) gene family.  
CC The cDNA was isolated from a human retinal cDNA library. The IMP 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bilateral choroidretinal atrophy, autosomal dominant Steargard's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IMPG1) and IPM 200 (or IMPG2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polynucleotides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression  
XX  
SQ Sequence 3261 BP, 1039 A, 721 C, 663 G, 837 T, 0 U, 1 Other;

Query Match	62.9%	Score 2094;	DB 9;	length 3261;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 2574;	Conservative	0;	Mismatches 0;	Indels 4;
			Gaps	4

753 AGATGTTGCCAACGTTCTCACTTGGGCTTTCCTCTCACTCTGATGACACCTCTCAA 812

Db 688 AGATGTTGCCAAGTCTCACTTGGCCTTCCCTCTCACTCCCTGATGACACCCCTCTCA 747

QY 813 TGAATTCTGATAATACACTCAACGACACCAAGATGCCCTACACAGAGAAGAAACAGA 872

Db 748 TGAATTCTCGATAATACACTCAACGACACCAAGATGCTTACAACAGAAAGAGAAACAGA 807

873 ATTCGCTGTGTGGAGGAGCAGAGGTTGAGCTCAGCGTCTCTCTGGTAAACCAAGATT 932

Db 808 ATTGGCTGTGTGAGGAGCAGAGGCTGAGCTCAGCGTCTCTCTGTAACCAAGAGTT 867

933 CAAGCAGAGCTCGCTGACTCCAGTCCCATATTACCAGAGCTAGCAGGAAGTCCA 992

Db 868 CAAGG CAGAGCTCGCTGACTCCAGTCCCATATTACCAGGAGCTAGCAGGAAGTCCA 927

993 ACTTCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAAAAAATCCATGTGTAGG 1052

Db 928 ACTTCAGATGC AAAAGATATTTAAGAACTTCCAGGATTC AAAAAAATCCATGTGTAGG 987

1053 ATTTAGACCAAGAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCAT 1112

Db 988 ATTGACCCAAGAAAGATGCTCAAGCTCCACAGAGATGCACTTACGGCCAT 1047

1113 CTTTAAAGACACAGTGCAGAGCAAAAAGCCCTGCAAGTGACCTCCTGTCTTTGATTC 1112

Db 1048 CTTTAAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGTGACCTCCTGTCTTTTGATTC 1107

QY 1173 CACCAAAATTGAAAGTGAGGAGTCTATCATGGAACCATGAGAGGACAAGCAACCAGA 1232

Db 1108 CAACAATAATGAACTGAGGAAGTCTATCATGGAACCATGGAGGAGACAAGCAACCAGA 1167

1233 AATCTATCTCAGCTACAGACCTCAAAGGCTGATCAGCAAGCACTAGAGGAGACA 1292

Db 1168 AATCTATCTACAGCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGGAGACA 1227

1293 ATCTTGGATGTGGGACAATTCAGTTCACGTGAAATTGCTGGATCACTGCCAGCCTT 1352

Db 1228 ATCTTTGGATGTGGGACAATTCAGTTCACGTGAAATGCTGGATCACTGCCAGCCTT 1287

1353 TGGTCCTGACACCAATCAGAGCTGCCACATCTTTGCTGTATACAGAGATGCTAC 1412

Db 1288 TGGTCCTGACACCCCAATCAGAGCTGCCACATCTTTGCTGTTATAACAGAGATGCTAC 1347

1413 TTGAGTCCAGACTTCTCTGTGAACCCAGCTTGAGACAGTGGACGGACGAGCA 1472

Db 1348 TTTGAGTCCAGACTTCCTCCTGTGAAACCCAGCTTGAGACAGTGGAACGAGCAGAGCA 1407

1473 TGGTCTACCTGACACTTCTTGGTCTCCACCTGCTATGGCCTTACCTCCCTGTCAGAAGC 1532

DB 1408 TGGTCTACCTGACACTTCTTGGTCTCCACCCTGCTATGGCCCTCTACCTCCCTGTGAGAGC 1467

OY	1533	TCGACCTTTCTTTATGGGATCGAATCTTCTCTGATCGATCAAGGCACCAAGATAC	1552
Db	1468	TCGACCTTTCTTTATGGGATCGAAGATCTTCTCTGATCGATCAAGGCACCAAGATAC	1557
OY	1593	AATGGCCACTACCAAGACAATGCTAGTATCGAAGGCTCACATCCCAACAGTGAATTATC	1652
Db	1528	AATGGCCACTACCAAGACAATGCTAGTATCGAAGGCTCACATCCCAACAGTGAATTATC	1587
OY	1653	TGCAATCAGCCCAATCGGCTCTGGGAAATTTCAATCCACCTGCATCTTCAATGACAGCG	1712
Db	1588	TGCAATCAGCCCAATCGGCTCTGGGAAATTTCAATCCACCTGCATCTTCAATGACAGCG	1647
OY	1713	ATCAAGTSCAGGTGGCGAAGATATGGTACAGACCTAGATGAATGATCTGTGACAC	1772
Db	1648	ATCAAGTSCAGGTGGCGAAGATATGGTACAGACCTAGATGAATGATCTGTGACAGC	1707
OY	1773	TCCTGCCCCATCTGAGGTACCAAGGCTCAGGAAATATGTTTCTGTCCAGATCAATTTCTT	1832
Db	1708	TCCTGCCCCATCTGAGGTACCAAGGCTCAGGAAATATGTTTCTGTCCAGATCAATTTCTT	1767
OY	1833	GGAGGATACCACTCCTGCTCAGGCTTACATATATGACCACTAGTCTTAAGACATATGC	1892
Db	1768	GGAGGATACCACTCCTGCTCAGGCTTACATATATGACCACTAGTCTTAAGACATATGC	1827
OY	1893	CCCCAAGGCGCAGAGCTGATAGTGTCTTCAGCTGCGTGTCTTAACATAGGCTTCTC	1952
Db	1828	CCCCAAGGCGCAGAGCTGATAGTGTCTTCAGCTGCGTGTCTTAACATAGGCTTCTC	1887
OY	1953	CAAGACCTGTTTCAACAAGAGCTCTCTGGAGTACCGAGCTTGGAGCACAATTCACACA	2012
Db	1888	CAAGACCTGTTTCAACAAGAGCTCTCTGGAGTACCGAGCTTGGAGCACAATTCACACA	1947
OY	2013	GCTGCTGGTTTCATATCTACAGATCCAACTCTTACAGATTTTAAGCACTTGAATACTTAA	2072
Db	1948	GCTGCTGGTTTCATATCTACAGATCCAACTCTTACAGATTTTAAGCACTTGAATACTTAA	2007
OY	2073	CTTCGAAACGGAGGTGATTTGTGAATAGCAAAATGAAAGTTTGTAAAGTCTGCGGTA	2132
Db	2008	CTTCGAAACGGAGGTGATTTGTGAATAGCAAAATGAAAGTTTGTAAAGTCTGCGGTA	2067
OY	2133	TAACTCTCAACAAAGCTGTGCAACGGGCTCTTGGAGATTTTGGTCTGCTGACGCCAACA	2192
Db	2068	TAACTCTCAACAAAGCTGTGCAACGGGCTCTTGGAGATTTTGGTCTGCTGACGCCAACA	2127
OY	2193	ACTCCATCTGGAATATAGACAGTACTCTCTGAACAATTGAACAGCTGATCAAGCAGATCC	2252
Db	2128	ACTCCATCTGGAATATAGACAGTACTCTCTGAACAATTGAACAGCTGATCAAGCAGATCC	2187
OY	2253	CTGCAAGTTCTTGCGCTCTGCGCGGAATTTGCCAATGTGTAAAGAACGAACGACTGAGGA	2312
Db	2188	CTGCAAGTTCTTGCGCTCTGCGCGGAATTTGCCAATGTGTAAAGAACGAACGACTGAGGA	2247
OY	2313	AGCGAGTGTGCTGSCAAACCAAGATATAGACAGCCAGGAGGAGCTGAGCGTCTGGAACC	2372
Db	2248	AGCGAGTGTGCTGSCAAACCAAGATATAGACAGCCAGGAGGAGCTGAGCGTCTGGAACC	2307
OY	2373	AGGCTCTGTGAGCCTTGCAACAAGAAATGCGAGGTCTCTCCAGGAAAGGAGCTCCATG	2432
Db	2308	AGGCTCTGTGAGCCTTGCAACAAGAAATGCGAGGTCTCTCCAGGAAAGGAGCTCCATG	2366
OY	2433	CAGGTGGCAATCTCTGAAAATCAAGCATCAAACTAGTGTAAAGAAAGTTCCAAA	2492
Db	2367	CAGGTGGCAATCTCTGAAAATCAAGCATCAAACTAGTGTAAAGAAAGTTCCAAA	2423
OY	2493	TCACAAATAATCAAGGTATCAGTAAAGAAATTCGAAATTAAGTACCTGACCTGAGATATGA	2552
Db	2424	TCACAAATAATCAAGGTATCAGTAAAGAAATTCGAAATTAAGTACCTGACCTGAGATATGA	2483
OY	2553	AGAAATTTAACATCAAGATTTGGGAAAGGAAATTTAAAACTGAAATATGATCAATTCACTT	2612
Db	2484	AGAAATTTAACATCAAGATTTGGGAAAGGAAATTTAAAACTGAAATATGATCAATTCACTT	2543

QY	2613	AGGCTATCTCAAGAGAGATGATTTGGCTTCTCAAGAAAAATGGAGACAGGCATATTGATG	2612
Db	2544	AGGCTATCTCAAGAGAGATGATTTGGCTTCTCAAGAAAAATGGAGACAGGCATATTGATG	2603
QY	2673	GGTCATCAAAATCCAGACATACAGTCAACACTGAGATTCAGACACACCATATTTCAAAT	2732
Db	2664	GGTCATCAAAATCCAGACATACAGTCAACACTGAGATTCAGACACACCATATTTCAAAT	2663
QY	2733	ATGAGAGATCATGTACTTGGCAACCACTAAATTCGAAAAAAAAGACCTTACTTTTA	2792
Db	2664	ATGAGAGATCATGTACTTGGCAACCACTAAATTCGAAAAAAAAGACCTTACTTTTA	2723
QY	2793	TTAAAAACCCAAATGCAATCAGGAAAAATATTTTTCATTCCTGGATATATGTCAAA	2852
Db	2724	TTAAAAACCCAAATGCAATCAGGAAAAATATTTTTCATTCCTGGATATATGTCAAA	2783
QY	2853	TGATCATTAAGCAGAGTTTGCTTCCACCTTCCCTGAAATTTTACTCAGATCATTTGCA	2912
Db	2784	TGATCATTAAGCAGAGTTTGCTTCCACCTTCCCTGAAATTTTACTCAGATCATTTGCA	2843
QY	2913	ACAAGCATAGCTTACTTATTTGTTTAAAGGACTGAACAAATTTATTTGGAGCAAACTTTTA	2972
Db	2844	ACAAGCATAGCTTACTTATTTGTTTAAAGGACTGAACAAATTTATTTGGAGCAAACTTTTA	2903
QY	2973	TATGCTAGAAAAGTACATTTTAAAAATATCTACTTACCGCAGGAGATACAGTCTCTTAA	3032
Db	2904	TATGCTAGAAAAGTACATTTTAAAAATATCTACTTACCGCAGGAGATACAGTCTCTTAA	2963
QY	3033	ACGCATGAATGTATGTAGTGTAGGACACTGTAGTGAAGTATATATGCTCCACACTACG	3092
Db	2964	ACGCATGAATGTATGTAGTGTAGGACACTGTAGTGAAGTATATATGCTCCACACTACG	3023
QY	3093	TCTGATAAACCAAAACCTCAGTATTCAGTTATTAGGCACACTAGTTTATACGCACTAC	3152
Db	3024	TCTGATAAACCAAAACCTCAGTATTCAGTTATTAGGCACACTAGTTTATACGCACTAC	3083
QY	3153	TGCTTACCATAGTACAGTGTTTTGTGGCAATATCTTTGAATTGTCTTTAAAAAGAACT	3212
Db	3084	TGCTTACCATAGTACAGTGTTTTGTGGCAATATCTTTGAATTGTCTTTAAAAAGAACT	3143
QY	3213	GAGGTTCAGATACATACATCGATGGAAAAATCTTCTTGTGTACTACAAAGCTAT	3272
Db	3144	GAGGTTCAGATACATACATCGATGGAAAAATCTTCTTGTGTACTACAAAGCTAT	3203
QY	3273	TTTAAAGAGATGCTATGTTGGAGAAAGGCGAAGTTGTACTATATGACATTAATCAAT	3330
Db	3204	TTTAAAGAGATGCTATGTTGGAGAAAGGCGAAGTTGTACTATATGACATTAATCAAT	3261
RESULT 7			
ADAI4866			
ID	ADAI4866	standard, cDNA, 3261 BP.	
XX	ADAI4866;		
DT	06-NOV-2003	(first entry)	
DE	Human cDNA encoding variant IPMC 150 isoform A.		
KM	88; gene; human; IPMC 150 isoform A; gene therapy; interphotoreceptor matrix component; IPMC; ocular disorder; macular degeneration; photoreceptor death; retinal detachment.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	CDS	128..2443	
FT		/*tag= A	
FT		/product= "Variant IPMC 150 isoform A"	
PD	US2002160954-A1.		
XX	31-OCT-2002.		

XX 08-NOV-2001; 2001US-00007270.  
PF  
XX 29-OCT-1998; 98US-00183972.  
PR  
XX 29-OCT-1999; 99US-00430195.  
PR  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA  
XX Hageman GS, Kuehn MH;  
PI  
XX MPI; 2003-238235/23.  
DR  
XX P-PSDB; ADA14667.  
XX  
PT New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.  
XX  
XX  
PS Claim 3; Page 63-66; 76pp; English.  
XX  
XX The invention relates to an isolated or recombinant interphotoreceptor  
XX matrix component (IPMC) polynucleotide. Also disclosed is a vector  
XX comprising a promoter of an interphotoreceptor matrix component (IPMC)  
XX gene operatively linked to the IPMC polynucleotide. The IPMC  
XX polynucleotide, polypeptides and antibodies are useful for diagnosing,  
XX preventing, treating or prognosticating ocular disorders, e.g. macular  
XX degeneration, photoreceptor death or retinal detachment. They are also  
XX useful for identifying a compound capable of modulating IPMC gene  
XX expression in a cell. The present sequence represents cDNA encoding  
XX variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
SQ  
Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;  
Query Match 62.9%; Score 2094; DB 10; Length 3261;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2574; Conservative 0; Mismatches 0; Indels 4; Gaps 4;  
QY 753 AGATGTGGCAACGCTCACTTGGGCTTTCCTCTCACTCTGATGACACCTCTCTCA 812  
DB 688 AGATGTGGCAACGCTCACTTGGGCTTTCCTCTCACTCTGATGACACCTCTCTCA 747  
QY 813 TGAATTCCTCGAATATACCTACGACGACCAAGATGCTTACAGAAAGAAACGA 872  
DB 748 TGAATTCCTCGAATATACCTACGACGACCAAGATGCTTACAGAAAGAAACGA 807  
QY 873 ATTCGCTGTGTGAGAGACAGAGGTGAGCTCAGCGTCTCTGTGTAACCAAGAGTT 932  
DB 808 ATTCGCTGTGTGAGAGACAGAGGTGAGCTCAGCGTCTCTGTGTAACCAAGAGTT 867  
QY 933 CAAAGCAGAGCTCGCTGACTCCCAAGTCCCATATTAACAGAGCTAGAGAAAGTCCA 992  
DB 868 CAAAGCAGAGCTCGCTGACTCCCAAGTCCCATATTAACAGAGCTAGAGAAAGTCCA 927  
QY 993 ACTTGAGATGCAAAAGATATTTAAAGAACTTCCAGATTCAGAAAAATCAAGTGTAG 1052  
DB 928 ACTTGAGATGCAAAAGATATTTAAAGAACTTCCAGATTCAGAAAAATCAAGTGTAG 987  
QY 1053 ATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCAGAGATGCACTTACGGCCAT 1112  
DB 988 ATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCAGAGATGCACTTACGGCCAT 1047  
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DB 1048 CTTTAAAGACACAGTGCAGAAACAAAAGCCCTGCAAGTGAACCTCTCTTTTGAATTC 1107  
QY 1173 CAACAAATTTGAAAGTGAAGTCTATCATGGAACATGGAAGGAGCAACCAACCA 1232  
DB 1108 CAACAAATTTGAAAGTGAAGTCTATCATGGAACATGGAAGGAGCAACCAACCA 1167  
QY 1233 AATCTATCTCAGAGCTACAGACTCAAAAGGCTGATCAGCAAAAGCACTAGAGAAAGACA 1292  
DB 1168 AATCTATCTCAGAGCTACAGACTCAAAAGGCTGATCAGCAAAAGCACTAGAGAAAGACA 1227

QY 1293 ATCTTTGATGAGGAGCAATCTCACTTGCATGANGAAATGCTGATGACATGCCACCTT 1352  
DB 1228 ATCTTTGATGAGGAGCAATCTCACTTGCATGANGAAATGCTGATGACATGCCACCTT 1287  
QY 1353 TGGTCTTGACACCCATCAGAGCTGCCACATCTTTTGTCTTATTAACAGAGATGCTAC 1412  
DB 1288 TGGTCTTGACACCCATCAGAGCTGCCACATCTTTTGTCTTATTAACAGAGATGCTAC 1347  
QY 1413 TTTGAGTCAGAACTTCTCTGTGAAACCCAGCTTGAGACAGTGAACGAGACAGACA 1472  
DB 1348 TTTGAGTCAGAACTTCTCTGTGAAACCCAGCTTGAGACAGTGAACGAGACAGACA 1407  
QY 1473 TGGTCTTACCTGACATCTTCTGTGCTCCACCTGCTATGAGCTTACCTCCTGTCAAGAC 1532  
DB 1408 TGGTCTTACCTGACATCTTCTGTGCTCCACCTGCTATGAGCTTACCTCCTGTCAAGAC 1467  
QY 1533 TCCACCTTTCTTATGAGATCAAGACATCTTCTCTGACTGATCAAGGACACAGATAC 1592  
DB 1468 TCCACCTTTCTTATGAGATCAAGACATCTTCTCTGACTGATCAAGGACACAGATAC 1527  
QY 1593 AATGACCACTGACAGACAAATGCTAGTACAGAGGCTCACATCCACCACTGATTTATTC 1652  
DB 1528 AATGACCACTGACAGACAAATGCTAGTACAGAGGCTCACATCCACCACTGATTTATTC 1587  
QY 1653 TGCATTCAGCCAACTGGCTCTGGGAATTTCAATCCACTGCACTTTCAGATGACAGCCG 1712  
DB 1588 TGCATTCAGCCAACTGGCTCTGGGAATTTCAATCCACTGCACTTTCAGATGACAGCCG 1647  
QY 1713 ATCAAGTCAGAGTGCAGAAAGATATGCTGACAGACCTGAGTGAATGATCTCTGACAC 1772  
DB 1648 ATCAAGTCAGAGTGCAGAAAGATATGCTGACAGACCTGAGTGAATGATCTCTGACAC 1707  
QY 1773 TCTTGCCTCATCTGAGATACCAAGCTCAGCGAATATGTTCTGTCCAGATCATTTCTT 1832  
DB 1708 TCTTGCCTCATCTGAGATACCAAGCTCAGCGAATATGTTCTGTCCAGATCATTTCTT 1767  
QY 1833 GGAGATACCACTCTGTCTCAGCTTTTACAGTATATCACCACTAGTTCTATGACATTTGC 1892  
DB 1768 GGAGATACCACTCTGTCTCAGCTTTTACAGTATATCACCACTAGTTCTATGACATTTGC 1827  
QY 1893 CCCGAAGGCGAGAGCTGTGTGTCTTCAAGTCTGAGTGTGCTTAAACATGAGCCCTTTC 1952  
DB 1828 CCCGAAGGCGAGAGCTGTGTGTCTTCAAGTCTGAGTGTGCTTAAACATGAGCCCTTTC 1887  
QY 1953 CAACGACCTGTTCACCAAGAGCTCTCTGAGTACCGAGCTCTGAGCAACATTTACACA 2012  
DB 1888 CAACGACCTGTTCACCAAGAGCTCTCTGAGTACCGAGCTCTGAGCAACATTTACACA 1947  
QY 2013 GCTGCTGTTCCATATCTACGATCCATCTTAACAGATTTTAAAGCACTTGAATACTTAA 2072  
DB 1948 GCTGCTGTTCCATATCTACGATCCATCTTAACAGATTTTAAAGCACTTGAATACTTAA 2007  
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DB 2008 CTTGAGAAACGGGAGTGTGATTGTGAATAGCAAAATGAAAGTTTGTAGTCTGTGCGCTGA 2067  
QY 2133 TAACTTCAACAAAGCTGTGACAGGGGTCTTGAGAGATTTTCGTTCTGTGACGCCAACA 2192  
DB 2068 TAACTTCAACAAAGCTGTGACAGGGGTCTTGAGAGATTTTCGTTCTGTGACGCCAACA 2127  
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DB 2188 CTGCAAGTTCTCGGCTCGGCGAATTTTGGCCCAATGCTGTAAAGAAAGCAAGCACTGAGGA 2247  
QY 2313 AGCGAGTGTGCTGCAAAACCAAGATATGACAGCAAGGAGAGCTGGAACGCTGGAACC 2372  
DB 2248 AGCGAGTGTGCTGCAAAACCAAGATATGACAGCAAGGAGAGCTGGAACGCTGGAACC 2307  
QY 2373 AGGCTCTGTGCGCTTGGAACCAAGGAATGCGAGGTCTCTCCAGGGAAGGAGCTCCATG 2432



Db 550 ACTTCGATGCAAAAGATATTTAAGAACTTCAGAGATTCAAAATTCATGTGTAG 609  
Qy 1053 ATTTAGACCAAGAAAGAAAAGATGGCTCCAGCTCAGAGATGCCATTCAGGCCAT 1112  
Db 610 ATTTAGACCAAGAAAGAAAAGATGGCTCAGCTCAGAGATGCCATTCAGGCCAT 669  
Qy 1113 CTTTAAGACACAGTCAGAGCAAAAGCCCTGCAAGTGAACCTCTCTTTTGAATTC 1172  
Db 670 CTTTAAGACACAGTCAGAGCAAAAGCCCTGCAAGTGAACCTCTCTTTTGAATTC 729  
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Db 790 AATCTATCTCAGCTACAGACTCTCAAAAGCTGATCAGCAAAAGCACTAGAGAGACA 849  
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Db 850 AATCTTGAATGAGGAGCAATTCAGTTCACTGATGAATTTGCTGATCACTGCAAGCCTT 909  
Qy 1353 TGGTCTGACACCCATCAGAGCTGCCACATCTTTTGTGTTATACAGAGATCTAC 1412  
Db 910 TGGTCTGACACCCATCAGAGCTGCCACATCTTTTGTGTTATACAGAGATCTAC 969  
Qy 1413 TTTGAGTCCAGAACTTCTCTGTGTGAACCCCAAGCTTGAAGACAGTGAACGAGCAGAGA 1472  
Db 970 TTTGAGTCCAGAACTTCTCTGTGTGAACCCCAAGCTTGAAGACAGTGAACGAGCAGAGA 1029  
Qy 1473 TGGTCTACCTGACACTTCTTGGTCTCCAGCTGTATGAGCTCTACCTCCCTGTCAAGAC 1532  
Db 1030 TGGTCTACCTGACACTTCTTGGTCTCCAGCTGTATGAGCTGTACCTCCCTGTCAAGAAC 1089  
Qy 1533 TCCACCTTCTTTATGAGCATCAAGCATCTTCTCTGACTGATCAAGGACCAAGATAC 1592  
Db 1090 TCCACCTTCTTTATGAGCATCAAGCATCTTCTCTGACTGATCAAGGACCAAGATAC 1149  
Qy 1593 AATGGCATTGACACGACATGCTAGTACAGAGGCTCACCATGCCCAAGATGATTTATTC 1652  
Db 1150 AATGGCATTGACACGACATGCTAGTACAGAGGCTCACCATGCCCAAGATGATTTATTC 1209  
Qy 1653 TGCATCAGCCAACTGGCTCTGGGAATTTCACTCCAGCTGATCTTCAGATGACAGCGG 1712  
Db 1210 TGCATCAGCCAACTGGCTCTGGGAATTTCACTCCAGCTGATCTTCAGATGACAGCGG 1269  
Qy 1713 ATCAAGTGAAGTGGGAGATATGCTCAGACACTAGATGAATGATCTGTCTGACAC 1772  
Db 1270 ATCAAGTGAAGTGGGAGATATGCTCAGACACTAGATGAATGATCTGTCTGACAC 1329  
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Db 1330 TCCGCCCCATCTGAGATACAGAGGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTT 1389  
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Db 1390 GGAAGATACCACTCCCTGTCTCAGCTTTACAGATATACCACTAGTCTTATGACCATTC 1449  
Qy 1893 CCCCAAGGCGAGAGCTGTAGTGTCTTCACTGCTGAGTGTGCTTAAATGAGCCCTTCTC 1952  
Db 1450 CCCCAAGGCGAGAGCTGTAGTGTCTTCACTGCTGAGTGTGCTTAAATGAGCCCTTCTC 1509  
Qy 1953 CAAGCACTGTTCACAAGAGCTCTCTGAGATACCGAGCTCTGAGCAACAATTCACACA 2012  
Db 1510 CAAGCACTGTTCACAAGAGCTCTCTGAGATACCGAGCTCTGAGCAACAATTCACACA 1569  
Qy 2013 GCTGCTGCTTCAATATCTACATCCAACTCTTACAGATTTAAGCACTTGAATATCTTAA 2072  
Db 1570 GCTGCTGCTTCAATATCTACATCCAACTCTTACAGATTTAAGCACTTGAATATCTTAA 1629  
Qy 2073 CTTTCAAGAAACGGGAGTGTATGTTGTAATAGCAAAATGAGTTGTCTAGTCTGTGCGCTA 2132  
Db 1630 CTTTCAAGAAACGGGAGTGTATGTTGTAATAGCAAAATGAGTTGTCTAGTCTGTGCGCTA 1689

Qy 2133 TTAACCTACCAAGGCTGTGACAGGGGCTTTGAGAGATTTTCGTTCTGTGCAAGCCCAACA 2192  
Db 1690 TTAACCTACCAAGGCTGTGACAGGGGCTTTGAGAGATTTTCGTTCTGTGCAAGCCCAACA 1749  
Qy 2193 ACTCCATCTGGAATATGACAGCTACTCTCTCAACAATTGAACAGAGCTATCAAGCAGATCC 2252  
Db 1750 ACTCCATCTGGAATATGACAGCTACTCTCTCAACAATTGAACAGAGCTATCAAGCAGATCC 1809  
Qy 2253 CTGCAAGTTCTGAGCTGTGCGGCGAATTTGCCAATGTGTAAAGAACGAACGACCTGAGGA 2312  
Db 1810 CTGCAAGTTCTGAGCTGTGCGGCGAATTTGCCAATGTGTAAAGAACGAACGACCTGAGGA 1869  
Qy 2313 AGCGAGTGTGCTGTCAAAACAGGATATGACAGCCAGGGGAGCTGTGACAGTCTGGAACC 2372  
Db 1870 AGCGAGTGTGCTGTCAAAACAGGATATGACAGCCAGGGGAGCTGTGACAGTCTGGAACC 1929  
Qy 2373 AGGCTCTGTGCGCTGTGCAAAAGGATGCGAGGCTCTCGAGGGAAAGGGAGCTTCATG 2432  
Db 1930 AGGCTCTGTGCGCTGTGCAAAAGGATGCGAGGCTCTCGAGGGAAAGGGAGCTTCATG 1988  
Qy 2433 CAGTTGCGCAGATCACTGTAAATCAAGCATACAAAATAGTGTAAAGTTCCAAAA 2492  
Db 1989 C-GGTT-CCAGATCACTGTAAATCAAGCATACAAAATAGTGTAAAGTTCCAAAA 2045  
Qy 2493 TCAACAAATTAACAAAGTATCAATGTAAGAAATTTGAAATTAAGTCAAGCTGTAATGTA 2552  
Db 2046 TCAACAAATTAACAAAGTATCAATGTAAGAAATTTGAAATTAAGTCAAGCTGTAATGTA 2105  
Qy 2553 AGAATTTAAACCAATGGAATTTGGAGAGAAATTTAAATCTGAAATGTAATTAATCACTT 2612  
Db 2106 AGAATTTAAACCAATGGAATTTGGAGAGAAATTTAAATCTGAAATGTAATTAATCACTT 2165  
Qy 2613 AGGCTATCTCAAGAGATGATTTGCTCTTCAAGAAATGAGACAGGCAATATTCATG 2672  
Db 2166 AGGCTATCTCAAGAGATGATTTGCTCTTCAAGAAATGAGACAGGCAATATTCATG 2225  
Qy 2673 GGTCAATCAAAATCCAGCATACGTAACAACCTGAGATTCAGCAACACCATATTTCAAAAT 2732  
Db 2226 GGTCAATCAAAATCCAGCATACGTAACAACCTGAGAAATCAGCAACACCATATTTCAAAAT 2285  
Qy 2733 ATAGAAGATCATGATCTTGGCAACAGTAATTTGAAAAAAGAGCACTTACTTATTA 2792  
Db 2286 ATAGAAGATCATGATCTTGGCAACAGTAATTTGAAAAAAGAGCACTTACTTATTA 2345  
Qy 2793 TTTAAACCCCAAAATGCAATCAGCGAAACATATTTTACTATCTTGTGATGATGTAACAAA 2852  
Db 2346 TTTAAACCCCAAAATGCAATCAGCGAAACATATTTTACTATCTTGTGATGATGTAACAAA 2405  
Qy 2853 TGATCATTAAGCCAGGTTGTCTTCACTTCCCTGAAAAATTTTACTCAAGATCATTTTGA 2912  
Db 2406 TGATCATTAAGCCAGGTTGTCTTCACTTCCCTGAAAAATTTTACTCAAGATCATTTTGA 2465  
Qy 2913 ACAAGCATATGCTTATTTATGTTTGAAGGACGTAACAATTTATGGAAGCAAACTCTTTA 2972  
Db 2466 ACAAGCATATGCTTATTTATGTTTGAAGGACGTAACAATTTATGGAAGCAAACTCTTTA 2525  
Qy 2973 TATGCTAAGAAATGATTTTAAAGATGACTCTTACGAGGAGGAGATGAGCTCTCTAA 3032  
Db 2526 TATGCTAAGAAATGATTTTAAAGATGACTCTTACGAGGAGGAGATGAGCTCTCTAA 2585  
Qy 3033 ACGCATGATATGATGTGTGTAGCACTGATGATGATATATATGCTCCACACTAG 3092  
Db 2586 ACGCATGATATGATGTGTGTGTAGCACTGATGATGATATATATGCTCCACACTAG 2645  
Qy 3093 TCTGATTAACCAAACTCTCAGATTAAGTATTAAGCACTAGTTTTATAGCAACTAC 3152  
Db 2646 TCTGATTAACCAAACTCTCAGATTAAGTATTAAGCACTAGTTTTATAGCAACTAC 2705  
Qy 3153 TGCTTACATAGTGACTGTTTGTGTCGAATATCTTGAATGTTGTTCTTTAAAGAAACT 3212  
Db 2706 TGCTTACATAGTGACTGTTTGTGTCGAATATCTTGAATGTTGTTCTTTAAAGAAACT 2765

QY 3213 GAGTTCAGATACACATACCATGAGAAAATCTTACTTCTTGTACTACACAAAGCAT 3272  
DB 2766 GAGGTTTCAGATACACATACCATGAGAAAATCTTACTTCTTGTACTACACAAAGCAT 2825  
QY 3273 TTTAAAGAAAGATGCTATGTTGGAGAGGCGAAGTTACTATATGACATATCAAT 3330  
DB 2826 TTTAAAGAAAGATGCTATGTTGGAGAGGCGAAGTTACTATATGACATATCAAT 2883

RESULT 9  
AAA46329  
ID AAA46329 standard; DNA; 2244 BP.  
AC AAA46329;  
XX  
XX  
DT 04-SEP-2000 (first entry)  
DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.  
XX  
XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
KM chromomere 6q13-q15; ocular disease; retinal detachment;  
KM choriorretinal degeneration; retinal degeneration; cone degeneration;  
KM age related macular degeneration; photoreceptor degeneration;  
KM retinal pigment epithelium degeneration; mucopolysaccharidosis;  
KM rod-cone dystrophy; cone-rod dystrophy; ss.  
XX Homo sapiens.  
OS  
PN WO200026367-A2.  
XX  
XX 11-MAY-2000.  
XX  
XX 29-OCT-1999; 99WO-US025440.  
XX  
XX 29-OCT-1998; 98US-00183972.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Hageman GS, Kuehn MH;  
XX  
XX WPI; 2000-365616/31.  
XX  
XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
PT preventing, diagnosing and treating ocular disorders such as retinal  
PT detachment and choriorretinal degeneration.  
XX  
XX Claim 3; Fig 19; 183pp; English.  
XX  
XX The present sequence represents a splice variant of an interphotoreceptor  
CC matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an  
CC additional intron after exon 5. The protein is an IPM component (IPMC).  
CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
CC is located on chromosome 6q13-q15, between markers CHC.GAT11F10 and  
CC D6S284. The IPM proteins may be used to supplement a patient's own  
CC production of the protein or to rectify alterations in their nucleic  
CC acids that result in expression of an inactive protein. The IPM nucleic  
CC acids may be used in this way to treat ocular diseases such as retinal  
CC detachment, choriorretinal degeneration, retinal degeneration, age related  
CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment  
CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
CC also be used to assay for other modulators of IPM proteoglycan expression  
CC and activity that may be used to treat ocular diseases. The nucleic acids  
CC and proteins may also be used as diagnostic reagents to detect the  
CC presence of IPM nucleic acids and their products in samples from patients  
CC according to standard methodologies  
CC  
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;

Query Match 45.1%; Score 1503; DB 3; Length 2244;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2123; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 90 TCTGATGTTTATCAGAAATACCAATGACCAAAAAGCAGATGATTTGGAAAATAGAA 149  
DB 110 TCTGATGTTTATCAGAAATACCAATGACCAAAAAGCAGATGATTTGGAAAATAGAA 169  
QY 150 GAGCTATTTTGTGTTTGTGATTTTCTCAAGTTCAAGGAAACCAAGATATCTTCATTA 209  
DB 170 GAGCTATTTTGTGTTTGTGATTTTCTCAAGTTCAAGGAAACCAAGATATCTTCATTA 229  
QY 210 ACATATACCATTCGAAATCTAAAGACATAGCAATCCCCCAAGAAATGAAACAATGAAA 269  
DB 230 ACATATACCATTCGAAATCTAAAGACATAGCAATCCCCCAAGAAATGAAACAATGAAA 289  
QY 270 GTACTGAAAAATGTAACAAATGTCAACTATGAGCAATATTCGATTTGGCAAAAGCATC 329  
DB 290 GTACTGAAAAATGTAACAAATGTCAACTATGAGCAATATTCGATTTGGCAAAAGCATC 349  
QY 330 GAACAAAAAGATCCGATTTTTCACACGAGGAGTTAAAGTGTGTCACAGGAATCCATGA 389  
DB 350 GAACAAAAAGATCCGATTTTTCACACGAGGAGTTAAAGTGTGTCACAGGAATCCATGA 409  
QY 390 AACGATTTTGAACAGTCTTCAAGCTTATTAATGATGAGAGTGTGTCAGGAAGCAT 449  
DB 410 AACGATTTTGAACAGTCTTCAAGCTTATTAATGATGAGAGTGTGTCAGGAAGCAT 469  
QY 450 GGGAAAGCATATCGATCTTCTGATCGCATCCCTGACACAGGGAATATCGACTGG 509  
DB 470 GGGAAAGCATATCGATCTTCTGATCGCATCCCTGACACAGGGAATATCGACTGG 529  
QY 510 TCAGCATCTGCAAGAGAGACCTTCTGCTCTTGTGACATTTGAAAAAATTCAGCAATT 569  
DB 530 TCAGCATCTGCAAGAGAGACCTTCTGCTCTTGTGACATTTGAAAAAATTCAGCAATT 589  
QY 570 CCCAGAGACCTGGATCTTCCACAGAGAAATTAACAGAGATTTCCCTGACAGAA 629  
DB 590 CCCAGAGACCTGGATCTTCCACAGAGAAATTAACAGAGATTTCCCTGACAGAA 649  
QY 630 AAGATGAATATATCTGACAGAGAAACATTTGGAGAGCTGTGAAACCAATTCATTTCAA 689  
DB 650 AAGATGAATATATCTGACAGAGAAACATTTGGAGAGCTGTGAAACCAATTCATTTCAA 709  
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DB 710 CAGCAATCTACATTTCAAAAAGCTTGGAGGATTTCTTAAGAAAACCTTCAGAAAGCAAT 769  
QY 750 TCAAGATGTGCAACGCTCTCACTTGGGCTTTTCCCTCTCACTCCTGATGACACCTCTCT 809  
DB 770 TCAAGATGTGCAACGCTCTCACTTGGGCTTTTCCCTCTCACTCCTGATGACACCTCTCT 829  
QY 810 CAATGAATTCCTGATATATACATCAACGACACCAAGATGCTTACACAGAAAGAGAAAC 869  
DB 830 CAATGAATTCCTGATATATACATCAACGACACCAAGATGCTTACACAGAAAGAGAAAC 889  
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DB 890 AGAATTCGCTGTGTTGAGAGAGCAGAGGTGAGCTCAGGCTCTCTGTGTTAAACAGAA 949  
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DB 1010 CCAATCTCAGATGCAAAAAGATATTTTAAGAAATCTTCAGAGATTTCAAAAATTCATGTGT 1069  
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DB 1070 AGAATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCAACTTACGCGC 1129  
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Db      1190 TTCCAAAGAAATTGAAAGTGAAGATCTATCATGGAACCATGAGAGAGACAGAAACC 1249
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Db      1370 CTTTGCTCTGACACCCCAATCAGAGCTGCCACATCTTTGCTGTTATTAAGAGAGATGC 1429
Qy      1410 TACTTGAATCCAGAACTTCTCTCTGTTGAACCCAGCTTGAGACAGTGAACGAGCAGA 1469
Db      1430 TACTTGAATCCAGAACTTCTCTCTGTTGAACCCAGCTTGAGACAGTGAACGAGCAGA 1489
Qy      1470 GGATGGTCACTGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1529
Db      1490 GGATGGTCACTGACACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1548
Qy      1530 AGCTCACCTTCTTATATGAGCATCAAGCATCTTCTCTGATGATCAAGCAGCAGACA 1589
Db      1549 AGCTCACCTTCTTATATGAGCATCAAGCATCTTCTCTGATGATCAAGCAGCAGACA 1608
Qy      1590 TACAATGGCACTGACAGACAAATGCTAGTACAGAGGCTCACATCCGACAGATGATTA 1649
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Db      1669 TTCTGCAATCAGCCCAATCTGGCTCTGGGAATTTCACTCCACTGCTCTTCAGATGACAG 1728
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Db      1729 CCGATCAAGTGAAGTGGGAGATATGCTGAGACACACTAGATGAAATGATCTGCTGA 1788
Qy      1770 CACTCTGCGCCCATCTGAGGTACAGAGCTCAGCGAATATGTTCTGCTCCAGATCATTT 1829
Db      1789 CACTCTGCGCCCATCTGAGGTACAGAGCTCAGCGAATATGTTCTGCTCCAGATCATTT 1848
Qy      1830 CTTGAGAGATACCATCTCTGCTCAGCTTTAAGATATACCACTAGTTCTATGACAT 1889
Db      1849 CTTGAGAGATACCATCTCTGCTCAGCTTTAAGATATACCACTAGTTCTATGACAT 1908
Qy      1890 TGCCCCCAAGGGCCGAGAGCTGTAGTGTCTTCACTGCTGCGGTGCTTAACATGCGCTT 1949
Db      1909 TGCCCCCAAGGGCCGAGAGCTGTAGTGTCTTCACTGCTGCGGTGCTTAACATGCGCTT 1968
Qy      1950 CTCGACGACCTGTTCAACAGAGCTCTCTGAGATACCGAGCTGAGCAACAATTCAC 2009
Db      1969 CTCGACGACCTGTTCAACAGAGCTCTCTGAGATACCGAGCTGAGCAACAATTCAC 2028
Qy      2010 AGAGCTGCTGTTCCATATCTACGATCCATCTTACAGATTTAAGCACTTGAATATCT 2069
Db      2029 AGAGCTGCTGTTCCATATCTACGATCCATCTTACAGATTTAAGCACTTGAATATCT 2088
Qy      2070 TAACTTCAGAAACGGGAGTGTATGTAATGACAAATGAAGTTGCTAAGCTGTGCGC 2129
Db      2089 TAACTTCAGAAACGGGAGTGTATGTAATGACAAATGAAGTTGCTAAGCTGTGCGC 2148
Qy      2130 GTATAAAGCTCAGCAAGGCTGTGACGGGGCTTGGAGAGATTTGCTTCTGCTGACGCCA 2189
Db      2149 GTATAAAGCTCAGCAAGGCTGTGACGGGGCTTGGAGAGATTTGCTTCTGCTGACGCCA 2208
Qy      2190 ACAAATCCATCTGGAATAGACAGCTACTCTCTC 2223
Db      2209 ACAAATCCATCTGGAATAGACAGCTACTCTCTC 2242

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RESULT 10

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ACCS7948
ID ACCS7948 standard; cDNA, 2244 BP.
XX
AC ACCS7948;
XX
DT 11-AUG-2003 (first entry)
XX
DB Human Interphotoreceptor matrix IPM 150, isoform C, cDNA.
XX
KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW receptor; ophthalmological; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 151..747
FT /*tag= a
FT /*product= "IPM 150"
FT sig_peptide 151..210
FT /*tag= b
FT /*tag= 265..267
FT /*tag= c
FT /*note= "encodes Pro"
FT 346..348
FT /*tag= d
FT /*note= "encodes His"
XX
PN WO2003039346-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036090.
XX
PR 08-NOV-2001; 2001US-00077270.
XX
PA (IOWA ) UNIV IOWA RES FOUNO.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2003-441440/41.
DR P-PSDB; ABR42344.
XX
PT New interphotoreceptor matrix proteins and polynucleotides, useful for
PT treating or preventing photoreceptor death or retinal detachment, or for
PT treating ocular disorders.
XX
PS Claim 1; Page 79-80; 105pp; English.
XX
CC The present sequence is that of cDNA encoding isoform C of novel human
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
CC is located on chromosome 6q13-q15, a region that also contains loci for
CC progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's
CC -like macular dystrophy, North Carolina macular dystrophy and Salla
CC disease. Members of the IPMC gene family have been identified in humans,
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
CC antibodies that specifically bind the polypeptides, and vectors
CC comprising the polynucleotides. A claimed method of treating or
CC preventing photoreceptor death or retinal detachment involves
CC administering an IPMC polynucleotide, polypeptide or antibody. Also
CC claimed is a method for identifying a compound capable of modulating IPMC
CC gene expression
XX
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
XX
Query Match 45.1%; Score 1503; DB 9; Length 2244;
Beat Local Similarity 99.5%; Pred. No. 0;
Matches 2123; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 90 TCTGTGATTTGTTATCAGAAATACCAATGACAGAAAGCAGATGATTTGGAATCTAGAA 149

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Db 110 TCTGTGATTGTTATCAGAAATACCAATGACAAAAGCCAGAAATGATTTGAAATCTAGAA 169  
Qy 150 GAGCATATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGAAACCAAGATATCTCATTA 209  
Db 170 GAGCATATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGAAACCAAGATATCTCATTA 229  
Qy 210 ACATATACCATTTCTGAAACCTAAAGACATAGACATCCCAAGAAATGAAACATGAAA 269  
Db 230 ACATATACCATTTCTGAAACCTAAAGACATAGACATCCCAAGAAATGAAACATGAAA 289  
Qy 270 GTAATGAAAAATGTACAAAATGTCAACTATAGACGAATATTCGATTTGGCAAAAGATC 329  
Db 290 GTAATGAAAAATGTACAAAATGTCAACTATAGACGAATATTCGATTTGGCAAAAGATC 349  
Qy 330 GAACAAAAAGATCCGATTTTCCCAAGGGGGTTAAAGTCTGTCCACAGGAATCCATGA 389  
Db 350 GAACAAAAAGATCCGATTTTCCCAAGGGGGTTAAAGTCTGTCCACAGGAATCCATGA 409  
Qy 390 AACAGATTTTAGACAGTCTTCAAGCTTATATAGATTGAGAGTGTCAAGAAAGCATAT 449  
Db 410 AACAGATTTTAGACAGTCTTCAAGCTTATATAGATTGAGAGTGTCAAGAAAGCATAT 469  
Qy 450 GGGAAAGCATATCGGATCTTTCTGATCGCATCCCTGACACAGGGGAATATCAGACTGG 509  
Db 470 GGGAAAGCATATCGGATCTTTCTGATCGCATCCCTGACACAGGGGAATATCAGACTGG 529  
Qy 510 TCGACATCTGCCAGACGAGGACCTTGTGCTCTTTGACATTTGAAAAAACTTCAGCAT 569  
Db 530 TCGACATCTGCCAGACGAGGACCTTGTGCTCTTTGACATTTGAAAAAACTTCAGCAT 589  
Qy 570 CCCAGAGACCTGAGATCTTCTCCAGCAGAGAATAAACAGAGAATTTCCCTGACAGA 629  
Db 590 CCCAGAGACCTGAGATCTTCTCCAGCAGAGAATAAACAGAGAATTTCCCTGACAGA 649  
Qy 630 AAGATGAATATCTGACAGAAAGACATTTGGAGAGCTGTGTAACCATTTGTCATTTCA 689  
Db 650 AAGATGAATATCTGACAGAAAGACATTTGGAGAGCTGTGTAACCATTTGTCATTTCA 709  
Qy 690 CAGCAATCTACATTTCAAGACCTTGGGCGATTTCTAAGAAAACTTCAGAAAGCAAT 749  
Db 710 CAGCAATCTACATTTCAAGACCTTGGGCGATTTCTAAGAAAACTTCAGAAAGCAAT 769  
Qy 750 TCAAGATGTGCAAGCTGCTCACTTGGGCTTTCCCTCTCACTCGATGACACCTCTCT 809  
Db 770 TCAAGATGTGCAAGCTGCTCACTTGGGCTTTCCCTCTCACTCGATGACACCTCTCT 829  
Qy 810 CAATGAATTTCTGATATATACCTCAAGACACCAAGATGCTTACCAAGAAAGAAAC 869  
Db 830 CAATGAATTTCTGATATATACCTCAAGACACCAAGATGCTTACCAAGAAAGAAAC 889  
Qy 870 AAGATTCGCTGTGTTGGAAGACAGAGGTTGAGCTCAAGCTCTCTGTGTTAAACCAAA 929  
Db 890 AAGATTCGCTGTGTTGGAAGACAGAGGTTGAGCTCAAGCTCTCTGTGTTAAACCAAA 949  
Qy 930 GTTCAAGGAGAGCTGCTGACTCCCAAGTCCCATTTTACCAAGAGCTGACAGAAAGTC 989  
Db 950 GTTCAAGGAGAGCTGCTGACTCCCAAGTCCCATTTTACCAAGAGCTGACAGAAAGTC 1009  
Qy 990 CCAACTTCAGATGCAAAAGATATTTAAGAACTTCCAGATTTCAAAAAATCATGTGTT 1049  
Db 1010 CCAACTTCAGATGCAAAAGATATTTAAGAACTTCCAGATTTCAAAAAATCATGTGTT 1069  
Qy 1050 AAGATTTTAACCAAGAAAGAAAGAAATGCTCAAGCTCAACAGAGATGCACTTAAGGCT 1109  
Db 1070 AAGATTTTAACCAAGAAAGAAAGAAATGCTCAAGCTCAACAGAGATGCACTTAAGGCT 1129  
Qy 1110 CATCTTTAAGAGACAGAGTGCAGAAAGCAAAAAGCCCTGCAAGTGAACCTCTGTCTTTGA 1169  
Db 1130 CATCTTTAAGAGACAGAGTGCAGAAAGCAAAAAGCCCTGCAAGTGAACCTCTGTCTTTGA 1189  
Qy 1170 TTCACACAAATTTGAAAGTGAAGAGTCTATCATAGAACCATGAGAGAGACAAAGCAAC 1229  
Db 1190 TTCACACAAATTTGAAAGTGAAGAGTCTATCATAGAACCATGAGAGAGACAAAGCAAC 1249

Qy 1230 AGAAATCTATCTCAAGCTACAGACCTCAAAAAGCTGATCAAGCAAAAGCACTTAGAGAA 1289  
Db 1250 AGAAATCTATCTCAAGCTACAGACCTCAAAAAGCTGATCAAGCAAAAGCACTTAGAGAA 1309  
Qy 1290 ACAATCTTTGATGTGGGAGCAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGC 1349  
Db 1310 ACAATCTTTGATGTGGGAGCAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGC 1369  
Qy 1350 CTTTGTCTCTGACACCCATACAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1409  
Db 1370 CTTTGTCTCTGACACCCATACAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1429  
Qy 1410 TACTTGTGTCAGACCTTCCCTGTTGAACCCCAAGCTTGAACAGTGGACGAGACGA 1469  
Db 1430 TACTTGTGTCAGACCTTCCCTGTTGAACCCCAAGCTTGAACAGTGGACGAGACGA 1489  
Qy 1470 GCATGCTTACCTGACACTTCTTGGTCTCACTGTGCTATGAGCTCTCACTCCCTGTGAGA 1529  
Db 1490 GCATGCTTACCTGACACTTCTTGGTCTCACTGTGCTATGAGCTCTCACTCCCTGTGAGA 1546  
Qy 1530 AGCTCCACCTTTCTTTATGGAATCAAGCATCTTCTCTGACTGATCAAGGACCAACAGA 1589  
Db 1549 AGCTCCACCTTTCTTTATGGAATCAAGCATCTTCTCTGACTGATCAAGGACCAACAGA 1608  
Qy 1590 TACAAATGACCTGACCAAGCAATGCTATGACAGAGGCTCAACATCCCAACCAAGATTA 1649  
Db 1609 TACAAATGACCTGACCAAGCAATGCTATGACAGAGGCTCAACATCCCAACCAAGATTA 1668  
Qy 1650 TTCTGCAATCAAGCAATGCTGCTGAGAAATTTCAATCACTGATCTTCAAGATGACAG 1709  
Db 1669 TTCTGCAATCAAGCAATGCTGCTGAGAAATTTCAATCACTGATCTTCAAGATGACAG 1728  
Qy 1710 CCGATCAAGTCAAGTGGCGAAGATATGTCAGACACCTTAGATGAATGATCTGTCTGA 1769  
Db 1729 CCGATCAAGTCAAGTGGCGAAGATATGACAGAGACCTTAGATGAATGATCTGTCTGA 1788  
Qy 1770 CACTCTGCCCCATCTGAGGTACCAAGAGCTCAGGAAATATGTTCTGCCCCAGATCATTT 1829  
Db 1789 CACTCTGCCCCATCTGAGGTACCAAGAGCTCAGGAAATATGTTCTGCCCCAGATCATTT 1848  
Qy 1830 CTTGAGGATACCACTCTGCTCACTGCTTACAGTATATACCACTAGTTCTATGACCAT 1889  
Db 1849 CTTGAGGATACCACTCTGCTCACTGCTTACAGTATATACCACTAGTTCTATGACCAT 1908  
Qy 1890 TGCCCCCAAGGCGGAGAGCTGTGATGTTCTTCAAGTCTGCGTGTGCTAACATGGCCTT 1949  
Db 1909 TGCCCCCAAGGCGGAGAGCTGTGATGTTCTTCAAGTCTGCGTGTGCTAACATGGCCTT 1968  
Qy 1950 CTCCAAGACCTGTTTCAACAGAGCTCTGGAAGTACCGAGCTCTGAGACCAAAATTCAC 2009  
Db 1969 CTCCAAGACCTGTTTCAACAGAGCTATTTGGAAGTACCGAGCTCTGAGACCAAAATTCAC 2028  
Qy 2010 ACAGCTGTGTTCCATATCTACGATCCATCTTACAGATTTAAGCACTTGAATACT 2069  
Db 2029 ACAGCTGTGTTCCATATCTACGATCCATCTTACAGATTTAAGCACTTGAATACT 2088  
Qy 2130 GTATTAACCTCAACAAAGCTGTGACAGGGGCTTGGAGAAATTTTGTCTGTGACGCCA 2189  
Db 2149 GTATTAACCTCAACAAAGCTGTGACAGGGGCTTGGAGAAATTTTGTCTGTGACGCCA 2208  
Qy 2190 ACAACTCCATCTGAAATATAGACAGCTACTCTC 2223  
Db 2209 ACAACTCCATCTGAAATATAGACAGCTACTCTC 2242

RESULT 11  
ADAI4844  
ID ADAI4844 standard; cDNA; 2244 BP.

XX AC ADA14844;  
XX XX 06-NOV-2003 (first entry)  
XX XX Human interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.  
XX DE  
XX XX ss; gene; human; IPMC 150 isoform C; gene therapy;  
XX KM interphotoreceptor matrix component; IPMC; ocular disorder;  
XX KM macular degeneration; photoreceptor death; retinal detachment.  
XX OS Homo sapiens.  
XX XX  
FH Key Location/Qualifiers  
FT CDS 151..747  
FT /tag= b  
FT /product= "IPMC 150 isoform C"  
FT sig\_peptide 151..200  
FT /tag= a  
FT /note= "Signal sequence"  
FT mat\_peptide 201..744  
FT /tag= c  
FT /note= "Mature IPMC 150 isoform C"  
FT unsure 265..267  
FT /tag= d  
FT /note= "Encodes Pro"  
FT unsure 346..348  
FT /tag= e  
FT /note= "Encodes His"  
XX PN US2002160954-A1.  
XX PD 31-OCT-2002.  
XX PF 08-NOV-2001; 2001US-00007270.  
XX PR 29-OCT-1998; 98US-00183972.  
XX PR 29-OCT-1999; 99US-00430195.  
XX PA (IOWA ) UNIV IOWA RES FOUND.  
XX PI Hageman GS, Kuehn MH;  
XX DR WPI; 2003-238235/23.  
XX DR P-PSDB; ADA14845.  
XX PT New isolated or recombinant interphotoreceptor matrix component  
XX PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
XX PT treating or prognosticating ocular disorders, e.g. macular degeneration  
XX PT or retinal detachment.  
XX PS Claim 3; Page 36-37; 76pp; English.  
XX XX  
XX CC The invention relates to an isolated or recombinant interphotoreceptor  
XX CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
XX CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
XX CC gene operatively linked to the IPMC polynucleotide. The IPMC  
XX CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
XX CC preventing, treating or prognosticating ocular disorders, e.g. macular  
XX CC degeneration, photoreceptor death or retinal detachment. They are also  
XX CC useful for identifying a compound capable of modulating IPMC gene  
XX CC expression in a cell. The present sequence represents cDNA encoding human  
XX CC interphotoreceptor matrix component, IPMC, 150 isoform C.  
XX XX  
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;

Query Match 45.1%; Score 1503; DB 10; Length 2244;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2123; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 90 TCTGTGATTGTTATCAGATTACCAATGACAAAGCCAGATGTTTGGAAACTAGAA 149  
DB 110 TCTGTGATTGTTATCAGATTACCAATGACAAAGCCAGATGTTTGGAAACTAGAA 169

QY 150 GAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGAAACCAAGATATCTCATTA 209  
DB 170 GAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGAAACCAAGATATCTCATTA 229  
QY 210 ACATATACCAATCTGAACCTAAAGACATAGACATCCCAAGAAATGAAACAAGTAA 269  
DB 230 ACATATACCAATCTGAACCTAAAGACATAGACATCCCAAGAAATGAAACAAGTAA 289  
QY 270 GTACTGAAAAATGTACAAAATGTCACTATGAGACGAATATTCGATTTGGCAAGCATC 329  
DB 290 GTACTGAAAAATGTACAAAATGTCACTATGAGACGAATATTCGATTTGGCAAGCATC 349  
QY 330 GAACAAAAAGATCCGATTTTCCCAAGGGGGTAAAGTCTGTCAACGAATCCATCA 389  
DB 350 GAACAAAAAGATCCGATTTTCCCAAGGGGGTAAAGTCTGTCAACGAATCCATCA 409  
QY 390 AACGATTTTGAACAGTCTTCAAGCTTATATATGATGAGAGTGTCAAGAAAGATAT 449  
DB 410 AACGATTTTGAACAGTCTTCAAGCTTATATATGATGAGAGTGTCAAGAAAGATAT 469  
QY 450 GGAAGCATATCGATCTTCTGATTCGATCCCTGACACAGGGGAATATCAGACTGG 509  
DB 470 GGAAGCATATCGATCTTCTGATTCGATCCCTGACACAGGGGAATATCAGACTGG 529  
QY 510 TCAGCATCTGCCAGACAGAGACCTTCTGCTCTTTGACATTTGAAAAAACTTCAGCAATT 569  
DB 530 TCAGCATCTGCCAGACAGAGACCTTCTGCTCTTTGACATTTGAAAAAACTTCAGCAATT 589  
QY 570 CCCAGAGACCTGGATCTTCTCCAGAGAGATTAACAGAGAGTTTCCCTGACAGA 629  
DB 590 CCCAGAGACCTGGATCTTCTCCAGAGAGATTAACAGAGAGTTTCCCTGACAGA 649  
QY 630 AAGATGAATATCTGACAGAGAGACATTTGGAGAGCTGTGTAACCATTTGATTTCA 689  
DB 650 AAGATGAATATCTGACAGAGAGACATTTGGAGAGCTGTGTAACCATTTGATTTCA 709  
QY 690 CAGCAATCTACATTTCAAAAGACTTGGGAGATTTTGAAGAAAACTTCAGAAAGCAAAAT 749  
DB 710 CAGCAATCTACATTTCAAAAGACTTGGGAGATTTTGAAGAAAACTTCAGAAAGCAAAAT 769  
QY 750 TCAAGATGTGCGAACGCTCACTTGGGCTTTCCCTCACTCCGTATGACACCTCCT 809  
DB 770 TCAAGATGTGCGAACGCTCACTTGGGCTTTCCCTCACTCCGTATGACACCTCCT 829  
QY 810 CAATGAATTTCTGATATATACACTCAAGACACCAAGATGCTTACACAGAAAGAAAC 869  
DB 830 CAATGAATTTCTGATATATACACTCAAGACACCAAGATGCTTACACAGAAAGAAAC 889  
QY 870 AGAATTCGCTGTGTGAGAGACAGAGAGGTGAGCTCAAGCTTCTGTGTAAACAGAA 929  
DB 890 AGAATTCGCTGTGTGAGAGACAGAGAGGTGAGCTCAAGCTTCTGTGTAAACAGAA 949  
QY 930 GTTCAAGGCAAGCTCGCTGACTCCCAATTAATCAAGAGGCTTAGAGAGAAAGTC 989  
DB 950 GTTCAAGGCAAGCTCGCTGACTCCCAATTAATCAAGAGGCTTAGAGAGAAAGTC 1009  
QY 990 CCAATCTGAGATGCAAAAGATATTTAAGAACTTCCAGATTTCAAAAAATCATGTGT 1049  
DB 1010 CCAATCTGAGATGCAAAAGATATTTAAGAACTTCCAGATTTCAAAAAATCATGTGT 1069  
QY 1050 AGGATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTTCCACAGAGATGCAACTTACGGC 1109  
DB 1070 AGGATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTTCCACAGAGATGCAACTTACGGC 1129  
QY 1110 CATCTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTGCCTCTGTTTGA 1169  
DB 1130 CATCTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTGCCTCTGTTTGA 1189  
QY 1170 TTCACAAATAATTGAAAGTGAAGAGTATCATGGAACCAATGAGAGAGCAACCAACC 1229  
DB 1190 TTCACAAATAATTGAAAGTGAAGAGTATCATGGAACCAATGAGAGAGCAACCAACC 1249

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QY 1230 AGAAATCTATCTCAGAGCTACAGACCTCAAAGGCTGATCAGCAAGCACTAGAGGAAGA 1289
DB 1250 AGAAATCTATCTCAGAGCTACAGACCTCAAAGGCTGATCAGCAAGCACTAGAGGAAGA 1309
QY 1280 ACAATCTTTGGATGTTGGGGCAATTCAGTTCACTGATGAATTTGCTGATCATCTCCAGC 1349
DB 1310 ACAATCTTTGGATGTTGGGGCAATTCAGTTCACTGATGAATTTGCTGATCATCTCCAGC 1369
QY 1350 CTTTGTCTCTGACACCCCAATCAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1409
DB 1370 CTTTGTCTCTGACACCCCAATCAGAGCTGCCACATCTTTTGTGTTATTAACAGAGATGC 1429
QY 1410 TACTTGTAGTCAGAACTTCTCTGTTGAACCCAGCTTGAGAGAGTGAAGAGCAGAGA 1469
DB 1430 TACTTGTAGTCAGAACTTCTCTGTTGAACCCAGCTTGAGAGAGTGAAGAGCAGAGA 1489
QY 1470 GCATGCTCTACCTGACACTTCTTGGTCTCCACCTGATAGGCTTACTCTCTGTCAGA 1529
DB 1490 GCATGCTCTACCTGACACTTCTTGGTCTCCACCTGATAGGCTTACTCTCTGTCAGA 1548
QY 1530 AGCTCACCTTTCTTTATGAGCAATCAAGCACTTCTCTGAGTGAATCAAGGACGACAGA 1589
DB 1549 AGCTCACCTTTCTTTATGAGCAATCAAGCACTTCTCTGAGTGAATCAAGGACGACAGA 1608
QY 1590 TACAATGGCACTGACAGACCAATGCTAGTACAGAGGCTCACCATCCCAACAGATGATTA 1649
DB 1609 TACAATGGCACTGACAGACCAATGCTAGTACAGAGGCTCACCATCCCAACAGATGATTA 1668
QY 1650 TTCTGCAATCAGCACTGCTCTGAGGAATTTTCACTCCACTGATCTTCAGATGACAG 1709
DB 1669 TTCTGCAATCAGCACTGCTCTGAGGAATTTTCACTCCACTGATCTTCAGATGACAG 1728
QY 1710 CCGATCAAGTGAAGGAGGCGAAGATATGTTTCTGAGACACCTAGATGAATGATCTGTGTA 1769
DB 1729 CCGATCAAGTGAAGGAGGCGAAGATATGTTTCTGAGACACCTAGATGAATGATCTGTGTA 1788
QY 1770 CACTCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATGTTTCTGTCGCCAGATCATTT 1829
DB 1789 CACTCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATGTTTCTGTCGCCAGATCATTT 1848
QY 1830 CTTTGAAGATCACTCTGCTCAGCTTTTACAGTATATCACCACCTAGTTCTATGACAT 1889
DB 1849 CTTTGAAGATCACTCTGCTCAGCTTTTACAGTATATCACCACCTAGTTCTATGACAT 1908
QY 1890 TGGCCCAAGGGGCGAGAGCTGTAAGTCTTCTCAGTGCAGTGGCTGCTCAATGAGCTT 1949
DB 1909 TGGCCCAAGGGGCGAGAGCTGTAAGTCTTCTCAGTGCAGTGGCTGCTCAATGAGCTT 1968
QY 1950 CTCGAACGACTGTTCAACAAGAGCTCTCTGAGTACCGAGCTGAGCAACAATTCAC 2009
DB 1969 CTCGAACGACTGTTCAACAAGAGCTCTCTGAGTACCGAGCTGAGCAACAATTCAC 2028
QY 2010 ACAAGCTGCTGTTCCATATCTAGATCAATCTTACAGATTTTAAAGCACTTGAATACT 2069
DB 2029 ACAAGCTGCTGTTCCATATCTAGATCAATCTTACAGATTTTAAAGCACTTGAATACT 2088
QY 2070 TAACTTCAGAAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTGCTAAGTCTGTC 2129
DB 2089 TAACTTCAGAAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTGCTAAGTCTGTC 2148
QY 2130 GTATTAACCTCACCAGAGCTGTGACCGGGTCTTGAAGATTTTCTGCTGACGCCA 2189
DB 2149 GTATTAACCTCACCAGAGCTGTGACCGGGTCTTGAAGATTTTCTGCTGACGCCA 2208
QY 2190 ACAACTCTCATCTGGAATATGACAGCTACTCTCTC 2223
DB 2209 ACAACTCTCATCTGGAATATGACAGCTACTCTCTC 2242
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RESULT 12
AAA46327
ID AAA46327 standard; DNA; 1858 BP.
XX
```

```
AC AAA46327;
XX
DT 04-SEP-2000 (first entry)
XX
DE Exon 1 and promoter of Interphotoreceptor matrix proteoglycan, IPM150.
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW chromosome 6q13-q15; ocular disease; retinal detachment;
KW choroidretinal degeneration; retinal degeneration; cone degeneration;
KW age related macular degeneration; photoreceptor degeneration;
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;
KW rod - cone dystrophy; cone-rod dystrophy; ss.
OS Homo sapiens.
PN WO200026367-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025440.
XX
PR 29-OCT-1998; 98US-00183972.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI, 2000-365616/31.
XX
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT preventing, diagnosing and treating ocular disorders such as retinal
PT detachment and choroidretinal degeneration.
XX
PS Claim 3; Fig 17; 183bp; English.
XX
CC The present sequence represents exon 1 and the promoter of human DNA
CC encoding interphotoreceptor matrix (IPM) proteoglycan, designated IPM150.
CC The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150
CC and IPM200, exist. The human IPM150 gene is located on chromosome 6q13-
CC q15, between markers CHLC.GATA11P10 and D6S284. The IPM proteins may be
CC used to supplement a patient's own production of the protein or to rectify
CC alterations in their nucleic acids that result in expression of an
CC inactive protein. The IPM nucleic acids may be used in this way to treat
CC ocular diseases such as retinal detachment, choroidretinal degeneration,
CC retinal degeneration, age related macular degeneration, photoreceptor
CC degeneration, RPE (retinal pigment epithelium) degeneration, cone
CC degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod
CC dystrophy. The nucleic acids and proteins may also be used to assay for
CC other modulators of IPM proteoglycan expression and activity that may be
CC used to treat ocular diseases. The nucleic acids and proteins may also be
CC used as diagnostic reagents to detect the presence of IPM nucleic acids
CC and their products in samples from patients according to standard
CC methodologies
XX
SQ Sequence 1858 BP; 667 A; 293 C; 316 G; 581 T; 0 U; 1 Other;
XX
Query Match 5.9%; Score 197; DB 3; Length 1858;
Beef Local Similarity 100.0%; Pred. No. 3.7e-85;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAACCAAGAGGTTATCTCATCATCTGATCATATATATATTTTTCACATTTTC 60
DB 1070 TAAACCAAGAGGTTATCTCATCATCTGATCATATATATATATTTTTCACATTTTC 1129
QY 61 TGTACTTTTATGATGATTTGAGGTTCTCTGATTTGTTATTCAGAAATACCAATGCAC 120
DB 1130 TGTACTTTTATGATGATTTGAGGTTCTCTGATTTGTTATTCAGAAATACCAATGCAC 1189
QY 121 AAAAGCCGAATGATTTTGGAAACTAGAAAGCTATTTTGTTTTGGATTTTCTCCA 180
DB 1190 AAAAGCCGAATGATTTTGGAAACTAGAAAGCTATTTTGTTTTGGATTTTCTCCA 1249
QY 181 AGTCAAGAACCAAG 197
```

Db 1250 AGTTCAGGACCAAG 1266

|||||

RESULT 13  
ID ACC57949 standard; DNA; 1858 BP.  
XX  
AC ACC57949;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Human interphotoreceptor matrix IPM 150 gene regulatory region.  
XX  
KW Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
KW receptor; ophthalmological; gene therapy; promoter; ss.  
OS Homo sapiens.  
XX  
PN MO2003039346-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 08-NOV-2002; 2002WO-US036090.  
XX  
PR 08-NOV-2001; 2001US-00077270.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Hageman GS, Kuehn MH;  
XX  
DR WPI; 2003-441440/41.  
XX  
PT New interphotoreceptor matrix proteins and polynucleotides, useful for  
PT treating or preventing photoreceptor death or retinal detachment, or for  
PT treating ocular disorders.  
XX  
PS Claim 12; Page 80-81; 105pp; English.

CC The present sequence is that of the regulatory region of the human human  
CC interphotoreceptor matrix 150 (IPM 150) gene on chromosome 6q13-q15. This  
CC chromosomal region also contains loci for progressive bifocal  
CC chorioretinal atrophy, autosomal dominant Stargardt's-like macular  
CC dystrophy, North Carolina macular dystrophy and Salla disease. IPM 150 is  
CC a member of the newly identified interphotoreceptor matrix component  
CC (IPMC) gene family. Members of the IPMC gene family have been identified  
CC in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polypeptides, and vectors  
CC comprising the polynucleotides, including claimed vectors in comprising a  
CC promoter obtained from the present sequence. A claimed method of treating a  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression  
XX  
SQ Sequence 1858 BP; 667 A; 293 C; 316 G; 581 T; 0 U; 1 Other;

Query Match 5.9%; Score 197; DB 9; Length 1858;  
Best Local Similarity 100.0%; Pred. No. 3.7e-85;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAAACCAAGAGGTTATCTCATCATCTGTATCATATATATATATATTTTTCACATTTC 60  
|||||  
Db 1070 TAAACCAAGAGGTTATCTCATCATCTGTATCATATATATATATTTTTCACATTTC 1129  
61 TGTACTTTTAAATGAGATTGAGTTGTTCTGTGATTTGTTATTCAGAAATTCAGATGCAC 120  
|||||  
Db 1130 TGTACTTTTAAATGAGATTGAGTTGTTCTGTGATTTGTTATTCAGAAATTCAGATGCAC 1189  
121 AAAAGCCAGATGTATTTGGAAGTGAAGAGCTATTTTGTATTTTGGATTTTCTCCA 180  
|||||

Db 1190 AAAAGCCAGATGTATTTGGAAGTGAAGAGCTATTTTGTATTTTGGATTTTCTCCA 1249

Qy 181 AGTTCAGGACCAAG 197  
|||||

Db 1250 AGTTCAGGACCAAG 1266

|||||

RESULT 14  
ID ADA14846 standard; cDNA; 1858 BP.  
XX  
AC ADA14846;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human interphotoreceptor matrix component, IPMC, 150 regulatory region.  
XX  
KW human; IPMC 150; gene therapy; interphotoreceptor matrix component; IPMC;  
KW ocular disorder; macular degeneration; photoreceptor death;  
KW retinal detachment; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2002160954-A1.  
XX  
PD 31-OCT-2002.  
XX  
PF 08-NOV-2001; 2001US-00007270.  
XX  
PR 29-OCT-1998; 98US-00183972.  
XX  
PR 29-OCT-1999; 99US-00430195.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Hageman GS, Kuehn MH;  
XX  
DR WPI; 2003-238235/23.  
XX  
PT New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.  
XX  
PS Claim 12; Page 38-39; 76pp; English.

CC The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding human  
CC interphotoreceptor matrix component, IPMC, 150 regulatory region.  
XX  
SQ Sequence 1858 BP; 667 A; 293 C; 316 G; 581 T; 0 U; 1 Other;

Query Match 5.9%; Score 197; DB 10; Length 1858;  
Best Local Similarity 100.0%; Pred. No. 3.7e-85;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAAACCAAGAGGTTATCTCATCATCTGTATCATATATATATATTTTTCACATTTC 60  
|||||  
Db 1070 TAAACCAAGAGGTTATCTCATCATCTGTATCATATATATATATTTTTCACATTTC 1129

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Qy 61 TGTACTTTTATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTACCAATGAC 120
Db 1130 TGTACTTTTATGAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTACCAATGAC 1189
Qy 121 AAAAGCCAGAAATGATTTTGGAAACTGAAAGACTATTTTGTGTTTGGATTTTCTCCA 180
Db 1190 AAAAGCCAGAAATGATTTTGGAAACTGAAAGACTATTTTGTGTTTGGATTTTCTCCA 1249
Qy 181 AGTTCAGGACCAAG 197
Db 1250 AGTTCAGGACCAAG 1266

RESULT 15
AAA46204
ID AAA46204 standard; cDNA, 555 BP.
XX
AC AAA46204;
XX
DT 04-SBP-2000 (first entry)
XX
DE cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
KW chromosome 6q13-q15; ocular disease; retinal detachment;
KW choriorretinal degeneration; retinal degeneration; cone degeneration;
KW age related macular degeneration; photoreceptor degeneration;
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;
KW rod-cone dystrophy; cone-rod dystrophy; ss.
XX
OS Macaca sp.
XX
PN WO200026367-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025440.
XX
PR 29-OCT-1998; 98US-00183972.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR MPI: 2000-365616/31.
DR P-PSDB; AAY93335.
XX
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT preventing, diagnosing and treating ocular disorders such as retinal
PT detachment and choriorretinal degeneration.
XX
PS Claim 2, Fig 2, 183pp; English.
XX
XX
CC The present sequence encodes an interphotoreceptor matrix (IPM)
CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).
CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
CC is located on chromosome 6q13-q15, between markers CHC.GAT11F10 and
CC D6S284. The IPM proteins may be used to supplement a patient's own
CC production of the protein or to rectify alterations in their nucleic
CC acids that result in expression of an inactive protein. The IPM nucleic
CC acids may be used in this way to treat ocular diseases such as retinal
CC detachment, choriorretinal degeneration, retinal degeneration, age related
CC macular degeneration, photoreceptor degeneration, RPS (retinal pigment
CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
CC also be used to assay for other modulators of IPM proteoglycan expression
CC and activity that may be used to treat ocular diseases. The nucleic acids
CC and proteins may also be used as diagnostic reagents to detect the
CC presence of IPM nucleic acids and their products in samples from patients
CC according to standard methodologies
XX
XX
SQ Sequence 555 BP; 162 A; 131 C; 131 G; 131 T; 0 U; 0 Other;

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Query Match 3.4%; Score 112; DB 3; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.3e-43;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 403 CAGTCTTCAGCTTATTTATGATTGAGGTGTGTCAGAGACGATATGGAAAGCATATCG 462
Db 60 CAGTCTTCAGCTTATTTATGATTGAGGTGTGTCAGAGACGATATGGAAAGCATATCG 119
Qy 463 GATCTTCTGATGCGATCCCTGACAGAGGGGAATATCAGGACTGGTCAAG 514
Db 120 GATCTTCTGATGCGATCCCTGACAGAGGGGAATATCAGGACTGGTCAAG 171

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Search completed: January 13, 2006, 15:35:12  
Job time : 1946 secs

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OM nucleic - nucleic search, using bw model

Run on: January 13, 2006, 11:50:05 ; Search time 16555 Seconds  
(without alignments)  
11433.929 Million cell updates/sec

Title: US-10-007-270-1  
Perfect score: 3330  
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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:\*  
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2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_cm:\*  
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6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_ses:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hfg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2578	77.4	3268	8 AF047492	AF047492 Homo sapi
2	1316	39.5	2009	6 CQ725539	CQ725539 Sequence
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6	534	16.0	816	8 HSIMP313	HSIMP313 Homo sapi
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8	249	7.5	444	8 HSIMP310	HSIMP310 Homo sapi
9	226	7.1	537	8 HSIMP302	HSIMP302 Homo sapi
10	236	7.1	132145	14 AL359817	AL359817 Homo sapi
11	236	7.1	186301	8 AL356962	AL356962 Human DNA
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13	197	5.9	310	8 HSIMP301	HSIMP301 Homo sapi
14	170	5.1	448	8 HSIMP314	HSIMP314 Homo sapi
15	169	5.1	422	8 HSIMP303	HSIMP303 Homo sapi
16	141	4.2	377	8 HSIMP307	HSIMP307 Homo sapi
17	112	3.4	555	8 AF047491	AF047491 Macaca fa
18	107	3.2	311	8 HSIMP306	HSIMP306 Homo sapi

19	81	2.4	438	8 HSIMP312	AF017771 Homo sapi
20	79	2.4	347	8 HSIMP311	AF017770 Homo sapi
21	79	2.4	380	8 HSIMP316	AF017775 Homo sapi
22	67	2.0	304	8 HSIMP305	AF017764 Homo sapi
23	62	1.9	300	8 HSIMP308	AF017767 Homo sapi
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25	42	1.3	3552	4 AB047844	AB047844 Bos tauru
26	39	1.2	259413	14 AC161554	AC161554 Bos tauru
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28	32	1.0	2850	9 AB047843	AB047843 Rattus no
29	32	1.0	2924	9 BC022970	BC022970 Mus muscu
30	32	1.0	3668	9 AF266478	AF266478 Mus muscu
31	32	1.0	3675	9 AF229922	AF229922 Mus muscu
32	32	1.0	41820	9 AC148244	AC148244 Mus muscu
33	32	1.0	110000	14 AC110108	AC110108 Rattus no
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38	24	0.7	149779	14 AL353583	AL353583 Homo sapi
39	24	0.7	162013	14 AC019347	AC019347 Homo sapi
40	24	0.7	166022	14 AC156794	AC156794 Mus muscu
41	24	0.7	184346	14 AC157902	AC157902 Mus muscu
42	24	0.7	216014	14 AC008823	AC008823 Homo sapi
43	23	0.7	294	8 HSIMP309	AF017768 Homo sapi
44	23	0.7	148747	14 AC140852	AC140852 Rattus no
45	23	0.7	153053	8 AL137179	AL137179 Human DNA
46	23	0.7	191166	8 AC009686	AC009686 Homo sapi
47	23	0.7	196806	8 AC104212	AC104212 Homo sapi
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54	22	0.7	70680	14 AC101265	AC101265 Mus muscu
55	22	0.7	102591	14 AC165023	AC165023 Bos tauru
56	22	0.7	103700	5 BX510946	BX510946 Zebrafish
57	22	0.7	110000	14 AC095248	AC095248 Homo sapi
58	22	0.7	110000	14 AC164423	AC164423 Homo sapi
59	22	0.7	110472	15 AC146709	AC146709 Homo sapi
60	22	0.7	112601	8 AP005140	AP005140 Homo sapi
61	22	0.7	119956	14 AC015789	AC015789 Homo sapi
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71	22	0.7	169361	5 CR762498	CR762498 Zebrafish
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76	22	0.7	173268	14 AC112087	AC112087 Rattus no
77	22	0.7	175945	9 AC124412	AC124412 Mus muscu
78	22	0.7	180668	14 AC020857	AC020857 Mus muscu
79	22	0.7	191898	8 AP003071	AP003071 Homo sapi
80	22	0.7	193373	9 AC134871	AC134871 Mus muscu
81	22	0.7	194781	14 AC019124	AC019124 Homo sapi
82	22	0.7	201670	14 AC158415	AC158415 Pongo pyg
83	22	0.7	202726	5 ALU773593	ALU773593 Zebrafish
84	22	0.7	202726	14 AC141507	AC141507 Rattus no
85	22	0.7	210913	9 AC093926	AC093926 Genomic s
86	22	0.7	216959	9 AC116998	AC116998 Mus muscu
87	22	0.7	217915	14 AC140432	AC140432 Mus muscu
88	22	0.7	233627	14 AC127968	AC127968 Rattus no
89	22	0.7	239840	14 AC094367	AC094367 Rattus no
90	22	0.7	244366	14 AC118363	AC118363 Rattus no
91	22	0.7	250029	8 AB014304	AB014304 Homo sapi











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## ALIGNMENTS

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VERSION AF047492.2 GI:6118565
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 3268)
AUTHORS Kuehn,M.H. and Hageman,G.S.
TITLE Expression and characterization of the IPM 150 gene (IMPG1)
JOURNAL chondroitin-sulfate proteoglycan
PUBMED 10601738
REFERENCE 2 (bases 1 to 3268)
AUTHORS Kuehn,M.H. and Hageman,G.S.
TITLE Direct Submision
JOURNAL Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190B PFP, Iowa City, IA
52240, USA
REFERENCE 3 (bases 1 to 3268)
AUTHORS Kuehn,M.H. and Hageman,G.S.
TITLE Direct Submision
JOURNAL Submitted (26-OCT-1999) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190B PFP, Iowa City, IA
52240, USA
REMARK Sequence update by submitter
COMMENT On Oct 26, 1999 this sequence version replaced gi:2906231.
FEATURES
Location/Qualifiers
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ORIGIN			
Query Match		77.4%; Score 2578; DB 8; Length 3268;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 2578; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
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DB	691	AGATGTTGCCAAGCTCTCACTTGAGGCTTTCCTCTCACTCTGATGACACCTCTCTCA	750
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RESULT 2  
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DEFINITION Sequence 11473 from Patent W002068579.  
ACCESSION CQ725539  
VERSION CQ725539.1 GI:42286477  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;



[http://www.sanger.ac.uk/Projects/C\\_elegans/wormmap](http://www.sanger.ac.uk/Projects/C_elegans/wormmap) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-755J17 is from the library RP11-11.3 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/dacpac/home.htm>  
VECTOR: pBAC3.6

----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)

This sequence was finished as follows unless otherwise noted: all clegions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

## FEATURES

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polya\_bite

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polyA\_signal

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## ORIGIN

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KEYWORDS Homo sapiens (human)  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 McIlroy, K.  
Direct Substitution  
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk

## COMMENT

On Jan 14, 2001 this sequence version replaced gi.12214326.  
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Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
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Project Information  
Center project name: ba505B21  
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Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
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Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality  
coverage: 2.65x in Q20 bases; agarose-fp  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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RESULT 5  
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DEFINITION  
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AF017776  
AF017776.1 GI:3800731

ACCESSION  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1235)  
Folbor, U., Gehrig, A., Sauer, C. G., Marguardt, A., Kohler, M., Schmid, M. and Weber, B. H.  
Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IPM1) gene: a candidate for 6q-linked retinopathies  
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
9691169

REFERENCE  
AUTHORS  
Gehrig, A., Folbor, U., Kelsell, R., Hunt, D. M., Maumenee-Husels, I. E. and Weber, B. H. F.  
Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bilateral choriorretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)

TITLE  
Unpublished  
3 (bases 1 to 1235)  
Folbor, U., Kuehn, M., Hageman, G. S. and Weber, B. H. F.  
Direct Submission  
Submitted (09-AUG-1997) HumanGenetic, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany  
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exon

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DB 471 AAGATTGGAGAGAAATTAAGAAATGTAACAATTAATCACTTAAGCTATCTCAAGA 530  
QY 2627 GAGATGATTCCTCTCAAGAAATGAGACAGGCAATTCATGCGTATCAAAAATCC 2686  
DB 531 GAGATGATTCCTCTCAAGAAATGAGACAGGCAATTCATGCGTATCAAAAATCC 590  
QY 2687 AGACATACAGTCAACACATGAAATCAGACACACATATTCAAATATAGAAAGTCAATG 2746  
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QY 3166 GACTGTTTGTGGCAATTAATCTTGAATTTGTTCTTTAAAGAACTGAGGTTCAATAC 3225  
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QY 3226 ACATACCATGAGAAAATCTTACTTTCTTGTTACTACACAAAGCTATTTAAAGAGATG 3285  
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 VERSION AF017772.1  
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 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 816)  
 REFERENCE  
 AUTHORS Felbor, U., Gehrig, A., Sauer, C.G., Marguardt, A., Kohler, M., Schmidt, M. and Weber, B.H.  
 TITLE Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IPM1) gene: a candidate for 6q-linked retinopathies  
 JOURNAL Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
 PUBMED 9691169  
 AUTHORS 2 (bases 1 to 816)  
 REFERENCE  
 AUTHORS Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.  
 TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bilateral choroideral atrophy (PBCRA), and North Carolina macular dystrophy (MCDN1)  
 JOURNAL Unpublished  
 AUTHORS 3 (bases 1 to 816)  
 REFERENCE  
 AUTHORS Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany  
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 Matches 534; Conservative 0; Mismatches 0;

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 Db 143 GACACTTTTGGATCCACCTGCTATAGGCTGCTTACTCTCCCTGACAGAGCTCCACCTTTC 202  
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QY 1543 TTTATGGATCAAGACATCTTCTCTGACTGATCAAGGACCAAGATCAATGGCCACT 1602  
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QY 1603 GACCAAGACATGCTAGTACCAAGGCTCACCATCTCCCAAGATGATTTCTGCAATCAGC 1662  
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 Db 263 GACCAAGACATGCTAGTACCAAGGCTCACCATCTCCCAAGATGATTTCTGCAATCAGC 322  
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QY 1663 CAAGTGGCTCTGGGAATTTCAATCCACTGATCTTTCAGATGACAGCCGATCAAGTGA 1722  
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 Db 323 CAAGTGGCTCTGGGAATTTCAATCCACTGATCTTTCAGATGACAGCCGATCAAGTGA 382  
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QY 1723 GGTGGCAAGATATGCTGACACACCTAGATGAATGATCTGTGACACTCTGCCCA 1782  
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 Db 383 GGTGGCAAGATATGCTGACACACCTAGATGAATGATCTGTGACACTCTGCCCA 442  
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 1 (bases 1 to 160719)  
 REFERENCE  
 AUTHORS Wall, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonequest@sanger.ac.uk  
 On Sep 12, 2001 this sequence version replaced gi:11991356.  
 COMMENT  
 ----- Genome Center  
 Center: Sanger Centre  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: d062L18  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Sequencing vector: plasmid; 108752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 160382 bases at least Q40  
 Consensus quality: 160493 bases at least Q20  
 Consensus quality: 160578 bases at least Q20  
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 \* NOTE: This is a 'working draft' sequence.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
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Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 7282 TTCACACAGAGCTCTCTGAGATACCGAGCTCTGAGCAACATTCACAGACTG 7229

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DEFINITION AF017769.1 GI:3800724  
ACCESSION  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
Homo sapiens (human)  
10 of 17  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 444)  
Schmid,M. and Weber,B.H.  
Genomic organization and chromosomal localization of the  
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate  
for 6q-linked retinopathies  
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
JOURNAL  
PUBMED 9691169  
AUTHORS Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.  
and Weber,B.H.F.  
TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150)

localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
macular dystrophy, progressive bilateral choroideremia atrophy  
(PBCRA), and North Carolina macular dystrophy (MCDRI)

## JOURNAL

Unpublished  
3 (bases 1 to 444)  
Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.

## AUTHORS

Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am  
Hubland, Wuerzburg D-97074, Germany

## JOURNAL

## FEATURES

## Source

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QY 1199 ATCATGGAACATGAGAGAGAGCAACCAAGAAATTAATCTCACACTACAGACTCA 1258  
DB 211 ATCATGGAACATGAGAGAGAGCAACCAAGAAATTAATCTCACACTACAGACTCA 270  
QY 1259 AAAGCTGATGAGCAAGACATAGAGAAACAATCTTGGATGTGGGACAATTCAGT 1318  
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ACCESSION  
VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM  
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2 of 17  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 537)  
Felbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,  
Schmid,M. and Weber,B.H.  
Genomic organization and chromosomal localization of the  
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate  
for 6q-linked retinopathies  
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)  
JOURNAL  
PUBMED 9691169  
AUTHORS Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.  
and Weber,B.H.F.  
TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150)  
localized to 6q14.2-q15 in autosomal dominant Stargardt-like  
macular dystrophy, progressive bilateral choroideremia atrophy  
(PBCRA), and North Carolina macular dystrophy (MCDRI)

JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 537)
AUTHORS	Felboj,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
TITLE	Direct Submission
JOURNAL	Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
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Matches 236; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Dd	95 AGATATCTCCATTAACTATATACCATTCCTGAAAAGTAAAGACATAGACATATCCCCCAAGAA 154
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Dd	155 TGAACAACACTGAAAGTAGTAAGAAAAATGTACAAAATGTCAAATAAGACAGATATTGCA 214
Oy	316 TTGGGCAGAAGCATCGAACAAAAAAGATCCGCATTTTCCCACACGGGGGTTAAAGTGTC 375
Dd	215 TTGGGCAGAAGCATCGAACAAAAAAGATCCGCATTTTCCCACACGGGGGTTAAAGTGTC 274
Oy	376 ACAGAAATCCATGAAACAGATTTTATAGACAGCTTCAAGCTATTATATAGATTGAGAG 431
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DEFINITION	Homo sapiens chromosome 1 clone RP11-505B21, 26 unordered pieces.
ACCESSION	ALJ59817
VERSION	ALJ59817.6 GI:12225447
KEYWORDS	HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 McJlay, K.
AUTHORS	Direct Submission
TITLE	Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL	CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
	requesters: clonerequest@sanger.ac.uk
	On Jan 14, 2001 this sequence version replaced gi:12214326.
COMMENT	----- Genome Center
	Center: Sanger Centre
	Center code: SC
	Web site: http://www.sanger.ac.uk
	Contact: humquery@sanger.ac.uk
	----- Project Information
	Center project name: ba505B21
	----- Summary Statistics
	Assembly program: XAPP4; Version 4.5
	Sequencing vector: Plasmid; L08752; 100% of reads
	Chemistry: Dye-terminator Big Dye; 100% of reads
	Consensus quality: 11761 bases at least Q40
	Consensus quality: 12343 bases at least Q30
	Consensus quality: 126505 bases at least Q20
	Insert size: 129645; sum-of-contigs
	Insert size: 166195; 8.3% error; agarose-fp

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Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality
coverage: 2.65x in Q20 bases; agarose-gel
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
*
* 1 8912: contig of 8912 bp in length
* 8913 9012: gap of 100 bp
* 9013 12665: contig of 3653 bp in length
* 12666 12765: gap of 100 bp
* 12766 16825: contig of 4060 bp in length
* 16826 16925: gap of 100 bp
* 16926 22958: contig of 6033 bp in length
* 22959 23058: gap of 100 bp
* 23059 25080: contig of 2022 bp in length
* 25081 25180: gap of 100 bp
* 25181 27272: contig of 2092 bp in length
* 27273 27372: gap of 100 bp
* 27373 40754: contig of 13382 bp in length
* 40755 40854: gap of 100 bp
* 40855 45147: contig of 4393 bp in length
* 45148 45247: gap of 100 bp
* 45248 48493: contig of 3246 bp in length
* 48494 48593: gap of 100 bp
* 48594 52861: contig of 4288 bp in length
* 52862 52981: gap of 100 bp
* 52982 57112: contig of 4131 bp in length
* 57113 57212: gap of 100 bp
* 57213 60637: contig of 3425 bp in length
* 60638 60737: gap of 100 bp
* 60738 62745: contig of 2008 bp in length
* 62746 62845: gap of 100 bp
* 62846 70684: contig of 7839 bp in length
* 70685 70784: gap of 100 bp
* 70785 74560: contig of 3776 bp in length
* 74561 74660: gap of 100 bp
* 74661 77242: contig of 2382 bp in length
* 77243 77342: gap of 100 bp
* 77343 81104: contig of 3762 bp in length
* 81105 81204: gap of 100 bp
* 81205 83750: contig of 2546 bp in length
* 83751 83850: gap of 100 bp
* 83851 92962: contig of 9112 bp in length
* 92963 93062: gap of 100 bp
* 93063 106092: contig of 13030 bp in length
* 106093 106192: gap of 100 bp
* 106193 110995: contig of 4803 bp in length
* 110996 111095: gap of 100 bp
* 111096 114862: contig of 3767 bp in length
* 114863 114962: gap of 100 bp
* 114963 118827: contig of 3665 bp in length
* 118828 118927: gap of 100 bp
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* 124085 124184: gap of 100 bp
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Query Match

7.1%; Score 236; DB 14; Length 132145;

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Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 AGATATCTCCATTACATATACATTTCTGAAACTTAAGACATAGCAATCCCCCAAGAAA 255
Db 130597 AGATATCTCCATTACATATACATTTCTGAAACTTAAGACATAGCAATCCCCCAAGAAA 130538
Qy 256 TGAACCAACTGAAGTACTGAAAAATGTACAAAATGCAACTATAGACGAATTTGCA 315
Db 130537 TGAACCAACTGAAGTACTGAAAAATGTACAAAATGCAACTATAGACGAATTTGCA 130478
Qy 316 TTTGGCAAGCATCGAACAACAAAGATCCGCAATTTTCCCAACGGGGGTTAAAGTGTGCC 375
Db 130477 TTTGGCAAGCATCGAACAACAAAGATCCGCAATTTTCCCAACGGGGGTTAAAGTGTGCC 130418
Qy 376 ACAGGAATCCATGAAACAGATTTTGAACAGTCTTCAAGCTTATATAGATTGAGAG 431
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RESULT 11
AL356962/186301 bp DNA linear PRI 18-MAY-2005
LOCUS Human DNA sequence from clone Rpl1-453C2 on chromosome 6 Contains
DEFINITION the 5' end of the IMPG1 gene for Interphotoreceptor matrix
proteinoglycan 1, complete sequence.
ACCESSION AL356962
VERSION AL356962.8 GI:11024485
KEYWORDS HTG, IMPG1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 186301)
REFERENCE Pearce,A.
AUTHORS Direct Submission
TITLE Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
JOURNAL Cambridgehire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Oct 26, 2000 this sequence version replaced gi:10944194.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
Rpl1-453C2 is from the library RPL1-11.2 constructed by the group
of Pletzer de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC63.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
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DB 32795 AGATATCTCCATTAAACATATACATCTGAAACTAAGACATAGCAATCCCCAAGAAA 32736
QY 256 TGAACAACATGAAAGTACTGAAAAAATGTACAAAATGTCAACTATGACGAAATTTGCA 315
DB 32735 TGAACAACATGAAAGTACTGAAAAAATGTACAAAATGTCAACTATGACGAAATTTGCA 32676
QY 316 TTGGCAAGCATGCAACAAAAGATCCGCAATTTTCCACGGGGTTAAAGTCTGCC 375
DB 32675 TTGGCAAGCATGCAACAAAAGATCCGCAATTTTCCACGGGGTTAAAGTCTGCC 32616
QY 376 ACAGAAATCCATGAAACAGATTTTGAAGAGCTTCAAGCTTATTTATTTAGATTGAGAG 431
DB 32615 ACAGAAATCCATGAAACAGATTTTGAAGAGCTTCAAGCTTATTTATGATTGAGAG 32560

RESULT 12
HSIMPG15 477 bp DNA linear PRI 28-OCT-1998
LOCUS Homo sapiens interphotoreceptor matrix gene (IPM150), exon 15.
DEFINITION AF017774.1 GI:3800729
ACCESSION AF017774.1
VERSION AF017774.1
KEYWORDS 15 of 17
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 477)
Felbor,U., Gehrig,A., Sauer,C.G., Marguardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
9691169
JOURNAL 2 (bases 1 to 477)
PUBMED Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Huissels,I.E.
and Weber,B.H.
AUTHORS Assessment of a novel interphotoreceptor matrix gene (IPM150)
located to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bilateral choriorrectinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDRI)
Unpublished
JOURNAL 3 (bases 1 to 477)
REFERENCE Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
AUTHORS Direct Submission
JOURNAL Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
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Best Local Similarity 100.0%; Pred. No. 7.9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2234 CAGCGATCAAGCATCCCTGCAAGTTCCGCGCTGCGAGGATTTGGCCCAATGTGTA 2293
DB 68 CAGCGATCAAGCATCCCTGCAAGTTCCGCGCTGCGAGGATTTGGCCCAATGTGTA 127
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Db	128	AGAAAGAA	CGGACTGATGAGAA	GCGGAGTGTCCGTCTGCAAA	CCAGGATATGACAC	CGCGGGA	187
QY	2354	GCGTCGAC	CGGCTTGGAAC	CGAGGCTCTGTGAGCCCTTGAGC	CAAAAGGAATGCGAGGTCCTCC		2413
Db	188	GCGTCGAC	CGGCTTGGAAC	CGAGGCTCTGTGAGCCCTTGAGC	CAAAAGGAATGCGAGGTCCTCC		247
QY	2414	AGGGAAAG	GGAGCTCCATGCAGGT				
Db	248	AGGGAAAG	GGAGCTCCATGCAGGT	271			
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DEFINITION	Homo sapiens interphotoreceptor matrix gene (IPM150), exon 1.						
ACCESSION	AF017760						
VERSION	AF017760.1	GI:3800715					
KEYWORDS							
SEGMENT							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
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QY	121	AAAGCCAGATGATATTGGAACTAGAGGCAATTTTGTCTTTGGATTTTCCTCA	180
Db	147	AAAAGCCAGATGATATTGGAACTAGAGGCAATTTTGTCTTTGGATTTTCCTCA	206
QY	181	AGTTCAGAGAACCAAG	197
Db	207	AGTTCAGAGAACCAAG	223
RESULT 14			
LOCUS	HSIMPG14	448 bp	DNA linear PRI 28-OCT-1998
DEFINITION	Homo sapiens interphotoreceptor matrix gene (IPM150), exon 14.		
ACCESSION	AF017773		
VERSION	AF017773.1	GI:3800728	
KEYWORDS			
SEGMENT	14 of 17		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Homnidae, Homo.		
AUTHORS	1 (bases 1 to 448) Felbor, U., Gehrig, A., Sauer, C.G., Marguardt, A., Kohler, M., Schmid, M. and Weber, B.H.		
TITLE	Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMP1) gene: a candidate for 6q-linked retinopathies		
JOURNAL	Cytogenet. Cell Genet. 81 (1), 12-17 (1998)		
PUBMED	9691169		
REFERENCE	2 (bases 1 to 448) Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maunee-Hussels, I.E. and Weber, B.H.F.		
AUTHORS	Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to 6q14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal chorioretinal atrophy (PBCRA), and North Carolina macular dystrophy (MCDRI)		
TITLE	Unpublished		
JOURNAL	3 (bases 1 to 448)		
REFERENCE	Direct Submission		
AUTHORS	Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.		
JOURNAL	Submitted (03-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hudland, Wuerzburg D-97074, Germany		
FEATURES	Location/Qualifiers		
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VERSION          AF017762.1  GI:3800717
KEYWORDS
SEGMENT
SOURCE
ORGANISM         Homo sapiens (human)
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                 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                 Homidae; Homo.
REFERENCE        1 (bases 1 to 422)
AUTHORS          Gehrig, A., Gehrig, A., Sauer, C.G., Marguardt, A., Kohler, M.,
                 Felbor, U., and Weber, B.H.
TITLE            Genomic organization and chromosomal localization of the
                 interphotoreceptor matrix proteoglycan-1 (IMPGL) gene: a candidate
                 for 6q-linked retinopathies
JOURNAL          Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
PUBMED           9691169
REFERENCE        2 (bases 1 to 422)
AUTHORS          Gehrig, A., Felbor, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E.
                 and Weber, B.H.F.
TITLE            Assessment of a novel interphotoreceptor matrix gene (IPM150)
                 localized to 6q14.2-q15 in autosomal dominant Stargardt-like
                 macular dystrophy, progressive bifocal choriorretinal atrophy
                 (PBCRA), and North Carolina macular dystrophy (MCDRI)
                 Unpublished
JOURNAL          3 (bases 1 to 422)
AUTHORS          Felbor, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
TITLE            Direct Submission
JOURNAL          Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2006, 07:32:00 ; Search time 12643 Seconds  
(without alignments) 12323.102 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_esc4:\*  
5: gb\_esc5:\*  
6: gb\_esc6:\*  
7: gb\_esc7:\*  
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9: gb\_esc9:\*  
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11: gb\_esc11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

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DEFINITION Homo sapiens mRNA; cDNA DKFZp686K0887 (from clone DKFZp686K0887).  
ACCESSION CR749572  
VERSION CR749572.1 GI:51476810  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fodor, G., Han, M. and Wiemann, S.  
1 (bases 1 to 5829)  
Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764

CONSRM  
TITLE The German cDNA Consortium  
JOURNAL Direct Submission  
COMMENT Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764

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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
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Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Interfering nonneutral evolution from human-chimp-mouse orthologous  
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JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1665)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
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361 GAGGAAGAACATCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
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1402 GAGATGCTACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1461  
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1462 GGAGCAGAGCAGTGGCTGCTGACACTTCTTGATGATGATGATGATGATGATGATGATGATG 1521  
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721 AGTATTTTTCGCAATGAGCAACTGGCTGAGGAAATTTTACATGATGATGATGATGATGATG 780

Accession	Version	Keywords	Source	Organism
AY415973	1	GI:39771933	Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
LOCUS	AY415973	1647 bp	DNA	linear
DEFINITION	Mus musculus IMPG1 gene, VIRUAL	TRANSCRIPT, partial	sequence,	genomic survey sequence.
Accession	AY415973			
Version	AY415973.1	GI:39771933		
Keywords	GSS.			
Source	Mus musculus (house mouse)			
Organism	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

REFERENCE	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
AUTHORS	Sciurognathi; Murioidea; Muridae; Murinae; Mus.
JOURNAL	1 (bases 1 to 1647)
PUBMED	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
AUTHORS	Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.U.,
	Adams,M.D. and Cargill,M.
	Direct Submission
	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
	Rockville, MD 20850, USA
	This sequence was made by sequencing genomic exons and ordering
	them based on alignment.
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Db	61 GGACAGTCCCAACTTCAGATGCAAAAAGATTTTAAGAACTTCCAGATTCGAGAAATC 120
OY	1042 CATGTGTAGGATTTAGACCAAGAAGAAAAAGATGGCTCAAGCTCCACAGAGATGCAA 1101
Db	121 CGTGAATTAGGATTTAGNNNNNNNNNNNNNNNNNNNNNTTCAAGCTCACAGAAATACAG 180
OY	1102 CTTAGGGCATCTTTAAGAGACACAGTGCACAAAGCAAAAAGCCCTGCAGAGACTCCTG 1161
Db	181 CTTATGGCATCTTTAAGAGGACCATGACAAAGCAAAAAGCCCTGATGATCTTACTG 240
OY	1162 TCTTTGATTCACAAAAAATTGAAAGTGAAGAGTCTATCATGTGAAACCATGAGAGAGAC 1221
Db	241 TCTCTGATTCACAAAAAATTGAAAGTGAAGATTCATCATGAGATCAT---AGAAAGC 297
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Qy      1642 AGTATATTTCTGCAATCAGCCACTGGCTGGAAATTTCACTTCACTTCATCTTCA 1701
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Qy      1762 CTGTCTGACACTCTGCCCCCATCTGAGGTACAGAGCTCAGGGAATATGTTCTGTCCCA 1821
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Db      949 GAGACATTTGCCACCAAGGGCAGAGAGCTGATGATTTCTTCACTGCTGCTGCTGCTAC 1008
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Qy      2122 TCTGCGGTATTAACCTACCAAGAGCTGTCAGCGGGTCTTGAAGATTTTCTGCTCTGT 2181
Db      1189 GCGGATACCTTCAACCTTCAAGAGCGGGTCTTGAAGATTTTCTGCTCAAC 1248
Qy      2182 GCAGCCCAACACTCTCTGTAATAGACAGTACTCTCTCAATTTGAACCACTGAT 2241
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Qy      2242 CAAGCAGATCCCTGCAAGTTCTGTGCGCGGCAATTTGCCCAATGTGTAAAGACGA 2301
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Qy      2362 GGTCTGGAACAGAGCTCTGTGCGCTGCAAGAAATGAGAGTCTCTCAGGGAAG 2421
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RESULT 4
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LOCUS
DEFINITION
Pan troglodytes IMP1 gene, VIRUAL TRANSCRIPT, partial sequence.
ACCESSION
AY415972
VERSION
AY415972.1 GI:39771932
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE
1 (bases 1 to 1587)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Fertiera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1587)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Fertiera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submision
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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location/Qualifiers
source
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
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Best Local Similarity 46.7%; Pred. No. 2.2e-180;
Matches 741; Conservative 0; Mismatches 846; Indels 0; Gaps 0;
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ACCESSION BI752112  
VERSION BI752112.1 GI:15743690  
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ORGANISM Homo sapiens  
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Homnidae; Homo.  
REFERENCE 1 (bases 1 to 836)  
NIH-MGC http://mhc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11482 row: 1 column: 16  
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(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."

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ACCESSION BX510244  
VERSION BX510244.1 GI:3205051

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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 690)  
Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,  
Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and  
Wiemann, S.  
TITLE EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,  
Wellenreuther, R., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp686P2496) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
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cDNA-collection"

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Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCAAGAGGATCTCTCAATCATCTGATCATATATATATATTTTTCACATTC 60  
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QY 61 TGTACTTTTATAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTCAGATGAC 120  
DB 117 TGTACTTTTATAGATTGAGGTTGTTCTGTGATTGTTATCAGAAATTCAGATGAC 176  
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QY 241 CAATCCCCCAAGAAATGAAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 300  
DB 297 CAATCCCCCAAGAAATGAAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 356  
QY 301 GAGAGCAATATTCGATTTGGCAAGCATTCGAAACAAAGATCCGATTTTCCCAACGGG 360  
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QY 361 GGTTAAGTCTGTCCACAGGAATCCATGAAACAGATTTTAGCAGTCTTCAAGCTTATTA 420  
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RESULT 8  
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LOCUS  
DEFINITION  
UI-E-CL1-afa-m-11-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone  
BM695987  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 633)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).  
Seq primer: M13 Reverse.  
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/mol\_type="mRNA"  
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/clone="UI-E-CL1-afa-m-11-0-UI"  
/tissue\_type="human retina"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CL1"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-E-CL1 is a normalized cDNA library containing the  
following tissue(s): retina. The library was constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pT73-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CCGCG. This library was  
created for the program, Gene Discovery in the Visual  
System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 18.8%; Score 628.8; DB 3; Length 633;  
 Best Local Similarity 99.5%; Pred. No. 8.5e-152;  
 Matches 630; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2529 TGAATTCAGCGGTGAATGAGAAATTTAAACATCAAGATTTGGGAGAAATTTAAA 2588  
 1 TGAATTCAGCGGTGAATGAGAAATTTAAACATCAAGATTTGGGAGAAATTTAAA 60

2589 ACTGAAATGTCACATTTACTTAGCTATCTCAAGAGATGATTTGCTTCTCAAG 2648  
 61 ACTGAAATGTCACATTTACTTAGCTATCTCAAGAGATGATTTGCTTCTCAAG 120

2649 AAAATGAGACAGGCTATTTGAGTCAATCAAAATCCAGACTATACATCACTGAGA 2708  
 121 AAAATGAGACAGGCTATTTGAGTCAATCAAAATCCAGACTATACATCACTGAGA 180

2709 ATCAGACACACATTTTCAATATAGAAAGTCAATGTTGCGACACAGTAAATCT 2768  
 181 ATCAGACACACATTTTCAATATAGAAAGTCAATGTTGCGACACAGTAAATCT 240

2769 GAAAAAAGACACTTACTTATATTTAAACCCCAATGCAATCAGCGAAATATTTT 2828  
 241 GAAAAAAGACACTTACTTATATTTAAACCCCAATGCAATCAGCGAAATATTTT 300

2829 ACTATTTCTGATGATGATCAAAATGATCATTAAGCCAGGTTGCTTCCACTTCCGAA 2888  
 301 ACTATTTCTGATGATGATCAAAATGATCATTAAGCCAGGTTGCTTCCACTTCCGAA 360

2889 AATTTTACTCAGACATTTTGGCAACACATAGCTTACTTATGTTTGGGACGTGAAC 2948  
 361 AATTTTACTCAGACATTTTGGCAACACATAGCTTACTTATGTTTGGGACGTGAAC 420

2949 ATTATTTGGGAAGCAACTCTTATATGCTAGAAATGATTTAAAGATGACTACTTAC 3008  
 421 ATTATTTGGGAAGCAACTCTTATATGCTAGAAATGATTTAAAGATGACTACTTAC 480

3009 GCAAGGAGATGCAAGTCTCTTAAACGATGAATGATGAGTGTAGGCACTGTAGTG 3068  
 481 GCAAGGAGATGCAAGTCTCTTAAACGATGAATGATGAGTGTAGGCACTGTAGTG 540

3069 AGTGTATATAGCTCCACACTGCTGTGATTAACAAACCTCAGATTCAGTTATTAAG 3128  
 541 AGTGTATATAGCTCCACACTGCTGTGATTAACAAACCTCAGATTCAGTTATTAAG 600

3129 CACACTAGTTTATACGCAACTACTGCTTACAT 3161  
 601 CACACTAGTTTATACGCAACTACTGCTTACAT 633

Db

RESULT 9  
 B0639265 626 bp mRNA linear EST 15-JUL-2002  
 LOCUS hd33d04.y1 Human Retina cDNA (Un-normalized, unambigified): hd/he  
 DEFINITION B0639265  
 VERSION B0639265.1 GI:21763724  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 626)  
 Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Petersen, K.,  
 Expressed sequence tag analysis of human retina for the NEIBank  
 Project: Rebinding, an abundant, novel retinal cDNA and alternative  
 splicing of other retina-preferred gene transcripts  
 Mol. Vis. 8 (4), 196-204 (2002)  
 JOURNAL PUBMED 12107411  
 COMMENT Contact: Wistow G

Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 33 row: d column: 04  
 Seq primer: M13RP1 reverse primer (AB1).  
 Location/Qualifiers

## FEATURES

source  
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 /db\_xref="taxon:9606"  
 /clone="hd33d04"  
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 /lab\_host="EMDH10B"  
 /clone\_1lb="Human Retina cDNA (Un-normalized,  
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 /note="Organ: Eye; Vector: pSPORT1. Neural retina tissue  
 was dissected from two 80 year old donors with no observed  
 eye disease. 100ug of total RNA was used for library  
 construction. A directionally cloned cDNA library in the  
 pSPORT1 vector (Life Technologies) was constructed at  
 Bioserve Biotechnology (laurel MD) essentially following  
 the protocols of the SuperScript Plasmid System full  
 details of which are contained in the manufacturer's  
 instruction manual (http://www.lifetech.com/). First  
 strand synthesis was carried out using a Not I  
 primer-adaptor  
 [5'-pGACTTACTTCTAGATCCGACCGCCGCTT5-3']. EST analysis  
 was performed on the unambigified library at the NIH  
 Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 18.8%; Score 626; DB 5; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-151;  
 Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

968 ACCAGAGCTAGCAGAAAGTCCCACTTCAGATGCAAAAGATTTTAAAGAACTTCCAG 1027  
 1 ACCAGAGCTAGCAGAAAGTCCCACTTCAGATGCAAAAGATTTTAAAGAACTTCCAG 60

1028 GATTCAAAAAATTCATGTGTTAGATTAGACCAAGAAAGAAAGATGCTCAAGCT 1087  
 61 GATTCAAAAAATTCATGTGTTAGATTAGACCAAGAAAGAAAGATGCTCAAGCT 120

1088 CCACAGAGTGAACCTTACGGCCATCTTAAAGACACAGTCCAGAGCAAAAGCCCTG 1147  
 121 CCACAGAGTGAACCTTACGGCCATCTTAAAGACACAGTCCAGAGCAAAAGCCCTG 180

1148 CAAGTGAACCTCTGTCTTTTGAATCCAAATAAATGGAAGTGAAGTCTATCATGAA 1207  
 181 CAAGTGAACCTCTGTCTTTTGAATCCAAATAAATGGAAGTGAAGTCTATCATGAA 240

1208 CCATGAGAGGAGCAAGCAACCAAAATCTATCTCAACAGTACAGACTTCAAAAGGCTGA 1267  
 241 CCATGAGAGGAGCAAGCAACCAAAATCTATCTCAACAGTACAGACTTCAAAAGGCTGA 300

1268 TCAGCAAGCACTAAGAGAAACAATCTTGGAGTGGGGCAATTCAGTCACTGAG 1327  
 301 TCAGCAAGCACTAAGAGAAACAATCTTGGAGTGGGGCAATTCAGTCACTGAG 360

1328 AAATGCTGATCATCTGCAAGCTTGTGCTGACACCAATCAGAGCTGCCACATCTT 1387  
 361 AAATGCTGATCATCTGCAAGCTTGTGCTGACACCAATCAGAGCTGCCACATCTT 420

1388 TTGCTGTTTAAACAGAGATGCTTCTTGAAGTCCGAAGTCTCTCTGTTGAACCCAGC 1447  
 421 TTGCTGTTTAAACAGAGATGCTTCTTGAAGTCCGAAGTCTCTCTGTTGAACCCAGC 480

1448 TTGAGACGTGACGAGAGAGAGCATGGTCTACGTGACACTTCTTGCTTCCAGCTGCTA 1507

Db

Db 481 TTGACAGAGTGGACGAGAGAGATGGTCTACCTTGACCTTCTGCTCCAGCTGTGA 540  
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Db 541 TGGCTCTACCTCCCTGTCAGAAAGCTCCACTTTCTTATGGCATCAAGCATCTTCTGC 600  
Qy 1568 TGACGATCAAGGACCAAGATAGA 1593  
Db 601 TGACGATCAAGGACCAAGATAGA 626

RESULT 10  
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LOCUS hd29a06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
DEFINITION Homo sapiens cDNA clone hd29a06 5', mRNA sequence.  
ACCESSION BQ638902.1 GI:21763361  
VERSION BQ638902.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 622)  
Wiscow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A.,  
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
Expressed sequence tag analysis of human retina for the NEIBank  
Project: Retbindin, an abundant, novel retinal cDNA and alternative  
splicing of other retina-preferred gene transcripts  
Mol. Vis. 8 (4), 196-204 (2002)  
12107411  
JOURNAL PUBMED  
COMMENT Contact: Wiscow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graham@helix.nih.gov  
Plate: 29 row: a column: 06  
Seq primer: M13RP1 reverse primer (AB1).  
Location/Qualifiers  
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/lab\_host="EMD110B"  
/clone\_1fb="Human Retina cDNA (Un-normalized,  
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/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
the protocols of the Superscript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-TGACTGATCTTGAATCGGACGCGCCGCTT)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

ORIGIN  
Query Match 18.5%; Score 617.2; DB 5; Length 622;  
Best Local Similarity 99.5%; Pred. No. 8.8e-149;  
Matches 619; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2480 AAAAGTCCAAATCAACAAATTAACAAAGTAATCAAGTAAGAAATCTGAATTACTGA 2539

Db 1 AAAAGTCCAAATCAACAAATTAACAAAGTAATCAAGTAAGAAATCTGAATTACTGA 60  
Qy 2540 CCGTGAATATGAAGAAATTTAAACATCAAGATTGGGAAGAAATTTAAACTGAAATAGT 2599  
Db 61 CCGTGAATATGAAGAAATTTAAACATCAAGATTGGGAAGAAATTTAAACTGAAATAGT 120  
Qy 2600 ACAATTAATCACTAGGCTATCTCAAGAGATGAATTTGCTTCTCAAGAAATAGGAGC 2659  
Db 121 ACAATTAATCACTAGGCTATCTCAAGAGATGAATTTGCTTCTCAAGAAATAGGAGC 180  
Qy 2660 AGGCATATTCATGGGTCAATCAAAATCCAGACATACATGCAACACTGAGAAATCAGACACA 2719  
Db 181 AGGCATATTCATGGGTCAATCAAAATCCAGACATACATGCAACACTGAGAAATCAGACACA 240  
Qy 2720 CCAATTTTCAATATGAAGAGTCAATGCTTGGCAACCATTAATTTCTGAAAAAATGA 2779  
Db 241 CCAATTTTCAATATGAAGAGTCAATGCTTGGCAACCATTAATTTCTGAAAAAATGA 300  
Qy 2780 CACTTACTTATTTAAACCCCAATGCAATGCAAGCAATATTTTACTATTTCTTGG 2839  
Db 301 CACTTACTTATTTAAACCCCAATGCAATGCAAGCAATATTTTACTATTTCTTGG 360  
Qy 2840 ATGATAGTCAAAATGATCATTAAGCCAGGTTGCTTCCACCTTCCCTGAAAAATTTACTCA 2899  
Db 361 ATGATAGTCAAAATGATCATTAAGCCAGGTTGCTTCCACCTTCCCTGAAAAATTTACTCA 420  
Qy 2900 CAGATCATTTGCAACAGCATATGCTTACTTATTTGTTAGGACATCAACATTTATTTGGA 2959  
Db 421 CAGATCATTTGCAACAGCATATGCTTACTTATTTGTTAGGACATCAACATTTATTTGGA 480  
Qy 2960 AGCAAACTCTTATATGCTAGTAAAGTACTTTAAAGATGACTTACTTACGAGGAGATG 3019  
Db 481 AGCAAACTCTTATATGCTTAAAGTACTTTAAAGTACTTACTTACGAGGAGATG 540  
Qy 3020 CAGGCTCTCTTAAAGCATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 3079  
Db 541 CAGGCTCTCTTAAAGCATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Qy 3080 GCTCCAGCTACGCTGTGATTA 3101  
Db 601 GCTCCAGCTACGCTGTGATTA 622

RESULT 11  
BQ685921 653 bp mRNA linear EST 27-FEB-2002  
LOCUS UI-E-CR0-sas-h-07-0-UI.r1 UI-E-CR0 Homo sapiens cDNA clone  
DEFINITION UI-E-CR0-sas-h-07-0-UI 5', mRNA sequence.  
ACCESSION BQ685921  
VERSION BQ685921.1 GI:18995817  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 653)  
Bonald, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL PUBMED  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Genetics (www.resgen.com).  
Seq primer: M13 Reverse.  
Location/Qualifiers

## FEATURES

SOURCE

1. .653  
/organism="Homo sapiens"  
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/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CK0"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; UI-E-CK0 is a cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 18.5%; Score 615.6; DB 3; Length 653;  
Best Local Similarity 99.4%; Pred. No. 2.3e-148;

Matches 618; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Oy 2709 ATCAGCACACCAATTTCAATATAGAGAGTCATGACTTGGACCAAGTAATCT 2768
Db 10 AACAGCACACCAATTTCAATATAGAGAGTCATGACTTGGACCAAGTAATCT 69
Oy 2769 GAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCAATATTTT 2828
Db 70 GAAAGAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCAATATTTT 129
Oy 2829 ACTATTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2888
Db 130 ACTATTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 189
Oy 2889 AATTTTACTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2948
Db 190 AATTTTACTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
Oy 2949 ATTTATTTGGGAAGCAAACTCTTATATGCTAGAAAGTACATTTAAAGTACTTAC 3008
Db 250 ATTTATTTGGGAAGCAAACTCTTATATGCTAGAAAGTACATTTAAAGTACTTAC 309
Oy 3009 GCAGGAGATGAGGCTCTCTTAAACGATGATGATGATGATGATGATGATGATG 3068
Db 310 GCAGGAGATGAGGCTCTCTTAAACGATGATGATGATGATGATGATGATGATG 369
Oy 3069 AGTATATATGATGCTCAGATGATGATGATGATGATGATGATGATGATGATGATG 3128
Db 370 AGTATATATGATGCTCAGATGATGATGATGATGATGATGATGATGATGATGATG 429
Oy 3129 CACACTAGTTTATAGCAACTACTGCTTACATAGTACAGTGTGTTGTTGCAATATCT 3188
Db 430 CACACTAGTTTATAGCAACTACTGCTTACATAGTACAGTGTGTTGTTGCAATATCT 489
Oy 3189 TTGAATTTGTTCTTTTAAAGAACTGAGTTGATGATGATGATGATGATGATGATG 3248
Db 490 TTGAATTTGTTCTTTTAAAGAACTGAGTTGATGATGATGATGATGATGATGATG 549
Oy 3249 TTTCTTTGTTACTACCAAGCTATTTTAAAGAAAGTGTGATGTTGGAGAAAGGGAAGT 3308
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Db 550 TTTCTGTTACTACCAAGCTATTTTAAAGAAAGTGTGATGTTGGAGAAAGGGAAGT 609
Oy 3309 TGTACTATATGACATATATCAAT 3330
Db 610 TGTACTATATGACATATATCAAT 631
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## RESULT 12

BM690735

LOCUS 675 bp mRNA linear EST 28-PEB-2002  
DEFINITION UI-E-CK0-aav-c-12-0-UI .r1 UI-E-CK0 Homo sapiens cDNA clone

UI-E-CK0-aav-c-12-0-UI 5', mRNA sequence.

ACCESSION BM690735  
VERSION BM690735.1 GI:19003993

KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.

1 (bases 1 to 675)

Bonaldo,M.P., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery  
Genome Res. 6 (9), 791-806 (1996)

8889548

## JOURNAL

PUBMED

COMMENT

Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

DNA library arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

## FEATURES

SOURCE

1. .675  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="UI-E-CK0-aav-c-12-0-UI"  
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/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CK0"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; UI-E-CK0 is a cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

## ORIGIN

Query Match 17.7%; Score 589.4; DB 3; Length 675;  
Best Local Similarity 99.7%; Pred. No. 1.6e-141;  
Matches 601; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY	2728	CAAAATATGAAAGAGCATGTCCTTGGCAACCAAGTAAATCTGAAAAAAAAGACCTTACT	2787
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Db	67	TATATATTTAAACCCCAATGCAATCAGGAAACAATATTTTACTATCTTCTGGATGATAGT	126
QY	2848	CAAAATGATCATTAAGCCAGGTTTGGCTTCCACCTTCCCTGAAAAATTTTACTCACAGATCAT	2907
Db	127	CAAAATGATCATTAAGCCAGGTTTGGCTTCCACCTTCCCTGAAAAATTTTACTCACAGATCAT	186
QY	2908	TTGCAACAGGATAGCTTACTTTATTTGTTTAGGGACCTGAACAATTTATTTGGGAAGCAACT	2967
Db	187	TTGCAACAGGATAGCTTACTTTATTTGTTTAGGGACCTGAACAATTTATTTGGGAAGCAACT	246
QY	2968	CTTTATATGCTAGAAAGTACATTTTAAAGATGACTTACTTACGACGGAGATGCAAGTCTC	3027
Db	247	CTTTATATGCTAGAAAGTACATTTTAAAGATGACTTACTTACGACGGAGATGCAAGTCTC	306
QY	3028	TCTTAAACGCATGAATGTATGTAGTGTAGGCACTGTAGTGAAGTATATATATGCTCCACA	3087
Db	307	TCTTAAACGCATGAATGTATGTAGTGTAGGCACTGTAGTGAAGTATATATATGCTCCACA	366
QY	3088	CTACGCTCTGATATTAACCAAAACCTCAGTATTCAGTTATATAGGCACACTAGTTTATACCA	3147
Db	367	CTACGCTCTGATATTAACCAAAACCTCAGTATTCAGTTATATAGGCACACTAGTTTATACCA	426
QY	3148	ACTACTGCTTACATAGTAGTACTGTTTGTGTGGCAATATCTTTGAAATGTGTTCTTTAAAG	3207
Db	427	ACTACTGCTTACATAGTAGTACTGTTTGTGTGGCAATATCTTTGAAATGTGTTCTTTAAAG	486
QY	3208	AACTGAGGTTCAGATATACATATCCATGGAATAATCTTACTTTCTTGTACTACACAA	3267
Db	487	AACTGAGGTTCAGATATACATATCCATGGAATAATCTTACTTTCTTGTACTACACAA	546
QY	3268	GCTATTTTAAAGAGATGCTATGTTGGAGAAAGGCGCAAGTTGTACTATATGACATATC	3327
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Db	607	AAT 609	
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DEFINITION	hd11h02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he		
ACCESSION	BO636596		
VERSION	BO636596.1	GI:21761055	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
TITLE	Homnidae; Homo.		
JOURNAL	1 (bases 1 to 598)		
PUBMED	Wielow,G., Bernstein,S.L., Wyalc,M.K., Ray,S., Behal,A.,		
COMMENT	Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.		
	Expressed sequence tag analysis of human retina for the NEIRank		
	Project: Rebrndin, an abundant, novel retinal cDNA and alternative		
	splicing of other retina-preferred gene transcripts		
	MOL. VIS. 8 (4), 196-204 (2002)		
	12107411		
	Contact: Wielow G		
	Section on Molecular Structure and Function		
	National Eye Institute		
	6/331, NIH, Bethesda, MD 20892-2740, USA		
	Tel: 301 402 3452		
	Fax: 301 496 0078		
	Email: gdraeme@helix.nih.gov		

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Plate: 11 row: h column: 02
Seq primer: M13R1 reverse primer (ABI).
Location/Qualifiers
source 1. 598

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unamplified) : hd/he"
/notes="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the Superscript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTGATTTCAGATCCGACGCCGCC(715-3')]. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."

```

**ORIGIN**

Query Match	17.3%	Score 577.6;	DB 5;	Length 598;
Best Local Similarity	99.3%	Pred. No. 1.8e-138;		
Matches 580;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1490	CTTGAGTCCACAGCTATGGCCCTTCAAGCTCCCTGTGAGAAGCTCCAACCTTTCTTTATGG	1549
DB	15	CTTGAGTCCACAGCTATGGCCCTTCAAGCTCCCTGTGAGAAGCTCCACCTTTCTTTATGG	74
QY	1550	CATCAAGCATCTTCTCTGTGACTGATCAAGGACCAAGATACATATAGCCACTGACCGA	1609
DB	75	CATCAAGCATCTTCTCTGTGACTGATCAAGGACCAAGATACATATAGCCACTGACCGA	134
QY	1610	CAATGCTAGTACCAAGGCTCAACATCCCAACAGTATTATTTGCAATACGCCAATCTGG	1669
DB	135	CAATGCTAGTACCAAGGCGACCAATCCCAACAGTATTATTTGCAATACGCCAATCTGG	194
QY	1670	CTCTGGGAATTTCAATCCACCTGATCTTTCAATGACGCCGATCAAGTGCAGGTGGCG	1729
DB	195	CTCTGGGAATTTCAATCCACCTGATCTTTCAATGACGCCGATCAAGTGCAGGTGGCG	254
QY	1730	AAGATATGTCAGACACTAGATGAATGAATCTGTCTGACACTCTGGCCCATCTGAGG	1789
DB	255	AAGATATGTCAGACACTAGATGAATGAATCTGTCTGACACTCTGGCCCATCTGAGG	314
QY	1790	TACCAAGCTCAGGAATATGTTCTGTCCAGATCAATTTCTTGAGAGATACACTCCTG	1848
DB	315	TACCAAGCTCAGGAATATGTTCTGTCCAGATCAATTTCTTGAGAGATACACTCCTG	374
QY	1850	TCTCAGCTTACAGATATACCACTAGATGTTCTATGACCATTTGCCCAAGGCGCAGAGAC	1908
DB	375	TCTCAGCTTACAGATATACCACTAGATGTTCTATGACCATTTGCCCAAGGCGCAGAGAC	434
QY	1910	TGTAATGTTCTCAGTCTGGCGTGTGCTAACATGACCCTTCTCCACGACCTGTTCACA	1968
DB	435	TGTAATGTTCTCAGTCTGGCGTGTGCTAACATGACCCTTCTCCACGACCTGTTCACA	494
QY	1970	AGAGCTCTGAGAGTACCGAGCTCTGAGCAACATTCACAACAGTGTGTTCCATATC	2028
DB	495	AGAGCTCTGAGAGTACCGAGCTCTGAGCAACATTCACAACAGTGTGTTCCATATC	554
QY	2030	TACGATCCATCTTACAGATTTTAAGCACTTGAATCTTTAC	2073
DB	555	TACGATCCATCTTACAGATTTTAAGCACTTGAATCTTTAC	598

RESULT 14  
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LOCUS cs44g04.y1 Human Retinal pigment epithelium/choroid cDNA  
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs44g04  
5', mRNA sequence.  
ACCESSION CA393958  
VERSION CA393958.1 GI:24728064  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 508)  
Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NEIbank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
JOURNAL 12107410  
PUBMED  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 402 0078  
Email: greene@helix.nih.gov  
Plate: 44 row: 9 column: 04  
Seq primer: M13RPI reverse primer (AB1).  
Location/Qualifiers  
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/dev\_stage="Adult"  
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/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the Superscript  
Plasmid System (Invitrogen Corp).  
http://www.invitrogen.com/>. The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

ORIGIN  
Query Match 15.0%; Score 498.4; DB 6; Length 508;  
Best Local Similarity 98.8%; Pred. No. 6,8e-118;  
Matches 502; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1442 CCCAGCTTGAGACAGTGAAGAGGAGAGCATGCTTACCTGACATCTTGGTCTCCAC 1501  
DB 1 CCCAGCTTGAGACAGTGAAGAGGAGAGCATGCTTACCTGACATCTTGGTCTCCAC 60  
QY 1502 CCGCATAGGCTCTCTACCTCCCTGTGAGAGCTCCACCTTCTTTATGAGATCAAGACTT 1561  
DB 61 CCGCATAGGCTCTCTACCTCCCTGTGAGAGCTCCACCTTCTTTATGAGATCAAGACTT 120  
QY 1562 TCTCTCTGACTGATCAAGGACCAAGATATCAATGAGCCACTGACAGACAATGCTAGTAC 1621  
DB 121 TCTCTCTGACTGATCAAGGACCAAGATATCAATGAGCCACTGACAGACAATGCTAGTAC 180

QY 1622 CAGGGCTGACCACTCCCAACAGTGATTTATTCGAATGAGCCAACTGGCTGGGAATTT 1681  
DB 161 CAGGGCTGACCACTCCCAACAGTGATTTATTCGAATGAGCCAACTGGCTGGGAATTT 240  
QY 1682 CACATCCACCTTGATCTTCAAGTGAACAGCCGATCAAGTGACAGTGGCGAATATGATGA 1741  
DB 241 CACATCCACCTTGATCTTCAAGTGAACAGCCGATCAAGTGACAGTGGCGAATATGATGA 300  
QY 1742 GACACCTGATGAATGAATGATCTGTCTGACACTCTGCCCATCTGAGGTACAGAGCTCA 1801  
DB 301 GACACCTGATGAATGAATGATCTGTCTGACACTCTGCCCATCTGAGGTACAGAGCTCA 360  
QY 1802 GCGAATATGTTTCTGTCCCAATCATTTCTTGAGAGATATCACTCTGTCTCACTTTAC 1861  
DB 361 TCGAATATGTTTCTGTCCCAATCATTTCTTGAGAGATATCACTCTGTCTCACTTTAC 420  
QY 1862 AGTATATGACCACTGATCTTATGACCAATTTGCCCCAAGGCGAGAGCTGTAGTGTCT 1921  
DB 421 AGTATATGACCACTGATCTTATGACCAATTTGCCCCAAGGCGAGAGCTGTAGTGTCT 480  
QY 1922 TCAGTCTGCGTGTGCTTAACATGACCTT 1949  
DB 481 TCAGTCTGCGTGTGCTTAACATGACCTT 508

RESULT 15  
BX097138 472 bp mRNA linear EST 04-FEB-2003  
LOCUS BX097138  
DEFINITION BX097138 Soares retina N2b4HR Homo sapiens cDNA clone  
IMAGE:988N11359 ; IMAGE:190666, mRNA sequence.  
ACCESSION BX097138  
VERSION BX097138.1 GI:27843098  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 472)  
Eberlt,U., Heil,O., Hennig,S., Neubert,P., Paratch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.  
Human Unigeneset - RZPD3  
Unpublished (2003)  
CONTACT: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGE988N11359.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/cloneCards/cgi-  
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heidenweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, primer sequence: TTTCACACAGAAACACTATGAC.  
Location/Qualifiers  
1..472  
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/db\_xref="taxon:9606"  
/clone="IMAGE988N11359 ; IMAGE:190666"  
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/dev\_stage="55 year old"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares retina N2b4HR"  
/note="Organ: eye; Vector: pTZ19 (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st

FEATURES  
SOURCE

strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)<sup>+</sup> RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Facina Bonaldo. "

## ORIGIN

```
Query Match      14.2%; Score 472; DB 5; Length 472;
Best Local Similarity 100.0%; Pred. No. 4.9e-111;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1307 GAGCAATTCAGTTCAGTGAATGCTGATCACTGCCAGCCTTGGTCTGACACCC 1366
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Db 1 GAGCAATTCAGTTCAGTGAATGCTGATCACTGCCAGCCTTGGTCTGACACCC 60
    |||

QY 1367 AATCAGAGTGGCCCATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCCAGAAC 1426
    |||
Db 61 AATCAGAGTGGCCCATCTTTTGTGTATTAACAGAGATGCTACTTTGAGTCCAGAAC 120
    |||

QY 1427 TTCCTCTGTTGAACCCCACTTTGAGACAGTGAACGAGCAGAGCATGCTTACTGACA 1486
    |||
Db 121 TTCCTCTGTTGAACCCCACTTTGAGACAGTGAACGAGCAGAGCATGCTTACTGACA 180
    |||

QY 1487 CTTCTTGGTCTGCACCTGCTATGAGCTTACCTCCCTGTGAGAACTCCACCTTCTTTA 1546
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Db 181 CTTCTTGGTCTGCACCTGCTATGAGCTTACCTCCCTGTGAGAACTCCACCTTCTTTA 240
    |||

QY 1547 TGGCATCAAGCATCTTCTCTGACTGATCAAGGCAACCAAGATCAATGGCACTGACC 1606
    |||
Db 241 TGGCATCAAGCATCTTCTCTGACTGATCAAGGCAACCAAGATCAATGGCACTGACC 300
    |||

QY 1607 AGACAATGCTAGTACCAAGGCTCACCATGCCCAAGATGATTATTCGCAATCAAGCAAC 1666
    |||
Db 301 AGACAATGCTAGTACCAAGGCTCACCATGCCCAAGATGATTATTCGCAATCAAGCAAC 360
    |||

QY 1667 TGGCTCTGGGAATTTTCACATCCACTGCACTTCAGATGACAGCCGATCAAGTGCAGGTG 1726
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Db 361 TGGCTCTGGGAATTTTCACATCCACTGCACTTCAGATGACAGCCGATCAAGTGCAGGTG 420
    |||

QY 1727 GCGAAGATATGGTGCAGACACCTAAGTGAATGATCTGTGACACTCTCTGC 1778
    |||
Db 421 GCGAAGATATGGTGCAGACACCTAAGTGAATGATCTGTGACACTCTCTGC 472
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Search completed: January 14, 2006, 16:49:06  
Job time : 12650 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 21:55:36 ; Search time 7693 Seconds  
(without alignments)  
4847.173 Million cell updates/sec

Title: US-10-007-270-2  
Perfect score: 4117  
Sequence: 1 MYLETRRAIFVFWIFLQVQ.....NSELLTVEYERHNDWEGN 797

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 2339354228 residues  
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame\_plus\_model -DEV=x1h  
-O=/cgn2.1/USPTO.spool/US10007270/runat\_11012006\_110803\_10633/esp\_query.fasta\_1.967  
-DB=EST -QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNIT=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=Pct -NORM=Est HENRIBS=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10007270@cgn2.1\_1\_5655@runat\_11012006\_110803\_10633 -NCPU=6 -ICPU=3  
-NO\_WMAP -LANG=QUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:\*  
1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_hic:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_esc7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3222.5	78.3	5829	4 CR749572	CR749572 Homo sapi
2	2801	68.0	1665	10 AY415971	AY415971 Homo sapi
3	1683	40.9	1647	10 AY415973	AY415973 Mus muscu
4	1054	25.6	626	5 B0639265	B0639265 hnd33d04.Y
5	971	23.6	1587	10 AY415972	AY415972 Pan trogl
6	955	23.2	598	5 B0636596	B0636596 hnd1h02.Y
7	902	21.9	3713	10 AY418611	AY418611 Homo sapi

8	893	21.7	690	5 BX510244	BX510244 DKFZp686P
9	829	20.1	963	5 BUS06195	BUS06195 AGENCOURT
10	819.5	19.9	3734	10 AY418613	AY418613 Mus muscu
11	817.5	19.9	3713	10 AY418612	AY418612 Pan trogl
12	815	19.8	508	6 CA393958	CA393958 cs44g04.Y
13	799	19.4	472	5 BX097138	BX097138 BX097138
14	759	18.4	510	1 AL713329	AL713329 DKFZp686P
15	751	18.2	618	6 CA391789	CA391789 csl1h07.Y
16	738	17.9	561	8 W26960	W26960 16h10 Human
17	737	17.9	754	8 CX568203	CX568203 UI-M-IBO-
18	730.5	17.7	914	5 BX743511	BX743511 BX743511
19	714.5	17.4	824	3 BI738733	BI738733 603358767
20	708	17.2	797	4 AK020862	AK020862 Mus muscu
21	707	17.2	624	7 CK619878	CK619878
22	688.5	16.7	722	8 DN897153	DN897153 nap1b09.Y
23	686	16.7	422	3 BM726533	BM726533 UI-B-EJO-
24	685	16.6	886	6 CF549501	CF549501 AGENCOURT
25	674	16.4	753	3 BI735383	BI735383 603356869
26	649	15.8	448	3 BM681190	BM681190 UI-E-EJO-
27	642.5	15.6	1447	4 CNS06F0V	CR688275 Tetradodon
28	637	15.5	393	5 B0636351	B0636351 hnd07h06.Y
29	636	15.4	851	3 BI733865	BI733865 603353151
30	634	15.4	836	3 BI752112	BI752112 603022362
31	631	15.3	813	5 BX743512	BX743512 BX743512
32	624	15.2	802	3 BI735091	BI735091 603356230
33	612.5	14.9	1146	4 CNS06G50F	CR702515 Tetradodon
34	612	14.9	405	8 H38604	H38604 yp48e04.r1
35	584	14.2	878	6 CF549297	CF549297 AGENCOURT
36	561.5	13.6	963	5 BU287197	BU287197 603604306
37	528	12.8	666	5 BY742200	BY742200 BY742200
38	508.5	12.4	642	7 CK617565	CK617565 mk06n08.Y
39	507	12.3	322	1 AA326863	AA326863 EST30113
40	493	12.0	309	8 H38594	H38594 yp48c06.r1
41	487	11.8	701	10 AG128736	AG128736 Pan trogl
42	466	11.3	611	7 CK621236	CK621236 ml12a05.Y
43	458.5	11.1	1167	8 DN682360	DN682360 CGX23-F08
44	437.5	10.6	567	9 AZ974344	AZ974344 200248P20
45	435.5	10.6	481	1 A1510373	A1510373 mp95e12.Y

## ALIGNMENTS

RESULT 1	CR749572	5829 bp	mRNA	linear	HTC 19-AUG-2004
LOCUS	CR749572				
DEFINITION	Homo sapiens mRNA; cDNA DKFZp686K0887 (from clone DKFZp686K0887).				
ACCESSION	CR749572				
VERSION	CR749572.1	GI:51476810			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 5829)				
AUTHORS	Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amld,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.				
CONSRMT	The German cDNA Consortium				
TITLE	Direct Submission				
JOURNAL	Submitted (17-AUG-2004) MIPS, Ingolstaedter Landerr.1, D-85764				
COMMENT	Neuberberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; Sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686K0887) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686K0887 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/. Location/Qualifiers				

## FEATURES

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 /note="interphotoreceptor matrix proteoglycan 1, differentially spliced"  
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 191..634  
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 ORIGIN

Alignment Scores:  
 Pred. No.: 3.7e-312 Length: 5829  
 Score: 3222.50 Matches: 719  
 Percent Similarity: 44.30% Conservative: 0  
 Best Local Similarity: 44.30% Mismatches: 0  
 Query Match: 78.27% Indels: 904  
 DB: 4 Gaps: 2

US-10-007-270-2 (1-797) x CR749572 (1-5829)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 DB 191 ATGTATTTGGAAACTGAGAGAGCTATTTTGTGTTTGGATTTTCTCCAGATTCAGAGA 250  
 QY 21 ThrLysAspIleSerIleAsnIleTyrIleSerGluThrLysAspIleAspAsnProPro 40  
 DB 251 ACCAAA----- 256  
 QY 41 AcGAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
 DB 256 ----- 256  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValIysVal 80  
 DB 256 ----- 256  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 256 ----- 256  
 QY 101 ValCysGlnGluAlaValAlaTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 257 GGTGTCTGAGAAAGAGAGTATGAGAGCATTCGATCTTTCTGATCGATCCCTGACACA 316  
 QY 121 GlyLysTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 317 GGGGAAATATCAGAGACTGGGTCAAGCATCTCCAGCAGAGAACCTTGTGCTTTTGACATT 376  
 QY 141 GlyLysAspPheSerAsnSerGlnGlnIleGluAspLeuLeuGlnGlnArgIleLysGln 160  
 DB 377 GGAAGAAACCTTCAGCAATTCAGAGGACCTGGATCTTCTCCAGAGAGAAATAAACAG 436  
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 DB 437 ABAAGTTTCCCTGACAGAAAGATGAATATCTGCAAGAAAGACATTGGGAGAGCTGGT 496  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 497 GAAACCATTTGTCTATTTCAACAGAAAGATTAAGGTAAACCAACCATTCATATCTTA 556

QY 187 ----- 187  
 DB 557 CAGTTTGAAGAAACCATCATGAAACATTACTGCCATATTTCTGGCTTCTTCTCTATT 616  
 QY 187 ----- 187  
 DB 617 ATATACATATTACTGAGACCATTTTACTAGAGTTGTATCATTTTTCCACTTAAC 676  
 QY 187 ----- 187  
 DB 677 CTGATGTAAAGATATTTATAGTCACTAAATTTCTCAAGTTATCATTTTAATGAC 736  
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 QY 187 ----- 187  
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 QY 187 ----- 187  
 DB 1337 CCGGCTGCGCATATTTCAATTTTCTCTAAGTTCAGCTAATTTATCATTTCTGAGACTG 1396  
 QY 187 ----- 187  
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 QY 187 ----- 187  
 DB 1457 GCATTTTAACATTAATAAAGAGAGCTACATATGTTAATTTCCCTATTAACAGCTCAA 1516  
 QY 187 ----- 187  
 DB 1517 TTGACCTGTGACACCTAATATCAAGTCTTATTCAAAAGATATTTAAGAGAGAGC 1576  
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 DB 1577 ATATAACATGTAAAGAGCGTTTGTACTGACTTCAATTTAATATGAGAGAAACAAATTT 1636

QY 187 ----- 187  
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 Db 1877 TTTTAGAATTATTTCCCACTACTTCTGGACACCTCCAGTTGAAGTATACACAGACA 1936  
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 Db 1937 GTTAAGATTAGATTTTGTATTGGGAAATGTTACTAGGTGCTAGGTGAAGAGAGTGA 1996  
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RESULT 2
AY415971
LOCUS AY415971 1665 bp DNA linear GSS 17-DEC-2003

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DEFINITION Homo sapiens IMPG1 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY415971
VERSION AY415971.1 GI:39771931
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1665)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Interfing nonneutral evolution from human-chimp-mouse orthologous
gene trles
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1665)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source location/Qualifiers
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Alignment Scores:
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Percent Similarity: 98.56% Conserved: 0
Best Local Similarity: 98.56% Mismatches: 8
Query Match: 68.03% Indels: 0
DB: 10 Gaps: 0
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QY 264 G1YrLysSerG1N1LleuG1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1 283
Db 61 GGAAGTCCCAACTTCAATGCAAGATATTGAAGAACTTTCAGAGATTCAAAAAATC 120
QY 284 H1Val1LleuG1YrPheA1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1G1N1 303
Db 121 CATGTGTAGGATTTAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTCAAGCTCCACAGAGATGCA 180
QY 304 LLeuThrAla1LlePheLysA1G1SerAlaG1U1AlaLysSerProAla1SerA1PheLleu 323
Db 181 CTACGGCCATCTTTAAAGACACAGCTGACAGAAAGCCCTGCAAGTGAAGCTCTG 240
QY 324 SerPheA1SerA1L1G1LysSerG1U1Val1YrH1G1YrThrMetG1U1Aup 343
Db 241 TCTTTTGAATTCACAAATTTGAAGTGAAGATCTATCATGGAACATGGAAGAGGAC 300
QY 344 LysG1N1ProG1U1L1YrLleuThrAlaThrA1PheLysValA1G1Lleu1L1SerLysAlaLleu 363
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Qy 444 LeuSerGluAlaAProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGly 463
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Qy 464 ThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThr 483
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Qy 484 SerAspTrpSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSer 503
Db 721 AGTGATTAATTCGCAATCAAGCACTGCTGGGAATTCACATCACTCACTGATCTTCA 780
Qy 504 AspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAsp 523
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Qy 564 MetThrIleAlaProGlyGlyArgGluLeuValIlePhePheSerLeuArgValAlaAsn 583
Db 961 ATGACCATTTGCCCCCAAGGCGAGAGCTGTGATGTTCTTCAAGTCTGCTGTGCTTAC 1020
Qy 584 MetAlaIlePheSerAspLeuPheAsnIleSerSerLeuGluTrpArgAlaLeuGluGln 603
Db 1021 ATGGCCCTTCTCAACAGCACTGTTCACAAAGAGCTCTGAGTACCGAGCTCTGGAGCAA 1080
Qy 604 GlnPheThrGlnLeuLeuValProTrpLeuArgSerAsnLeuThrGlyPheIleGlnLeu 623
Db 1081 CAATTCACACAGCTGTGCTGATTCATATTCATCAATTCATCAAGATTTTAAGCAACTT 1140
Qy 624 GlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerIleMetLeuPheAlaIle 643
Db 1141 GAAATATCTTAATCTCGAAGAACGGAGTGTGATTCGAATAGCAAAATGAAGTTCTGAAG 1200
Qy 644 SerValProTrpAsnLeuThrIleValAlaHISglYValLeuGluAspPheArgSerAla 663
Db 1201 TCAGTGCCGTATTAACCTCAACCAAGGCTGTGACAGGGGTCTTGAAGGATTTTCTGTCT 1260
Qy 664 AlaAlaGlnGlnLeuHISleuGlnIleAspSerTrpSerLeuAsnIleGluProAlaAsp 683
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Db 1381 CGAGCTGAGGAAGCGAGTGTGCTGCAAAACAGGATATGACAGCCAGGGAGCTGTGAC 1440
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Qy 764 IysPheGlnAsnGlnAlaAsnAsnValIleSerIleArgAsnSerGluLeuLeuThr 783
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RESULT 3
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LOCUS        Mus musculus IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION   genomic survey sequence.
ACCESSION    AY415973
VERSION      AY415973.1 GI:39771933
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 1647)
              Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarival, A.,
              Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, P., Murphy, B.,
              Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.D.,
              Adams, M.D. and Cargill, M.
              Direct Submission
              Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
              This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
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ORIGIN
Alignment Scores:
Pred. No.:      5,86e-158      Length:      1647
Score:          1683.00      Matches:      354
Percent Similarity: 73.47%      Conservative: 53
Best Local Similarity: 63.90%      Mismatches: 141
Query Match:    40.88%      Indels:      6
DB:              10      Gaps:      5

US-10-007-270-2 (1-797) x AY415973 (1-1647)

Qy 244 AsnGlnIlePheIleValIGluLeuAlaAspSerGlnSerProTrpTrpGlnGluLeuAla 263
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[illegible]

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OY		664	Ala1aagInglIneuh1sleugluileapSerTyrsertleuanilleguPro1aAp	683
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OY		664	GlN1laaRPProCyelyvRphelEuLlCYeg1yluIheha1gInCYsvallYaaNg1u	703
Dd		1309	CAGCGGATCCCTTCAAACCTTCTAGACTGTGGCAAAATTTGCCAGTGTGTAAAGAATGAG	1368
OY		704	ArgThrgluglu1a1a1uCYaRGcyARgCYvlyvProgl1yTraarSergInglySer1euAsp	723
Dd		1369	TGGACAGAGAGAACGAGAGTGTCTGTCAGACAGGACAATGAGACCAAGGACCTTGAC	1428
OY		724	GLyleugluProgl1yeuCYeg1yPRog1yThrlysgucyvgoluval1eugInglylys	743
Dd		1429	TACAGAGACCTGAAACCTGTGTCCCCCTGGA---AAGACTGTGTGTGGCCGGCGAGAAACA	1485
OY		744	GLy1alAProCYsaRg1euProarPHisSerg1ueuIngl1atrylvyrThrservAllys	763
Dd		1486	GCAACTCCTATGACAGCCCAACAGATCACTTCAAAACAAGCTCAGAAACCTGTGTAAA	1545
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Dd		1546	AAGCTACGT---CAGCAAAATAAGTGTGTGTGTCAAGAAAGAAATTTCAAATCTACAGCT	1602
OY		784	Va1glutrytGlu1upRheaenH1glnaBPTrpGlu1yaBn	797
Dd		1603	ATAGGATTGTGAAGATTGTAAGAACAGAGACTGGAGAGGAAAT	1644
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DEFINITION		B0639265	hd33d04.y1 Human Retina cDNA (Un-normalized, unamplified) : hd/he	
ACCESSION		B0639265	Homo sapiens CDNA clone hd33d04 5', mRNA sequence.	
VERSION		B0639265.1	GI:21763724	
KEYWORDS			EST.	
SOURCE			Homo sapiens (human)	
ORGANISM			Homo sapiens	
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS			Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
TITLE			Hominiidae; Homo	
JOURNAL			1 (bases 1 to 626)	
PUBMED			Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,	
COMMENT			Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.	
			Expressed sequence tag analysis of human retina for the NEIBank	
			Project: Retinidin, an abundant, novel retinal cDNA and alternative	
			splicing of other retina-preferrred gene transcripts	
			MOJ. V18. 8 (4), 196-204 (2002)	
			12107411	
			Contact: Wistow G	
			Section on Molecular Structure and Function	
			National Eye Institute	
			6/331, NIH, Bethesda, MD 20892-2740, USA	
			Tel: 301 402 3452	
			Fax: 301 496 0078	
			Email: ggreene@helix.nih.gov	
			Plate: 33 row: d column: 04	
			Seq primer: M13Rp1 reverse primer (ABI).	
FEATURES			Location/Qualifiers	
source			1..626	
			/organism="Homo sapiens"	
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			/tissue_type="Retina"	
			/dev_stage="Adult"	
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			/clone_id="Human Retina cDNA (Un-normalized,	

## FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
db_xref="taxon:9606"
clone="hd3d04"
tissue_type="Retina"
dev_stage="Adult"
lab_host="EMD1108"
clone_lib="Human Retina cDNA (Un-normalized)

```

unamplified): hd/he"

15'-pGACCTGCTCTGATGCGAGCGCCGCC(7)15-3'. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NIHSC)."

## ORIGIN

**Alignment Scores:**

Pred. No.:	2.67e-95	Length:	62e
Score:	1054.00	Matches:	20e
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	25.60%	Indels:	0
DB:	5	Gaps:	0

US-10-007-270-2 (1-797) X BQ639265 (1-626)

Qy	260	GIIGIuIeuNlaGIlySserGIuIeuGIuImetGIuNlySIephelySyleuProGIy	279
Db	3	CAGAGCTAGCAGAAAGTCCCACTTCAGATGCAGAAAGATTTTAAGAAATTCACAGA	62
Qy	280	PhelyyelySIehIvalleuGIyPheATProLyGlyGlyySAspGIySerSerSer	299
Db	63	TTCAAAAAATCATGTGGATTGAGATTAGCCAAAAGAAAGAAAGATGGCTCAAGCTCC	122
Qy	300	ThnGIuMetGIuNeuThraIalIephelySAtgHISerIaGIuaIalySerProIa	319
Db	123	ACGAGATGCACCTTCGGCCATCTTTAAAGACACAGTGCAGAGCAAAAAGCCCTGCA	182
Qy	320	SeTAspIeuNeuSerPheAspSerAnlySIegIuSerGIuGIuValTyHISGIyThr	339
Db	183	AGTGAACCTCTGTCTTTGATTCCAACAAATTTGAAGTGAAGAGTCTATCATGAAAC	242
Qy	340	MetGIuGIuNlySgIInProGIuIleTyLeuThraIaThraSpleuLySArgLeuIle	359
Db	243	ATGAGAGAGACACAGCAACCAAAATCTATCTCACAGCTACAGACTCAAAAGCTGATC	302
Qy	360	SeTlySAlaIeuGIuGIuGIuInSerIeuAspValGIyThrIleGIuPheThraSpgIu	379
Db	303	AGCAAGACACTAGAGAGAACATCTTTGATGGGGACAAATTCAGTTCATCATGAA	362
Qy	380	IlaIaGIySerIeuProAlaPheGIyProAspThrGIuInSerGIuIeuProThSerPhe	399
Db	363	ATTGCTGGATCATGTGCACCTTTGGTCTGTGACCCCATAGAGCTGCCACATCTTTT	422
Qy	400	AlaValIleThnGIuNlySAlaThrIleuSerProGIuIeuProProValGIuProGIuIeu	419
Db	423	GCCTTATTAACAGAGATGCTACTTTGAATCCAGAACTTCTCTCTGTGAAACCCACTT	482
Qy	420	GIuThraValAspGIyAlaGIuHISGIyIeuProAspThrSerTTPSerProProIaMet	439
Db	483	GAAACAGTGGACGGACAGACATGGTCTACCTGACACTTCTGGTCTCCACCTGTATG	542
Qy	440	AlaSerThnSerIeuSerGIuAlaProProPhePheMetAlaSerSerIlePheSerIeu	455
Db	543	GCCTTACCTCCCTGTGCAGAGTCCACCTTCTTTATGGATCAAGCATCTTCTCTG	602
Qy	460	ThraSpgInGIyThraThraSPTHr	467
Db	603	ACTGATCAAGCACCAAGATACA	626
RESULT 5			
RY415972			

## LOCUS

**DEFINITION** Pan troglodytes IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION	AY415972
VERSION	AY415972.1
KEYWORDS	GI:39771932
	CC

**KEYWORDS**  
**SOURCE**  
**ORGANISM**

100

## REFERENCE

## AUTHORS

3  
4  
3  
4  
1

FILE

[DOI: 10.1002/for](#)  
[PUBMED](#)  
[REFERENCE](#)

## AUTHORS

**TITLE**  
**JOURNAL**

**COMMENT**

## FEATURES

100

gene

**ORIGIN**

**Alignment Scores:**

Pred. No.:	2,89e-86	Length:	158
Score:	971.00	Matches:	239
Percent Similarity:	45.21%	Conservative:	0
Best Local Similarity:	45.21%	Mismatches:	289
Query Match:	23.55%	Indels:	0
DB:	10	Gaps:	0

US-10-007-270-2 (1-797) x AY415972 (1-1587)

[illegible]

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QY 390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409
DB 391 GACACCCCAATCAGAGCTGCCCATCTTGTCTGTTATACAGAAATGCTACTTGGAGT 420
QY 410 ProGluLeuProProValGluProGluLeuGluThrValAspGlyValAspGlyLeu 429
DB 421 CCAGAACTTCTCTTGTGAAACCCAGCTTGAGACAGTGCAGAGCAGAGCATGCTGTA 480
QY 430 ProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449
DB 481 CCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 540
QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
DB 541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600
QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle 489
DB 601 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 660
QY 490 SerGlnLeuAlaLeuGlyIleSerThrIleProProAlaSerSerAspAspSerArgSerSer 509
DB 661 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720
QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
DB 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
QY 530 ProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAsp 549
DB 781 CCATCTGAGAGTACAGAGCTCAGCGAAATGTTTCTGCTCCAGATCATTTCTTGGAGAT 840
QY 550 ThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProIlys 569
DB 841 ACCACTCCCTGCTCTGCTTACAGATATACACACTAGTCTATGACCATTCGCCCCAG 900
QY 570 GlyArgGluLeuValPhePheSerLeuArgValAlaAspMetAlaPheSerAsp 589
DB 901 GGCAGAGAGCTGATGATGTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 590 LeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609
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QY 610 ValProTyrLeuArgSerAsnLeuThrGlyPheIleGlnLeuGluIleLeuAsnPheArg 629
DB 1021 GTTCCATATCTACGATCCATCTNNCAGGATTTAAGCAACTTGAATCTTAACCTTCA 1080
QY 630 AsnGlySerValIleValAsnSerLysPheAlaLysSerValProTyrAsnLeu 649
DB 1081 AACGGAGAGTATGCTGATGCAATGCAAAATGAAGTTTNCATAGTCCGCTATNNNNNC 1140
QY 650 ThrIleValAlaIleGlyValLeuGluAspPheArgSerAlaAlaAlaGlnLeuLeuHis 669
DB 1141 ACCAAGAGCTGTCAAGGGGCTTGGAGGATTTTGGTTGCGNCCAGCCCAACACTCCAT 1200
QY 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
DB 1201 CTGGAAATAGANANCACTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1260
QY 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709
DB 1261 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1320
QY 710 CysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729
DB 1321 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1380
QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyValProCysArgLeu 749
DB 1381 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1440

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QY 750 ProAspHisSerGluAsnGluAlaTyrLysThrSerValLysLysPheGlnAsnGln 769
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QY 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGluGluPhe 789
DB 1501 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1560
QY 790 AsnHisGlnAspTyrProGluGlyAsn 797
DB 1561 AACCATCAAGATGGAGAAAT 1584

RESULT 6
LOCUS B0636596
DEFINITION hdl1h02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
ACCESSION B0636596
VERSION B0636596.1 GI:21761055
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 598)
Wietow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
12107411
COMMENT Contact: Wietow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graham@helix.nih.gov
Plate: 11 row: h column: 02
Seq primer: M13P1 reverse primer (ABI).
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source
1..598
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/db_xref="taxon:9606"
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/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMH10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ng of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTAGTCTAGATCGAGCGCGCCGCT(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
```

Alignment Scores:  
Pred. No.: 2.5e-85  
Score: 955.00  
Percent Similarity: 98.47%

Length: 598  
Matches: 190  
Conservative: 3

Best Local Similarity: 96.94% Mismatches: 3  
 Query Match: 23.20% Indels: 0  
 DB: 5 Gaps: 0

US-10-007-270-2 (1-797) x B0636596 (1-598)

QY 432 ThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPhePhe 451  
 : : : : :  
 DB 11 TCGCTTGCTTCACCTGCTATGCGCTTCACTCCCTGTCAGAAAGCTCCACTTCTTT 70

QY 452 MetAlaSerSerLeuPheSerLeuThrAspGlnGlyThrThraPheThrMetAlaThrAsp 471  
 : : : : :  
 DB 71 ATGGCATCAAGCATCTTCTCTGCTGATGATCAAGGACCAAGATCAATGCGCACTGAC 130

QY 472 GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491  
 : : : : :  
 DB 131 CAGACAACTGCTATGATACAGGCGACCATCCCAAGATTAATCTGCAATCAGCCAA 190

QY 492 LeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerAspSerSerAlaGly 511  
 : : : : :  
 DB 191 CTGGCTCTGGAAATTTCAATCACTCACTTCTTCAATGACAGCCGATCAAGTGAAGT 250

QY 512 GlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSer 531  
 : : : : :  
 DB 251 GGGAGATATGCTGAGACCTAGATGAATGATGATCTGTCACACTCTGCGCCATCT 310

QY 532 GluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThr 551  
 : : : : :  
 DB 311 GAGGTACCAAGACTCAGCAATATGTTTCTCCCAATCATTTCTTGGAGATACACT 370

QY 552 ProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProGlyArg 571  
 : : : : :  
 DB 371 CCGTCTCAGCTTACAGTATACACACACTGATTCATGACCAATGCCCCAAGGCGCA 430

QY 572 GluLeuValValPhePheSerLeuArgValAlaAspMetAlaPheSerAspLeuPhe 591  
 : : : : :  
 DB 431 GAGCTGATGATGTTCTTCAATCGCTGTTGCTTAACATGCGCTTCCAAAGACTGCTTC 490

QY 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPheThrGlnLeuValPro 611  
 : : : : :  
 DB 491 AACAGAGCTCTCTGAGTACCGAGCTGAGCAACAATTCCACAGCTGCTGGGTCCA 550

QY 612 TyrLeuArgSerAspLeuThrGlyPheLeuGlnLeuGluIleLeuAsn 627  
 : : : : :  
 DB 551 TACTTACGATCCAACTTACAGGATTTAAGCAACTTGAATACTTAC 598

RESULT 7  
 AY418611 3713 bp DNA linear GSS 17-DEC-2003  
 LOCUS  
 DEFINITION Homo sapiens IMPG2 gene, VIRUTUAL TRANSCRIPT, partial sequence.  
 ACCESSION AY418611  
 VERSION AY418611.1 GI:39774571  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 3713)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Adame,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3713)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Sniatsky,J.J.,  
 Adame,M.D. and Cargill,M.

TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT These sequences were made by sequencing genomic exons and ordering  
 them based on alignment.  
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 source 1..3713  
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 /db\_xref="taxon:9606"  
 <1..>3713  
 /gene="IMPG2"  
 /locus\_tag="HGM615"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 9,98e-79 Length: 3713  
 Score: 902.00 Matches: 290  
 Percent Similarity: 39.08% Conservative: 145  
 Best Local Similarity: 26.06% Mismatches: 274  
 Query Match: 21.91% Indels: 405  
 DB: 10 Gaps: 34

US-10-007-270-2 (1-797) x AY418611 (1-3713)

QY 2 TyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThr 21  
 : : : : :  
 DB 11 TTCCCTTTTGGAGATTTCTCTCGGTATTTTG-ATATTTGCTCCTGATTAAGAGAGAC 69

QY 22 ---LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro--- 39  
 : : : : :  
 DB 70 TTTCATCATTAACAGCAACAACCTACTATCT---ATAGAGAGATTCAGAACCCAG 126

QY 40 -----ProArgAsnGluThr-----Thrgluser 47  
 : : : : :  
 DB 127 AGTGCAGTTCTTTCTCTCCTGCTGAAGATCAAGACAGACTTCTTACTGACCAAAAG 186

QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67  
 : : : : :  
 DB 187 AAACAGCCCTCGACCGCAGAGAACTGAAAGACAGTGGTTA-----ATCAGA 234

QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnIleSerMetLys 87  
 : : : : :  
 DB 235 AGCGGAGATCTATTTCTGTTCTTAATGAGGAAATCTGCCAGATGAAGTGTGCA 294

QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGlnAlaValTyrP 107  
 : : : : :  
 DB 295 GAGGCTGGGCAAAATCAATGATGATTTTAAGTCCAGATGTGTGAGAAAGCTGTCTGG 354

QY 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTyrVal 127  
 : : : : :  
 DB 355 GAAGCTTCAGAGACTTTTGGATGAGACTTCTCGGCGCGAGAAATATCATTAACAGGATG 414

QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAspPheSerAsnSer 147  
 : : : : :  
 DB 415 AATTGTGTGAGAGATGAGACTCAAGATATATTGAAATGGGCAAAATTTTATGTAATCT 474

QY 148 GlnGluHisLeuAspLeuLeuGlnArgIleLysGlnArgSerPheProAspArgLys 167  
 : : : : :  
 DB 475 GTGGAACATGAAAGCTTAATCATGAGAAACTGACTTAT-----GCMAAG 519

QY 168 AspGluIleSerAlaGluLysThrLeuGlyGluPro-----GlyGluThrIleVal 184  
 : : : : :  
 DB 520 GAAAGCTGAAAGAGCTGGA---CTGTCTTCCAGTTCTGTGGTGTATCTTCAACA 576

QY 185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200  
 : : : : :  
 DB 577 TTGGAGACACTACTCTCAGTGT-----CCACATCCAGAGGTGAGCCCTATGAA 627

QY 201 -----ProAspAspThrLeuLeuAsnGluIleLeuAsp 211  
 : : : : :  
 DB 628 GGTGCTCAGAGAGAGAGCTTGGAAAGGCCAGAGAGATTAAGCAATGAATTT---GAG 684



FEATURES	SOURCE
Db	2779 CTGGAGCAAAAGATTCTTGAAATGCTGGTTCCTTACTTCACGTAAATCTCACGGGGTTC 2833
Qy	621 LysglnLeuGluIleLeuAspPheArganglySerValIleValAsnSerIysMetIys 640
Db	2839 CAGAATTAGAAATCTCAACTTCAAGAAATGGCACATTTGGTGAACAGCTGAATGAAG 2898
Qy	641 PheAlaIysSerValProTyrPheMetLeuThrIysAlaValIleGlyValLeuGluAspPhe 660
Db	2899 TTGGCAATTCTGTCTCCCTCCTTAACCTCAACAATGGGGTGTATCATGATCTGGAGACATT 2958
Qy	661 ArgSerAlaAlaIleGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680
Db	2959 TGTACACTGCTCTACAAATACCATCAATCTGGTATTTGAATTAATCTCTCTTGATGTGAA 3018A
Qy	661 ProAlaAspGlnAlaAspProCysAlaPheLeuAlaCysGlyGluPheAlaGlnCysVal 700
Db	3019 TCAGGTGTAGTAAGCCACCTTGCAAGTTTCAGGCGCTGTAAATGAATTTTCAGAGTGTCTG 3078B
Qy	701 LysAsnGluAArgThrGlnGluAlaGluCysArgCysIysProGlyTyrAspSerGln--- 719
Db	3079 GTCAACCCCTGGAGAGGAGAACCAAGACAGATCTTCCCTGTGATACCTGAGGTGTGAA 3138B
Qy	720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyTyrHis 735
Db	3139 GACGGCCCTGTGCAGAGTCTCTGTACCTACCTACGCTTGCTTGTAAATGATGAAG 3198B
Qy	736 GluCysGluValLeuGlnGlyLysGlyValaProCysArg 748
Db	3199 ---TGTGACATTATGCTGTGGGACGGGGCCATTGTTAG 3234
RESULT 8	
LOCUS	BX510244 690 bp mRNA linear EST 04-SEP-2003
DEFINITION	DKFZp686P2496.r1.686 (synonym: h1cc3) Homo sapiens cDNA clone
ACCESSION	DKFZp686P2496.5, mRNA sequence.
VERSION	BX510244
KEYWORDS	BX510244.1 GI:32050551
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE	1 (bases 1 to 690)
AUTHORS	Poustka,A., Albert,R., Moosmayer,P., Schnupp,I., Wellenreuther,R., Mewes,H.W., Well,B., Amlid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE	EST (Poustka,A., Albert,R., Moosmayer,P., Schnupp,I., Wellenreuther,R., et al.)
JOURNAL	Unpublished (2003)
COMMENT	Contact: MIPS
	MIPS
	Incoltaedter Landstr.1, D-85764 Neuherberg, Germany
	This is the 5' sequence of the clone insert
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
	Sequenced by DKFZ (German Cancer Research Center,
	Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
	No BL sequence available.
	This clone (DKFZp686P2496) is available at the RZPD in Berlin.
	Please contact the RZPD: Ressourcenzentrum, Heuberweg 6, 14059 Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.
	Location/Qualifiers
	1..690
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="DKFZp686P2496"
	/dev_stage="adult"
	/lab_host="DH10B"
	/clone_id="686 (synonym: h1cc3)"
	/note="Vector: pTritEX3; Site.1: SfilA; Site.2: SfilB;

ORIGIN	CDNA-collection"
Alignment Scores:	5.53e-79
Pred. No.:	Length: 690
Score:	893.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	21.69%
DB:	5
US-10-007-270-2 (1-797) x BK510244 (1-690)	
QY	1 MetYrLcngluthrAgaRgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
DB	187 ATGATATTTGGAAACTGAGAGAGCTATTTTGTGTTTGGATTTCCTCAAGTTCACAGA 246
QY	21 ThrLYsaPILeserIleasnIleTyrHisSerGluThrLYsaPILesAsPProRo 40
DB	247 ACCAAGATATCTCCATTACATATACCATTCGAACTAAAGACATAGACATCCCA 306
QY	41 ArgAsngluthrthrgluserThrglulysMetYrLYsMetSerThrMetArgArgile 60
DB	307 AGAATGAAACACCTGAAGATGTAAGAAATATGACAAATGTCACTATGAGCGATA 366
QY	61 PheAspleuAlaLYsHlaRgThrLYsArgSerAlaPhePheProthrglValLYsAl 80
DB	367 TTCATTTTGGCAAGCATCGAACAAAGATCCCATTTTCCCAACGGGGTTAAAGTC 426
QY	81 CysProGlnGlnuserMetLYsGlnIleLeuAspSerLeuGlnAlaTyrTrpArgLeuArg 100
DB	427 TGTCACAGGATCCATCGAAACAGATTTTAAACAGCTCTCAAGCTTATATAGATTGAGA 486
QY	101 ValCYsGlnGlnAlaValATrpglAlaTyrArgIlePheLeuAsPArgIlePAsPthr 120
DB	487 GTGTGTACGAGAGAGATGAGGAGCATATCGATCTTCTCGATTCGATCCCTGACACA 546
QY	121 GLYgluTYrglnAspTPValSerIleCYsGlnGlnGluThrPheCYsleuPheAspIle 140
DB	547 GGGGAATATCAGAGCTGGGTACAGCATCGCACAGAGAGACCTTCGCGCTTGTGACATT 606
QY	141 GLYLYsaPheAsPheSerAsnSerGlnGlnIleuAspleuLeuGlnGlnAlaGlyLeuGln 160
DB	607 GGAAGAAACCTTCACCAATCCACAGACACCTGATCTTCTCCAGCAGAGATAAACAG 666
QY	161 ArgSerPheProAsPArgLYsaAsp 168
DB	667 AGAAGTTCCCTGACAGAAAGAT 690
RESULT 9	
BUS06195	963 bp mRNA linear EST 12-SEP-2002
LOCUS	
DEFINITION	AGENCOURT_10015502 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6494245
ACCESSION	BUS06195
VERSION	BUS06195.1 GI:22812428
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 963)
TITLE	NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-rc@mail.nih.gov Tissue Procurement: The Cepko Laboratory CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Data distribution: MGC clone distribution information can be

Found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNL14050 row: c column: 14  
High quality sequence stop: 637.  
Location/Qualifiers

## FEATURES

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1..963

/organism="Mus musculus"

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/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by lile technologies. Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.:	2,636-72	Length:	963
Score:	829.00	Matches:	182
Percent Similarity:	74.13%	Conservative:	30
Best Local Similarity:	63.64%	Mismatches:	65
Query Match:	20.14%	Indels:	11
DB:	5	Gaps:	2

US-10-007-270-2 (1-797) x BUS06195 (1-963)

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QY 61 PheAspLeuAlaIleHisIleArgThrTyrAspSerAlaPhePheProThrGlyValIleVal 80
DB 298 TTCGATTTGCCAAGCTTCGAAACCAAAATGATCAGCATTTTCCCA---GCTGCTAACATC 354
QY 81 CysProGlnGluSerMetLeuGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
DB 355 TGTCCACAGGAATCCTTGAGACAGATTTTGAAGATCTTCAAGATATTATATAGACTGAGA 414
QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
DB 415 GATATGCAAGAGTCTGTGGAGAGCATATCGATCTTTCTGACCGAATTCCTAGACACA 474
QY 121 GlyIuTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
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QY 141 GlyTyrAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLeuGln 160
DB 535 GGGAAAAAATCTCAGCAACTCCAGAGACACTAGATCTTCTCAGAGAGAAATTAACACG 594
QY 161 ArgSerPheProAspArgTyrAspArgIleSerAlaGluTyrThrLeuGlnIleGluProGly 180
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QY 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrTyrAspPro 220
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QY 237 GluLeuSerValSerLeuValAsnGluIlePheIleValAla-GluLeuAlaAspSer-Glns 256

DB 833 GAATTCAGCATCTCTGCGCCACACACAGATTTCAGGCGACAGAGCTCACCAACTCTGGGCT 892

QY 256 expTyrTyrGlnGluLeuAla--GlyTyrSerGlnLeuGlnIleGlnIlePheIle 275

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QY 275 slyLeuPro 278

DB 953 GAAACTCCA 962

## RESULT 10

AY418613

LOCUS

DEFINITION Mus musculus IMPG2 gene, VIRUTAL TRANSCRIPT, partial sequence,

AY418613 genomic survey sequence.

ACCESSION AY418613.1 GI:39774573

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

14671302

2 (bases 1 to 3734)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,

Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,

Adams,M.D. and Cargill,M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

These sequences were made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

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/gene="IMPG2"

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ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-007-270-2 (1-797) x AY418613 (1-3734)

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QY 47 SerThrGluYswetYrlyswetSer-----ThwArArgAllepheApleu 63  
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 QY 64 AlaYsHis-----ArgThrLyAsrSerAlapheProthrgly 77  
 DB 205 ACCGAGACTGGGAGAGTGGCTGTAGAAAGCGCGATCTATCTGTGTTCCCAATGGG 264  
 QY 78 ValIlyValCyProoIngluSerMetLySgInIleuabpSerleuInalalyrYr 97  
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 QY 178 GluProGly----- 180  
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 DB 685 AATGTV----- 690  
 QY 211 AspAsnThrLeuabpAspThrLySweTProThrThrGluArgGluThrgluPheAlaVal 230  
 DB 691 -----ACAGAGAGGCCACACACACAGCTGCT 717  
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genomic survey sequence.
ACCESSION AY148612
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
REFERENCE
1 (bases 1 to 3713)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsny,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene clusters
JOURNAL
Science 302 (5652), 1960-1963 (2003)
14671302
PUBMED
2 (bases 1 to 3713)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsny,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
These sequences were made by sequencing genomic exons and ordering
them based on alignment.
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 CA393958 508 bp mRNA linear EST 06-NOV-2002  
 c844g04.y1 Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone c844g04  
 5', mRNA sequence.  
 ACCESSION  
 VERSION  
 CA393958  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE  
 AUTHORS  
 1 (bases 1 to 508)  
 Mielow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
 Touchman,D.W., Bouffard,G., Smith,D. and Peterson,K.  
 Expanded sequence tag analysis of human RPS/choroid for the  
 NIBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 JOURNAL  
 PUBMED  
 Mol Vis. 8 (4), 205-220 (2002)  
 12107410  
 COMMENT  
 Contact: Mielow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: gmiel@helix.nih.gov  
 Plate: 44 row: 5 column: 04  
 Seq primer: M13RPI reverse primer (ABI).

FEATURES  
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 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="c844g04"  
 /tissue\_type="RPS/choroid"  
 /dev\_stage="Adult"  
 /lab\_host="EMD10B"  
 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPS/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD), now part of Invitrogen Corp.,  
 essentially following the protocols of the Superscript  
 plasmid system (Invitrogen Corp).  
 <http://www.invitrogen.com/> The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,44e-71 Length: 508  
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 Best Local Similarity: 97.02% Mismatches: 5  
 Query Match: 19.80% Indels: 0  
 Ds: 6 Gaps: 0  
 US-10-007-270-2 (1-797) x CA393958 (1-508)  
 Qy 418 GlnLeuGluThrValAspGlyAlaGluLeuProAspThrSerTyrSerProPro 437  
 Db 3 CAGCTTGAGACAGTGGACGAGCAGACATGCTTCACTGACATCTTGTGCTCCACT 62  
 Qy 438 AlaMetAlaSerThrSerLeuSerGlnAlaProPhePheMetAlaSerSerIlePhe 457  
 Db 63 GCTATGGCCTTCACTCCCTGTCAGAGCTCACTTCTTATGATCAAGCATCTTC 122  
 Qy 458 SerLeuThrArgGlnGlyThrThrAspThrMetAlaThrArgGlnThrMetLeuValPro 477  
 Db 123 TCTTGACTGATCAAGGACCAAGATCAATGGCCATGACCAAGACATGCTACTACCA 182  
 Qy 478 GlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSer 497  
 Db 183 GGGCTCACATCCCAACAGATGATTTCTGCAATACCACTGGCTCTGGAAATTTCA 242  
 Qy 498 HisProProAlaSerSerAspAspSerArgSerSerAlaGlyGlyAlaAspMetValArg 517  
 Db 243 CATCACTGATCTTTCAGATGACAGCGCAATCAAGTCAAGTGGGGAATATGCTCA 302  
 Qy 518 HisLeuArgGluMetAspLeuSerAspThrProAlaProSerGluVal1ProGluLeuSer 537  
 Db 303 CACCTAGATGAAGAATGATCTGTGACACTCTCTGCCATCTGAGTACCGAGAGCTCATC 362  
 Qy 538 GluTyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557  
 Db 363 GAAATGTTCTGTCCAGATCATTTCTTGAAGATACACTCTCTGCTACGCTTACAG 422  
 Qy 558 TyrIleThrThrSerSerMetThrIleAlaProArgGlyArgGluLeuVal1PhePhe 577  
 Db 423 TATATCAACACTAGTTCATATGACATTCGCCACAAAGCCGATAGCTGTAAAGTTCTTC 482  
 Qy 578 SerLeuArgVal1Alaametal 585  
 Db 483 AGTCTGCTGATGATCAATGAGCC 506  
 RESULT 13

BX097138  
 LOCUS BX097138 472 bp mRNA linear EST 04-FEB-2003  
 DEFINITION BX097138 Soares retina N2b4R Homo sapiens cDNA clone  
 IMAG9998N11359 ; IMAGE:190666, mRNA sequence.  
 ACCESSION BX097138  
 VERSION BX097138.1 GI:27843098  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 472)  
 Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
 Radtke,U., Schneider,D. and Korn,B.  
 Human UniGeneSet - RZPD3  
 Unpublished (2003)  
 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD, IMAG998N11359.  
 RZPDLIB, I.M.A.G.E. cDNA Clone Collection;  
 Human UniGeneSet - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showlib.pl.cgi?response=libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r. Primer sequence:TTTTCACACGGAACGCTATGAC.  
 Location/Qualifiers  
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 /clone="IMAG998N11359 ; IMAGE:190666"  
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 /clone\_lib="Soares retina N2b4R"  
 /note="Organ: eye; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dt) primer (5'  
 TGTTCACATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3'),  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). The retinas were obtained from a 55 year old  
 Caucasian and total cellular poly(A)+ RNA was extracted 6  
 hrs after their removal. The retina RNA was kindly  
 provided by Roderick R. McInnes M.D. Ph.D. from the  
 University of Toronto. Library constructed by Bento  
 Soares and M.Facima Bonaudo."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 8, 89e-70 Length: 472  
 Score: 799.00 Matches: 156  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 19.41% Indels: 0  
 DB: 5 Gaps: 0

US-10-007-270-2 (1-797) x BX097138 (1-472)  
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QY 393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412  
 DB 63 TCAGAGCTCCCAACATCTTTGCTTTATPACAGAGATGCTACTTGGATCCAGAACTT 122  
 QY 413 ProProValIGluProGluLeuGluThrValAaPGLyAlaGluHISgLyLeuProAspThr 432  
 DB 123 CCTCGTGTGAACCCAGCTTGAGACAGTGAACGAGACGAGCATGTCTTACTGACACT 182  
 QY 433 SerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPheMet 452  
 DB 183 TCTTGCTCCCACTGCTATGCGCTTACTCTCCCTGTGAGAAGCTCCACCTTCTTTTANG 242  
 QY 453 AlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGln 472  
 DB 243 GCATCAAGCATCTTCTCTGACTGATCAAGGACACACAGATPACATGAGCCACTGACAG 302  
 QY 473 ThrMetLeuValProGlyLeuThrIleProThrSerAspTrpSerAlaIleSerGluLeu 492  
 DB 303 ACAATGCTAGTACAGAGGCTCAACATCCCAACAGATATTCTTGCATTCAGCCAACTG 362  
 QY 493 AlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGly 512  
 DB 363 GCTCTGGGAATTTTCATCATCTCAGATCTTCAGATGACAGCCGATCAAGTCAGAGTGGC 422  
 QY 513 GluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrPro 528  
 DB 423 GAAGATATGATGACACCTAGATGAATGATGATCTGTGACACATCTCT 470

RESULT 14  
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 LOCUS AL713229  
 DEFINITION DKFZp6686P1295\_r1 686 (synonym: hlc3) Homo sapiens cDNA clone  
 DKFZp686P1295\_5', mRNA sequence.

ACCESSION AL713229  
 VERSION AL713229.1 GI:19696585  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 510)  
 Bloeker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and  
 Wiemann,S.  
 EST (Bioecker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and  
 Wiemann,S.)  
 Unpublished (1999)  
 JOURNAL Contact: MIPS  
 COMMENT MIPS  
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
 Braunschweig/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No si sequence available.  
 This clone (DKFZp686P1295) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
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 cDNA-collection"

ORIGIN

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 DB: 1 Gaps: 1

US-10-007-270-2 (1-797) x AL713229 (1-510)

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DB 97 ACCAAA----- 102
QY 41 ArgAsnGluThrThrGluSerThrGluLYsMetTYrLYsMetSerThrMetArgArgIle 60
DB 102 ----- 102
QY 61 PheAspLeuAlaLYsHisArgThrLYsArgSerAlaPhePheProThrGlyValLYsVal 80
DB 102 ----- 102
QY 81 CysProGlnGluSerMetLYsGlnIleLeuAspSerLeuGlnAlaTYrTYrArgLeuArg 100
DB 102 ----- 102
QY 101 ValCYsGlnGlnAlaValTYrGlnAlaTYrArgIlePheLeuAspArgIleProAspThr 120
DB 103 GGTGTGCGAGGAGCAGTATGGGAGACATTCGATCTTCGATCGCATCCCTGACACA 162
QY 121 GlyGluTYrGlnAspTYrValSerIleCYsGlnGlnGluThrPheCYsLeuPheAspIle 140
DB 163 GGGGATATCAGAGACCTGGCTCAGCATCTCCAGCAGAGAACCTTCGCTTGTGACATT 222
QY 141 GlyLYsAsnPheSerAsnSerGlnGlnIleLeuAspLeuGlnGlnArgIleLYsGln 160
DB 223 GGAATAAACTTCAGCAATTCAGAGAGACCTGGATCTTCTCAGAGAGAAATAAAAACG 282
QY 161 ArgSerPheProAspArgLYsAspGlnIleSerAlaGlnLYsThrLeuGlnValProGly 180
DB 283 ABAAGTTTCCCTGACAGAAAGATGAATATCTCGAGAGAAACATTTGGAGAGAGCTGCT 342
QY 181 -GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuTh 200
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QY 200 rProAspAspThrLeuLeuAsnGlnIleLeuAspAsnThrIleAsnAspThrLYsMetPr 220
DB 403 TCTGTATGACACCTCTCTCAATGAATTTCTGATTAATACATCAACAGAACCAAGATGCC 462
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RESULT 15  
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 LOCUS ca18h07.y1 Human Retinal pigment epithelium/choroid cDNA  
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 5', mRNA sequence.

ACCESSION CA391789  
 VERSION CA391789.1 GI:24723977  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 618)

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## COMMENT

Miatow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
 Expressed sequence tag analysis of human RPE/choroid for the  
 NEI Bank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 Mol. Vis. 8 (4), 205-220 (2002)  
 12107410  
 Contact: Miatow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: gmatow@helix.nih.gov  
 Plate: 18 row: h column: 07  
 Seq primer: M13RPI reverse primer (ABI).  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /dev\_stage="Adult"  
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 /clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs"  
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD, now part of Invitrogen Corp),  
 essentially following the protocols of the Superscript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>". The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/MluI sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC).

## FEATURES

## source

## ORIGIN

## Alignment Scores:

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 Percent Similarity: 66.09% Conservative: 0  
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 Query Match: 18.24% Indels: 78  
 DB: 6 Gaps: 1

US-10-007-270-2 (1-797) x CA391789 (1-618)

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DB 161 ATGTATTTGGAACTAGAGAGACTATTTTGTGTTTGGATTTTCTCAAGTTCAAGGA 220
QY 21 ThrLYsAspIleSerIleAsnIleTyRHisSerGluThrLYsAspIleAspAsnProPro 40
DB 221 ACCAAA----- 226
QY 41 ArgAsnGluThrThrGluSerThrGluLYsMetTYrLYsMetSerThrMetArgArgIle 60
DB 226 ----- 226
QY 61 PheAspLeuAlaLYsHisArgThrLYsArgSerAlaPhePheProThrGlyValLYsVal 80
DB 226 ----- 226
QY 81 CysProGlnGluSerMetLYsGlnIleLeuAspSerLeuGlnAlaTYrTYrArgLeuArg 100
DB 226 ----- 226
QY 101 ValCYsGlnGlnAlaValTYrGlnAlaTYrArgIlePheLeuAspArgIleProAspThr 120

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Db      287 GGGGAATATCAGGACTGGGTCAAGCATCTGCCAGCAGAGACCTTGCTTGCTTTGACATT 346
Qy      141 GlyValAsnPheserAsnSerGInGInIleLeuAspLeuLeuGInGInArgIlelyGIn 160
Db      347 GGAATAAACTTCAGCAATCCAGAGCACTGGATCTTCTCCAGCAGAGAAATAAAACAG 406
Qy      161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
Db      407 AGAAGTTTCCTGACGAAAGATGAAATATCTGCAGAGAGACATTGGGAGAGCCTGGT 466
Qy      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db      467 GAACCATTTGTCACTTTCACAGATGTTGCCAAGTCTCACTTGGGCTTTCCCTCTCACT 526
Qy      201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
Db      527 CCTGATGACACCCCTCTCAATGAAATTCGATTAATACACTCAACGACACCAAGATGCCT 586
Qy      221 ThrThrGluArgGluThrGluPheAlaVal 230
Db      587 ACAACGAAAGAGAAACAGAAATTCGCTGTG 616
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2006, 02:03:01 ; Search time 1526 Seconds

(without alignments)  
4318.935 Million cell updates/sec

Title: US-10-007-270-2

Sequence: 1 MYLTERRAIFWVWIFLQVQ.....NSELTVEYERPHODMEGN 797

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA Main:\*

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9: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

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# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4073	98.9	3330	5	US-10-007-270-1
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3	3619	87.9	2887	5	US-10-007-270-3
4	3323	80.7	2244	5	US-10-007-270-5
5	2548.5	61.9	3668	5	US-10-007-270-8
6	1342.5	32.6	1726	5	US-10-007-270-10
7	929.5	22.6	1321	5	US-10-007-270-12
8	927	22.5	4165	8	US-10-783-528-9

9	927	22.5	4166	5	US-10-007-270-16	Sequence 16, Appl
10	885	21.5	555	5	US-10-007-270-14	Sequence 18, Appl
11	846.5	20.6	2864	5	US-10-007-270-18	Sequence 14, Appl
12	841	20.4	4204	5	US-10-007-270-23	Sequence 23, Appl
13	248.5	6.0	592	9	US-10-972-079-61156	Sequence 61156, A
14	248.5	6.0	599	9	US-10-972-079-61152	Sequence 61152, A
15	248.5	6.0	600	9	US-10-972-079-61153	Sequence 61153, A
16	248.5	6.0	600	9	US-10-972-079-61154	Sequence 61154, A
17	248.5	6.0	600	9	US-10-972-079-61155	Sequence 61155, A
18	194.5	4.7	2026	3	US-10-198-846-12589	Sequence 12589, A
19	189.5	4.6	4139	3	US-09-964-824A-105	Sequence 105, App
20	189.5	4.6	4139	3	US-09-964-824A-578	Sequence 578, App
21	189.5	4.6	4139	3	US-09-864-864-334	Sequence 334, App
22	189.5	4.6	4139	3	US-09-880-107-2121	Sequence 2121, App
23	189.5	4.6	4139	3	US-09-968-007A-751	Sequence 751, App
24	189.5	4.6	4139	3	US-10-171-311-157	Sequence 157, App
25	189.5	4.6	4139	6	US-10-177-293-310	Sequence 310, App
26	189.5	4.6	4139	7	US-10-440-464-155	Sequence 155, App
27	189.5	4.6	4139	7	US-10-734-564-53	Sequence 53, Appl
28	189.5	4.6	4139	8	US-10-775-920-80	Sequence 80, Appl
29	189.5	4.6	4139	8	US-10-775-920-85	Sequence 85, Appl
30	189.5	4.6	4139	9	US-10-843-641A-5408	Sequence 5408, Ap
31	189.5	4.6	4139	9	US-10-843-641A-5881	Sequence 5881, Ap
32	189.5	4.6	4139	9	US-10-843-641A-7221	Sequence 7221, Ap
33	189.5	4.6	4139	9	US-10-997-055-1	Sequence 1, Appl
34	189.5	4.6	4139	10	US-11-009-533-1	Sequence 1, Appl
35	188.5	4.6	1572	10	US-11-055-119-1	Sequence 280, Appl
36	188.5	4.6	1721	3	US-09-864-864-280	Sequence 280, Appl
37	188.5	4.6	1721	3	US-09-967-768A-224	Sequence 224, App
38	188.5	4.6	1721	5	US-10-097-340-211	Sequence 211, App
39	188.5	4.6	1721	5	US-10-171-311-155	Sequence 155, App
40	188.5	4.6	1721	6	US-10-007-926A-58	Sequence 58, Appl
41	188.5	4.6	1721	6	US-10-029-517-3	Sequence 3, Appl
42	188.5	4.6	1721	6	US-10-172-118-775	Sequence 775, App
43	188.5	4.6	1721	7	US-10-342-887-775	Sequence 775, App
44	188.5	4.6	1721	8	US-10-775-920-88	Sequence 88, Appl
45	188.5	4.6	1721	9	US-10-843-641A-6369	Sequence 6369, Ap

## ALIGNMENTS

RESULT 1  
US-10-007-270-1  
Sequence 1, Application US/10007270  
Publication No. US20020160954A1  
GENERAL INFORMATION:  
APPLICANT: Hageman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
FILE REFERENCE: 020618-000120US  
CURRENT APPLICATION NUMBER: US/10/007,270  
CURRENT FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US 09/430,195  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: US 09/183,972  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 3330  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 150 cDNA, isoform A  
US-10-007-270-1  
Alignment Scores:  
Pred. No.: 0  
Score: 4073.00  
Percent Similarity: 97.31%  
Best Local Similarity: 97.31%  
Query Match: 98.93%  
Length: 3330  
Matches: 796  
Conservative: 0  
Mismatches: 1  
Indels: 22

DB: 5 Gaps: 1  
US-10-007-270-2 (1-797) x US-10-007-270-1 (1-3330)  
Qy 1 MetYrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
Db 131 ATGTATTGGAAACATAGAAAGACCTATTGTTGTTTGGATTTTCTCCAAGTCAAGGA 190  
Qy 21 ThrIleAspPheIleSerIleAsnIleTyrHisSerGluThrIleAspPheIleAspAspProPro 40  
Db 191 ACCAAAGATATCTCAATTAACATATACCTTCTGAACATTAAGACATAGACATATCCCCCA 250  
Qy 41 ArgAsnGluThrThrGluSerThrGluIleuMetYrIleuMetSerThrMetArgArgIle 60  
Db 251 AGAATGAAACAACTGAAAGTACTGAAAAAATGTCAAAAATCTCAACATAGAGAGAAATA 310  
Qy 61 PheAspLeuAlaIleHisIleArgThrIleYrAspSerAlaPhePheProThrGlyValIleVal 80  
Db 311 TTGATTTGGCAAAACATCGAACAAGATCCGATTTTTCCTCAACGGGGGTAAAGTC 370  
Qy 81 CysProGlnGluSerMetIleGlnIleLeuAspSerLeuGlnAlaTyrTyrArgIleuArg 100  
Db 371 TGTCACAGGAATCCATGAAACAGATTTTGAACAGTCTTCAAGCTTATTATAGATTGAGA 430  
Qy 101 ValCysGlnGluAlaValTyrPgluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
Db 431 GTGTCTCAGGAAGCATATGGGAAGCATATCGGATCTTTCGATCGCATCCCTGACACA 490  
Qy 121 GlyIleuYrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
Db 491 GGGGAATATCAGAGCATGGGTGAGCATCTGCCAGCAGAGACCTTCGTGCTTTGACATTT 550  
Qy 141 GlyIleAspPheSerPheAsnSerGlnGlnIleLeuAspLeuGlnGlnArgIleIleGln 160  
Db 551 GAAAAAACTTCAGCAATTCCTCAGAGACCTGGAATCTTCTCCACAGAGAAATAAAACAG 610  
Qy 161 ArgSerPheProAspArgIleAspPgluIleSerAlaGluIleYrThrLeuGlyValuProGly 180  
Db 611 AGAATTTTCCCTGACAGAAAAGATGAATATCTGCAGAGAAACATTTGGAGAGCTGCTGT 670  
Qy 181 GluThrIleValIleSerThr----- 187  
Db 671 GAAACATGTCTATTCAAC-AGCAATCTACATTTCAAAAGACTTGCGGCGATTTCTAAGA 729  
Qy 188 -----AspValAlaAsnValIleSerLeuGlyProPheProLeu 199  
Db 730 AAACCTCAGAAAGACAAATTCAGAGATGTGGCCACGCTCACTTGCGGCTTTTCCCTGTC 789  
Qy 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrIleuMet 219  
Db 790 ACTCTGATGACACCTCTCTCAATGAAATTCCTCGATATACCTCAACGACACCAAGATG 849  
Qy 220 ProThrThrGluArgGluThrGluPheAlaValIleuGluGluGlnArgValGluLeuSer 239  
Db 850 CCTAACACAGAAAGGAAACAGAAATTCGCTGTGTGGAGAGACAGAGGCTGAGACTCAGC 909  
Qy 240 ValSerLeuValIleAsnGluIlePheIleValIleGluIleuAlaAspSerGlnSerProTyrTyr 259  
Db 910 GCTCTCTGTGTAACCAAGATTCAGAGGAGAGCTGCTGACTCCACAGTCCCAATATTAAC 969  
Qy 260 GlnGluLeuAlaGlyIleSerGlnIleuGlnMetGlnIleValIlePheIleYrLeuProGly 279  
Db 970 CAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAACTTCCAGGA 1029  
Qy 280 PheIleYrIleHisIleValIleuGlyPheArgProIleYrGluIleYrAspGlySerSerSer 299  
Db 1030 TTCAAAAAATCCATGTGTAGATTAGACCAAGAAAGAAAGAAAGATGCTCAAGCTCC 1089  
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Qy 320 SerAspLeuLeuSerPheAspSerAsnIleGluSerGluGluValTyrHisGlyThr 339

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Db 1210 ATGAGAGAGAGCAAGCAACCAAGAAATCTATCTCACAGCTACAGAGACTCAAAAGCTGATTC 1269  
Qy 360 SerIleValIleuGluGluGlnGlnSerLeuAspValIleGlyThrIleGlnPheThrAspGlu 379  
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Qy 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
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Qy 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
Db 1390 GCTGTATTAACAGAGAGATCTTATGATCCAGAACTTCTCTGTGAAACCCAGCTT 1449  
Qy 420 GluThrValAspGlyAlaGluHisGlyIleuProAspThrSerTrpSerProProAlaMet 439  
Db 1450 GAGACATGAGAGAGAGAGAGATGTCTTACCTGACACTTCTTGCTTCCACTGCTATG 1509  
Qy 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
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Qy 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyIleu 479  
Db 1570 ACTGATCAAGGACACACAGATACATATGCCACTGCCAGCAATGCTATGACAGGGCTC 1629  
Qy 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnIleuAlaIleuGlyIleSerHisPro 499  
Db 1630 ACCATCCCAACAGGATTAATTCGCAATCAAGCAACTGGGCTTGGGAATTTCAATCCA 1689  
Qy 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyIleAspMetValArgHisLeu 519  
Db 1690 CCTGATCTTCAGATGACAGCGCATCAAGTGCAGGTGGCAAGATATGTCAACACTA 1749  
Qy 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlyIle 539  
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Qy 540 ValSerValProAspPheIlePheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
Db 1810 GTTCTGTCAGATCATTTCTTGAGAGATACCACTCTGTCTCAGCTTTACAGTATATC 1869  
Qy 560 ThrThrSerSerMetThrIleAlaProIleGlyArgGluLeuValIlePhePheSerLeu 579  
Db 1870 ACCACTAGTCTTATGACCAATTTGCCCAAGGGCCGAGAGCTGTGTGTTCTTCACTGTCG 1929  
Qy 580 ArgValAlaAsnMetAlaPheSerAsnAspIleuPheAsnIleYrSerSerLeuGluIleYrArg 599  
Db 1930 CGTGTGTCTTAACATGGCTTCTCCAAACGACTGTTCACCAAGAGCTCTCTGAGATACCGA 1989  
Qy 600 AlaLeuGluGlnGlnPheThrGlnIleuIleuValProTyrLeuAspSerAsnLeuThrGly 619  
Db 1990 GCTCTGAGCAACAATTCACAGCTGCTGTTCCATATCTACATCCAAITTTACAGGA 2049  
Qy 620 PheIleGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValIleAsnSerIleMet 639  
Db 2050 TTTTAAGCAACTTGAATATCTTAATCTTCAAGAAACGAGAGATGTGATTAAGCAAAATG 2109  
Qy 640 LysPheAlaIleSerValProTyrAsnLeuThrIleValIleHisGlyValIleuGluAsp 659  
Db 2110 AAGTTTGTAAAGTGTGTCCGTATTAACCTCAACAAAGCTGTGACAGGGGTCTTGAAGAT 2169  
Qy 660 PheArgSerAlaAlaIleGlnGlnIleuHisIleuGlnIleAspSerTyrSerLeuAsnIle 679  
Db 2170 TTTGCTTGTGTCAGCCCAACACTCATCTGAGAAATGACAGTACTCTTCAACATTT 2229  
Qy 680 GluProAlaAspGlnAlaAspProCysIlePheLeuAlaCysGlyGluPheAlaGlnCys 699

Db 2230 GAACACGATGATCAAGACAGATCCCTGCAGATTCTGCGCCGCGGAGAAATTTGCCCAATG 2289  
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 Qy 780 GluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGluAsn 797  
 Db 2530 GAATTACTGACCTAGAAATATGAAATTTAACCATCAAGATTGGAGAGAAAT 2583  
 RESULT 2  
 US-10-007-270-27  
 ; Sequence 27, Application US/10007270  
 ; Publication No. US20020160954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hegeman, Gregory S.  
 ; APPLICANT: Kuehn, Markus H.  
 ; APPLICANT: University of Iowa Research Foundation  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ; FILE REFERENCE: 020618-000120US  
 ; CURRENT APPLICATION NUMBER: US/10/007,270  
 ; CURRENT FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/430,195  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; PRIOR FILING DATE: 1998-10-29  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 27  
 ; LENGTH: 3261  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Human IPM 150 isoform A variant cDNA sequence  
 ; NAME/KEY: CDS  
 ; LOCATION: (128)..(2440)  
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 Alignment Scores:  
 Pred. No.: 0 Length: 3261  
 Score: 4024.50 Matches: 793  
 Percent Similarity: 99.62% Conservative: 1  
 Best Local Similarity: 99.60% Mismatches: 3  
 Query Match: 97.75% Indels: 3  
 DB: 5 Gaps: 0  
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 Qy 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTyrIlePheLeuGlnValGlnGly 20  
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 Qy 21 ThrIleAspIleSerIleAsnIleTyrHisSerGluThrIleAspIleAsnAspPro 40  
 Db 188 ACTAAAGATATCTCCATTACATATACATTCTGAAACTAAGACATAGCAATCCCA 247  
 Qy 41 ArgAsnGluThrThrGluSerThrGluIleMetTyrIleMetSerThrMetArgArgIle 60  
 Db 248 AGAAATGAAACAACTGAAAGTACTGAAAAATGTACAAAATGTCACTATGAGACGAATA 307

Qy 61 PheAspLeuAlaIleValHisArgThrIleAspArgSerAlaPhePheProThrGlyValIleVal 80  
 Db 308 TTGATTTTGGCAAGATCTGAACAAAGATCGCATTTTTCCAACGGGGGTAAAGTC 367  
 Qy 81 CysProGlnIleSerMetCysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 368 TCTCCACAGGATTCATGAAACAGATTTTATAGACAGTCTTCAAGCTTATATGATTGAGA 427  
 Qy 101 ValCysGlnIleAlaValIleTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
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 Db 488 GGGAAATATCAGAGCTGGTCAAGATCTGCGACAGAGAACCTTGTGCTCTTTCATATT 547  
 Qy 141 GlyIleAsnPheSerAspSerGlnGluHisLeuAspLeuLeuGlnArgIleIleArgGln 160  
 Db 548 GGAAGAAATCTCAGCAATTCAGAGGACCTCGATCTTCTCAGACAGAGAAATTAAGACG 607  
 Qy 161 ArgSerPheProAspArgIleAspGluIleSerAlaGluIleThrLeuGlyGluProGly 180  
 Db 608 AGAAGTTTCCCTGACAGAAAGATGAAATATCTGCAGAGAAACATTTGGAGAGCCTGAT 667  
 Qy 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
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 Qy 301 GluMetGlnLeuThrAlaIlePheIleArgHisSerAlaGluAlaIleAspSerProAlaSer 320  
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 Qy 361 IlyValIleGluGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
 Db 1208 AAAGCATAGAGAGAAACAACTTTGATGAGGAGCAATTCAGATTCATGATGAAAT 1267  
 Qy 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
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 Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu 420  
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 Qy 421 ThrValAspGlyAlaGluHisGlyLeuProAspThrSerThrProProAlaMetAla 440



QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
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 QY 208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrgluArgGluThrglu 227  
 DB 371 GAAATTCGTGATTAATCACTCAACGACACCAAGATCCTTACACAGAAAGAAACAGAA 430  
 QY 228 PheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
 DB 431 TTCGCTGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 490  
 QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGln 267  
 DB 491 AAGGCGAGAGCTCGTCACTCCGAGTCCCATATTACAGAGCTACAGAAAGATGCCAA 550  
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 DB 551 CTTCAATGCAAAAGATATTAAAGAACTTCCAGATTCAGAAAAATCCATGTGTAGGA 610  
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 DB 731 AACAAATTTGAAAGTGAAGAGTCTATCAAGAACATGAGAGAGGACAGGACACAGAA 790  
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 DB 791 ACTATCTCAGAGCTACAGACCTCAAAAGCTGATAGAGAAAGCACTTACAGAAAGACA 850  
 QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
 DB 851 TCTTTGAGATGTGGGGCAATTCATGATGAAATTCGTGGATCCTGCTGCTTTCATCTT 910  
 QY 388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
 DB 911 GGTTCGACCAACCAATCAGAGCTGCCACATCTTTGCTGATTAACAAGAGATGTACT 970  
 QY 408 LeuSerProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlnHis 427  
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 DB 1031 GGTCTACCTGACACTTCTGCTGCTCCACCTGCTATGAGCTTACCTCCCTGCAGAGCT 1090  
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 QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArg 507  
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 QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787  
 DB 2051 CAACAAATTAACAAGTAAATCAGTAAAGAAATTCGAATTACTGACCTAGAAATATGA 2110  
 QY 788 GluPheAsnHisGlnAspTyrGluGlnValAsn 797  
 DB 2111 GAATTTAACATCAAGATTGGGAGGAAT 2140  
 RESULT 4  
 US-10-007-270-5  
 ; Sequence 5, Application US/10007270  
 ; Publication No. US20020160954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hageman, Gregory S.  
 ; APPLICANT: Kuehn, Markus H.  
 ; APPLICANT: University of Iowa Research Foundation  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ; FILE REFERENCE: 020618-000120US  
 ; CURRENT APPLICATION NUMBER: US/10/007.270  
 ; CURRENT FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/430,195  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; PRIOR FILING DATE: 1998-10-29  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 2244  
 ; TYPE: DNA

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/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(2244)
/ OTHER INFORMATION: n is a, c, g, or t.
US-10-007-270-5

Alignment Scores:
Pred. No.: 5,97e-312 Length: 2244
Score: 3323.00 Matches: 667
Percent Similarity: 95.56% Conservative: 0
Best Local Similarity: 95.56% Mismatches: 10
Query Match: 80.71% Indels: 23
DB: 5 Gaps: 1

US-10-007-270-2 (1-797) x US-10-007-270-5 (1-2244)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
DB 151 ATGTATTGGAAACCTGAAAGAGCTATTTTGTGTTTGGATTCTCCAACTTCAGGA 210
QY 21 ThrIysAspIleSerIleAsnIleTyrHisSerGluThrIysAspIleAspAsnPro 40
DB 211 ACCAAGATATCTCCATTACATATACCATCTGAAACTTAAGACATAGACAAATGCCCA 270
QY 41 ArgAsnGluThrThrGluSerThrGluIysMetTyrIysMetSerThrMetArgArgIle 60
DB 271 AGAAATGAAACCACTGAAAGTACTGAAAAATGTCAAAATGTCAACTATGAGAGCAATA 330
QY 61 PheAspLeuAlaIleHisArgThrIysArgSerAlaPhePheProThrGlyValIysVal 80
DB 331 TTCGATTGGCAAGATGCAAGATGCAAAAGATCCGATTTTCCCAACGGGGTTAAAGTC 390
QY 81 CysProGlnGluSerMetIysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
DB 391 TGTCCACAGGATTCATGAAACAGATTTTAGACAGCTTCAAGCTTATATGATTGAGA 450
QY 101 ValCysGlnGlnAlaValAlaTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
DB 451 GTGTCTCAGGAAGCAGCATGGAGACATATCGAATCTTCTGATCGCATCCCTGACACA 510
QY 121 GlyIuThrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
DB 511 GGGGAATTCAGGACTGGGTCAGCATCTGCCACGAGAGACCTTCTGCTCTTTGACATT 570
QY 141 GlyIysAsnPheSerAsnSerGlnGlnHisLeuAspLeuLeuGlnArgIleIysGln 160
DB 571 GGAATAAACTTCAGCAATCCCAAGAGCAGCTGGATCTTCTCCACAGAGATTAACAG 630
QY 161 ArgSerPheProAspArgIysAspGluIleSerAlaGluIysThrLeuGlnGluProGly 180
DB 631 AGAAGTTCCTCTGACAGAAAGATGAAATATCTGCAGAGAGACATTTGGAGAGGCTGGT 690
QY 181 GluThrIleValIleSerThr----- 187
DB 691 GAAACATTGTCTATTTCACACAGCAATCTACATTCAAAAGACTTGGGCGATTTCTAAGA 749
QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199
DB 750 AAACCTCAGAGAGCAATTCAGATGTTGCCAAGCTCTCACTTGGGCTTTCCCTGTC 809
QY 200 ThrProAspAspThrIleLeuAsnGluIleLeuAspAspThrLeuAsnAspThrIysMet 219
DB 810 ACTCTGATGACACCTCTCTCAATGGAATTCGAAATACCACTCAACACACCAAGATG 869
QY 220 ProThrThrGluArgGluThrGluPheAlaValIleGluGlnGluArgValGluLeuSer 239
DB 870 CTTACACAGAAAGAGAAACAGAAATTCGCTGTGTGGAGAGAGGAGGAGGCTCAGC 929
QY 240 ValSerIleValAsnGlnIysPheIysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259
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DB 930 GTCTCTGTGTAACCAAGATTCAAGCAGAGCTCGCTGACTCCAGTCCCATATTAC 989
QY 260 GlnIuLeuAlaGlyIysSerGlnLeuGlnMetGlnIysIlePheIysLeuProGly 279
DB 990 CAGAGCTGACGAGGAAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCAGGA 1049
QY 280 PheIysIleHisValIleGluIysPheArgProIysIysGluIysAspGlySerSerSer 299
DB 1050 TTCAAAAATCCATGTGTATAGATTTTAAACCAAGAAAGAAAGAAATGGCTCAAGCTCC 1109
QY 300 ThrGluMetGlnLeuThrAlaIlePheIysArgHisSerAlaGluAlaIysSerProAla 319
DB 1110 ACAGAGATGCAACTTACGCGCCATCTTAAAGACACAGTGCAGAAAGCAAAAGCCCTGCA 1169
QY 320 SerAspLeuLeuSerPheAspSerAspIysIleGluSerGlnGluValIysHisGlyThr 339
DB 1170 AGTACCTCTGCTCTTGTGATTCACAAATTAAGATGAGAAAGTCTATCATGGAACC 1229
QY 340 MetGluGluAspIysGlnProGluIleTyrLeuThrAlaThrAspLeuIysArgLeuIle 359
DB 1230 ATGAGAGAGGACAAAGCAACGAAATCTATCTCACAGCTACAGACTCAAAAGGCTGATC 1289
QY 360 SerIysAlaLeuGlnGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379
DB 1290 AGCAAGCAGCTAGAGGAAGAAACAATCTTGATGTGGGAGCAAAATTCAGTTCAGTGA 1349
QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399
DB 1350 ATTCTGTGATCAGCCAGCTTGTGCTTACACCCCATGAGAGCTGCCACATCTTT 1409
QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419
DB 1410 GCTGTATTAACAGAGAGATGCTACTTGTAGTCCAGAACTCTCCGTGTTAAACCCAGCTT 1469
QY 420 GluThrValAspGlyAlaGlnHisGlyLeuProAspThrSerTrpSerProProAlaMet 439
DB 1470 GAGACAGTGGACGAGAGCAGACATGCTTACCTGACATCTTGGTCTCCACCTGCTATG 1529
QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459
DB 1530 GCCCT-ACCTCCGTCGAGAGCTCCACCTTCTTATGGATCAAGCATCTTCTCTG 1588
QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479
DB 1589 ACTGATCAAGGACCAACAGATACATGCGCCTGACCAAGACATGCTAGTCCAGGGCTC 1648
QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499
DB 1649 ACCATCCCAACAGTGAATATTCTGCATCAGCCAATGGCTCTGGGAAATTTCAATCCA 1708
QY 500 ProIaSerSerAspAspSerArgSerSerAlaGlyGlyIysAspMetValArgHisLeu 519
DB 1709 CCTGCATTTAGATGACAGCGGATCAAGTCCAGGTGGCAAGGTATGACAGAGACCTTA 1768
QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGlnValProGluLeuSerGlnTyr 539
DB 1769 GATGAATGATCTGTCTGACATCTGCCCATCTGAGTACGATACCAAGACTCAGGCAATAT 1828
QY 540 ValSerValProAspHisPheLeuGluIysAspThrThrProValSerAlaLeuGlnTyrIle 559
DB 1829 GTTCTGTGCCAGATCATTTCTTGGAGATATCCACTCTGCTCAGCTTTACAGATATATC 1888
QY 560 ThrThrSerSerMetThrIleAlaProIysGlyArgGluLeuValValPhePheSerLeu 579
DB 1889 ACCACTAGTTCTATGACCATTTGCCCCCAAGGCGCAGAGCTGTAGTGTCTTCAAGTGTG 1948
QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnIysSerSerLeuGlnTyrArg 599
DB 1949 CGTGTGCTTACATGCTTCTTCCACGACCTGTTCAACAAGAGATATTGGAGTACCGA 2008
QY 600 AlaLeuGlnGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGly 619
DB 2009 GCTGTGAGCAACATTCACACAGCTGCTGTTTCAATATCAAGATCCAAATCTTACAGGA 2068
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QY 620 PheVbGlnLeuGluIleLeuAenPheAgaNGlySerValIleValIenSerIyMet 639  
DB 2069 TTTAAGCACTGGAATACCTTAATCAAAAAGGAGTGTGTGTAATGCAAAAAG 2128  
QY 640 LysPheAlaIySerValProTyrAenLeuThrIyAlaValIleGlyValIleuGluAap 659  
DB 2129 AGTTTGTCTGACGTGCGGTATTAACCTCAACCAAGGCTGTGCAAGGAGT 2188  
QY 660 PheAgaSerAlaAlaIleuGlnLeuIleuGluIleAapSerTyrSerIeu 677  
DB 2189 TTTGCTTGTGTGAGCCCAACACTCCATCTGAAATAGACAGTACTCTCTC 2242  
RESULT 5  
US-10-007-270-8  
Sequence 8, Application US/10007270  
Publication No. US20020160954A1  
GENERAL INFORMATION:  
APPLICANT: Hageman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
APPLICANT: University of Iowa Research Foundation  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
FILE REFERENCE: 020618-000120US  
CURRENT APPLICATION NUMBER: US/10/007,270  
PRIOR FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US 09/430,195  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 09/183,972  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 3668  
TYPE: DNA  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform A  
NAME/KEY: misc\_feature  
LOCATION: (1)..(3668)  
OTHER INFORMATION: n is a, c, g, or t.  
US-10-007-270-8  
Alignment Scores:  
Pred. No.: 2,25e-236 Length: 3668  
Score: 2548.50 Matches: 528  
Percent Similarity: 75.12% Conservative: 79  
Best Local Similarity: 65.35% Mismatches: 180  
Query Match: 61.90% Indels: 21  
DB: 5 Gaps: 9  
US-10-007-270-2 (1-797) x US-10-007-270-8 (1-3668)  
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DB 136 ATGAATTTTCAATTAACATGCTATCTTGTGTTTGGATTTTCTCAAGTCAAGGA 255  
QY 21 ThrIyAspIleSerIleAsnIleTyrIleSerGluThrIyAspIleAspAnProPro 40  
DB 256 ATCAAAAGATACCTCTATTAATATTCAGTCTGAAATTAABAACTACAAACCCCA 315  
QY 41 ArgAnGluThrThrGluSerThrGluIyMetTyrIyMeSerThrMetArgArgIle 60  
DB 316 AATAATCGAAACATTTGAAGTACTTCAACAGTCACAAAGTGTCAACATGAAACGAATA 375  
QY 61 PheAspLeuAlaIySerIleArgThrIyAspSerAlaPhePheProThrIyValIyVal 80  
DB 376 TTCGATTTCCAAAGCTTGAACCAAAAGATCAGCACTTTCCCA--GCTGCTAACATC 432  
QY 81 CybProGlnIySerMetIyGlnIleLeuAapSerIleuGlnAlaTyrTyrArgLeuArg 100  
DB 433 TGTTCACAGAAATCTCTGAGACAGATTTTAGCAAGTCTTCAGAAATATATAGACTGAGA 492

QY 101 ValCybGlnIyAlaValITrGluAlaTyrArgIlePheLeuAapArgIleProAspThr 120  
DB 493 GTATGTCAAGAGTGTGTGGAGACATATCTATCTTTCGAGCCGAATTTCTACACA 552  
QY 121 GlnIyTyrGlnAapTrpValSerIleCybGlnGlnIyThrPheCybLeuPheAspIle 140  
DB 553 GAGGAATATCAAGATCTGGGTACGCTCTGCCGAAAGAACTTGTGCTCTTTAGACAT 612  
QY 141 GlnIyAspAnPheSerAsnSerGlnIyIleLeuAapLeuLeuGlnIyArgIleIyGln 160  
DB 613 GGGAAAACTTCAGCACTCCAGAGGACCTAGATCTTCTTCAAGAGAAATTAACAG 672  
QY 161 ArgSerPheProAspArgIyAspGluIleSerAlaGlnIySerThrLeuGlnIyGluProGly 180  
DB 673 AAGACCTTCCCTGGAGGAAAGATAGACAGCTCTCAGAGACACTGAAACACTTACT 732  
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
DB 733 GAAGCCCTGTGTGTATCCACAGATTTTCCAGAGATGTCCTGGGCTCTCCACTTCT 792  
QY 201 ProAspAspThrLeuLeuAenGluIleLeuAapAnThrLeuAapThrIyMetPro 220  
DB 793 TCTGATGACACAGACTCTCAAGAGATTTCAAGTGTCACTCAAGGACATTCAAAAGCC 852  
QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGlnIyGln 234  
DB 853 ACAACAGAAAGTAAACAGAACCTATTCACTGTGTCTGAATTTCA-----TCAAGAGAG 906  
QY 235 ArgValIleLeuSerValSerLeuValAsnIyIlePheIyAlaGluLeuAlaAspSer 254  
DB 907 AAGGTGAATTCAGCATCTCTTGCACAAACACAGATTCAGGAGAGCTCACCACTCT 966  
QY 255 GlnSerProTyrTyrGlnIyLeuAlaGlyIySerGlnLeuGlnIyMetGlnIyIlePhe 274  
DB 967 GGGTACCACTACTACAGAACTGTGTGGAGACAGTCCCACTCAGTCAAAAGATATT 1026  
QY 275 LysIyIleuProGlyIlePheIyAlaIleIleValIleuGlyPheArgProIyIyGlnIy 294  
DB 1027 AAGAACTTCCAGGATTCGAGAAATCCGTGTATTAGATTTAGACCAAAAGAAAGAA 1086  
QY 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheIyArgHisSerAlaGlu 314  
DB 1087 GATGATTCAGCTCCACAGAAATACAGCTTATGCGCATCTTTAAGAGGACCATGACAGA 1146  
QY 315 AlaIySerProAlaSerAspLeuLeuSerPheAspSerAsnIyIleGluSerGlnIy 334  
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QY 335 ValTyrIleGlyThrMetGlnIyAspIyGlnProGluIleTyrLeuThrAlaThrAsp 354  
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QY 355 LeuIyAspGlnIleSerIyAlaLeuGlnIyGlnIyGlnIySerLeuAspAlaGlyThrIle 374  
DB 1264 CTCAAATACTCATATCACTACTAGTAGAGACCTGTCTTGTGAAAGGAAATTT 1323  
QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
DB 1324 CCATTCCGGATGATGATGATGATGAGACCTC-----TTCAGACCTGTCACTGAACAGAT 1377  
QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
DB 1378 CTGCCCAAGCCCTTGTGATGTCTCAAGAGATGCTCACTTGTGATGCTCAGAACTTCTTC 1437  
QY 415 ValGluProGlnIyGlnIyThrValAspGlyAlaGlnIyGlyLeuPro----- 430  
DB 1438 GTTAGGCTTAGCTTAGGAGCTGAGACAGAGAGATCTGAGCTCTCGAAATGCTCC 1497  
QY 431 --AspThrSerTrpSerProProAlaMetAlaSerThrSerIleSerGlnIyAlaProPro 449  
DB 1498 AAAGACAGTTCGTGTCTCCACTGTATCAGCTCAATTTCCGATCAGAAATCTACTCT 1557  
QY 450 PhePheMetAlaSerSerIlePheSerIleuThrAspGlnIyThrThrAspThrMetAla 469

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Db      1558 TCGATT---ACACCTAGCATCTTCTCTAGATGCTCAAGCCCTCCCTTGATGACC 1614
Qy      470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThSerAspThrSerAlaIle 489
Db      1615 ATGGGCCCAACAGCACTATCCCAAGCCCACTCTCCCACTATGATTAATCTCACTC 1674
Qy      490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSer 509
Db      1675 CGCCATATGCTCTGGAATCGTCACTTGGCTGCATCTCTCAAGTACAGAAAGCTGATC 1734
Qy      510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
Db      1735 ACAAGACGCATGACCAATCCGAGACCTAGATGATGATGATGATGATGATGATGATG 1794
Qy      530 ProSerGluValProGlyLeuSerGluValSerValProAspHisAspLeuGluAsp 549
Db      1795 TTGTCAAGAAATATCAAGACTGAGTGGATGCAATTCGCTCGGCTCAGTTCTTGAAGATG 1854
Qy      550 ThrThrProValSerAlaLeuGlnIleThrThrThrSerSerMetThrIleAlaProIys 569
Db      1855 ACCACACCCATCCCAACAGTACAGTTTCATCACCACAGCTCCGAGACCATTCGCCACCAAG 1914
Qy      570 GlyArgGluLeuValValPhePheSerLeuArgValAlaAspMetAlaPheSerAsnAsp 589
Db      1915 GCCCAGAGACTAGTGGTATCTTCAAGCCGCGTGTGCTAACAATGCGCTTCTCTATGAC 1974
Qy      590 LeuPheAsnIleSerSerLeuGluIleThrArgAlaLeuGlnGlnPheThrIleLeu 609
Db      1975 CTGTTCACAAAGATCTCTGAGATCAAGCCCTGGAACAACAGTTCACAACTCGCTG 2034
Qy      610 ValProTyrLeuArgSerSerAsnLeuThrGlyPheGlyGlnLeuGluIleLeuAsnPheArg 629
Db      2035 GTTCCCTATCTACGATCGAATCTTACGGGATTTAAGCACTGGAATATCTCAGCTTCAGA 2094
Qy      630 AsnGlySerValIleValAsnSerIleMetLysPheAlaLysSerValProTyrAsnLeu 649
Db      2095 AACGGAAGTGATCTGTGAACAGCAAGCGGTTGGCAAAAGCGGTACCTTCAACACCTC 2154
Qy      650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669
Db      2155 ACCCAGGCGGTGCGCGGATCTTGGAGATCTTGGTCCACCGCAGCTCAAGGCGCTCAAT 2214
Qy      670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
Db      2215 CTGGAATCGAAAGCTACTCCCTCCGACATTGAACCAAGCTGATCAGCGGATCCCTGCAAA 2274
Qy      690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709
Db      2275 CTCTAGACTGTGGCAATTTGCCAGTGTGAAGAATGAGTGGACAGAGAGAGAGAG 2334
Qy      710 CysArgCysLysProGlyTyrAspSerGlnIleSerLeuAspGlyLeuGluProGlyLeu 729
Db      2335 TGTCTGTCGACAGAGGACATGAGACCCAGGACCTTGGACTCACCAGACCTTGAACCTC 2394
Qy      730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749
Db      2395 TGTCCCTCGGA---AAGACTGTGTGGCGCGCGGAGCAAGCAACTCAATGAGGCGCA 2451
Qy      750 ProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsnGlnGln 769
Db      2452 CCAGATCAGCTTCAAAACCAAGCTCAGAACCTGTGTTAAAAAGCTA-----CGTCAG 2505
Qy      770 AsnAsnLeuValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGluGluPhe 789
Db      2506 CAATAATAGGTAGTCAAGAAAGAAATTTCTAAACTATCAGCTATAGATTTGAAGAATTT 2565
Qy      790 AsnHisGlnAspTyrGluGluAsn 797
Db      2566 GAAAGACCAAGACTGGGAGGGAAT 2589

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/ Sequence 10, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuenn, Markus H.
/ APPLICANT: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-000120US
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ PRIOR APPLICATION NUMBER: 2001-11-08
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ PRIOR FILING DATE: 1998-10-29
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10
/ LENGTH: 1726
/ TYPE: DNA
/ ORGANISM: Mus sp.
/ FEATURE:
/ OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D
US-10-007-270-10

Alignment Scores:
Pred. No.: 1,1e-119 Length: 1726
Score: 1342.50 Matches: 310
Percent Similarity: 44.96% Conservative: 51
Best Local Similarity: 38.61% Mismatches: 99
Query Match: 32.61% Indels: 343
Gaps: 9

US-10-007-270-2 (1-797) x US-10-007-270-10 (1-1726)
Qy      1 MetTyrLeuGlnThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
Db      140 ATGAAATTTCAAAATTAACAGTACTATCTTGTGTTGGATTTTCTCAAGTTCAGAGCA 199
Qy      21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
Db      199 ----- 199
Qy      41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60
Db      199 ----- 199
Qy      61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
Db      199 ----- 199
Qy      81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
Db      200 -----ATCAAA 205
Qy      101 ValCysGlnGluAlaValIleProGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
Db      206 GATATCAAGAAAGTGTGTGGGAAGCATATGATCTTCTGAGACCGAATTCCTGACACA 265
Qy      121 GlyIleTyrGlnAspTyrValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle 140
Db      266 GAGGAATATCAAGACTGGGTGAGCTCTCGCGCAAGAAACCTTGTGCTCTTACACTT 325
Qy      141 GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuLeuGlnGlnArgIleLysGln 160
Db      326 GGGAAATCTTCAAGCACTCCAGAGACCTTAGATCTTCTTCAAGAGAAATTAACAG 385
Qy      161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
Db      386 AGAAGCTTCTCCGAGGAGAAAGATGACAGAGCTCAATGAGACACTGAAGACACTACT 445
Qy      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db      446 GAAAGCCCTGTGTATCCCAAGATGTTCACAGATGTTCCTGGGCGCAATTCACACTTCT 505

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QY 201 ProAspArgThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrIleMetPro 220
Db 506 TCTGATGACAGACCTCAAGAGATTCCTCACTGTCACTTCAAGACATTTCAAAAGCC 565
QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln 234
Db 566 ACAACGAAAGATTAACAGAACCTATTCAGTCTGTAATCTCA-----TCAGAGGAG 619
QY 235 ArgValGluLeuSerValSerLeuValAsnGlnIlyPheValGluLeuAlaAspSer 254
Db 620 AAGGTGAGATTACAGATCTCTGCAAAACACAGGTTCAAGACGAGCTCAACACTCT 679
QY 255 GlnSerProTyrTyrGlnGluLeuAlaGlyIlySerGlnLeuGlnMetGlnIlyIlePhe 274
Db 680 GGGTACCACTACTACAGGAACTGGTGGGACAGTCCCACTCAGTTGGCAAAAGATATT 739
QY 275 LysIlyPheLeuProGluPheIlySerIleHISValLeuGluPheArgProIlySerGluIlyS 294
Db 740 AAGAACTTCAGAGATTCGAGAAATCCGTGATTAGATTAGACCAAGAAAGAGAGA 799
QY 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheIlyArgHISSerAlaGlu 314
Db 800 GATGTTCAAGCTCCACAGAAATACAGCTTATGGCCATTTAAGAGGAGCATCCAGAA 859
QY 315 AlaIlySerProAlaSerAspLeuLeuSerPheAspSerAsnIlyIleGlnSerGluGlu 334
Db 860 GCAAAAGCCCTGATGATCATCTACTGTCTTGATTCCACAAATTTGAAAGTCAAAAGA 919
QY 335 ValTyrHISGlyThrMetGluGluAspIlyGlnProGluIleTyrLeuThrAlaThrAsp 354
Db 920 ATCCATCATGAGTCACTA---GAGACAAACACCAAGAACTTACCTCACTCACTCAAGC 976
QY 355 LeuIlyArgLeuIleSerIlyAlaLeuGluGluGlnGlnSerLeuAspValGlyThrIle 374
Db 977 CTCAAAACATCATATCACTACTAGATGAGACCTGTCTTGGTGAAGAGGAAATTT 1036
QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394
Db 1037 CCATTCCGGTGAATGAACTTACTGGGACACTC-----TTCAGACCTGTCTCAACAGAT 1090
QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414
Db 1091 CTGCCCAAGCCCTTGTGATGTCAACAGAGATGCCACTTGTAGTCCAGAACTTCTTTC 1150
QY 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHISGlyLeuProAspThrSerTrp 434
Db 1151 GTTAGGCTAGGCTTAGGACAGTGCAC----- 1177
QY 435 SerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSer 454
Db 1177 ----- 1177
QY 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474
Db 1177 ----- 1177
QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494
Db 1177 ----- 1177
QY 495 GlyIleSerHISProProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAsp 514
Db 1177 ----- 1177
QY 515 MetValArgHISLeuAspGluMetAspLeuSerAspThrProAlaProSerGluValPro 534
Db 1177 ----- 1177
QY 535 GluLeuSerGluTyrValSerValProAspHISPheLeuGluAspThrThrProValSer 554
Db 1177 ----- 1177

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QY 555 AlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProIyGlyArgGluLeuVal 574
Db 1177 ----- 1177
QY 575 ValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnIlySer 594
Db 1177 ----- 1177
QY 595 SerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArg 614
Db 1177 ----- 1177
QY 615 SerAsnLeuThrGlyPheIlyGlnLeuGluIleLeuAsnPheArgAsnGlySerValIle 634
Db 1178 -----AGAAAGGATCTAGCTG 1195
QY 635 ValAsnSerIlyMetIlyPheAlaIlySerValProTyrAsnLeuThrIlyAlaIleHIS 654
Db 1195 ----- 1195
QY 655 GlyValLeuGluAspPheArgSerAlaAlaIleGlnGlnLeuHISLeuGluIleAspSer 674
Db 1195 ----- 1195
QY 675 TyrSerLeuAsnIleGluProAlaAspGlnAlaAspProGlyIlyPheLeuAlaCysGly 694
Db 1196 -----CTGTGATCATGAGCGGATCCCTGCAAACTTCTAGACTGTGC 1237
QY 695 GluPheAlaGlnCysValIlyAsnGluIlyArgThrGluGluAlaGluCysArgCysIlyPro 714
Db 1238 AATTTGCCCTGCTGTAAAGATGATGACAGACAGAAAGAGATGTGCTGTCAGACAG 1297
QY 715 GlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThr 734
Db 1298 GACATCATGAGACCGAGGAGCTGTGATACAGACCTGTAACCTGTGCTGCTGGA--- 1354
QY 735 LysGluCysGluValLeuGlnGlyIlySerIlyAlaProCysArgLeuProAspHISerGlu 754
Db 1355 AAGACTTGTGTGGCCGGCCGAGAACCAACTCATGACAGGCCAAAGATCACTTACA 1414
QY 755 AsnGlnAlaTyrIlyThrSerValIlyIlyAspPheGlnAsnGlnGlnIlyAsnAllyValIle 774
Db 1415 AACCAAGCTCAGAACTCGGTGTTAAAGCTA-----CTCAGCAAAATTAAGTAGTC 1468
QY 775 SerIlyArgAsnSerGluLeuLeuThrValGluTyrGluGluPheAsnHISGlnAspTrp 794
Db 1469 AAGAAAGAAATTTCAAACTATCAGCTATAGGATTTGAAGAAATTTGAAGACAGGACTGG 1528
QY 795 GluGluAsn 797
Db 1529 GAGGGAAT 1537

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RESULT 7  
 US-10-007-270-12  
 ; Sequence 12, Application US/1007270  
 ; Publication No. US20020160954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hageman, Gregory S.  
 ; APPLICANT: Kuehn, Markus H.  
 ; APPLICANT: University of Iowa Research Foundation  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ; FILE REFERENCE: 020618-000120US  
 ; CURRENT APPLICATION NUMBER: US/10/007,270  
 ; CURRENT FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/430,195  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; PRIOR FILING DATE: 1998-10-29  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 1321  
 ; TYPE: DNA

ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform E  
US-10-007-270-12

Alignment Scores:  
Pred. No.: 9,93e-80 Length: 1321  
Score: 929.50 Matches: 185  
Percent Similarity: 79.41% Conservative: 31  
Best Local Similarity: 68.01% Mismatches: 53  
Query Match: 22.58% Indels: 3  
DB: 5 Gaps: 2

US-10-007-270-2 (1-797) x US-10-007-270-12 (1-1321)

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QY 526 AepThrProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHis 545
DB 320 GAAAGCGCAGCTTGTGAGAAATATCAGAACTGAGTGAATGATTCGCTCGGATCAG 379
QY 546 PheLeuGluAepThrTherProValSerAlaLeuGlnTyrIleThrTherSerSerMetThr 565
DB 380 TTCTTGAGATGATCAACACCCATCCCAACAGTACGGTTCATACCAACGCTCCAGACC 439
QY 556 IleAlaProLysGlyArgGluLeuValAlaPhePheSerLeuArgValAlaAsnMetAla 585
DB 440 ATTGCACCAAGGCGCAGAGAGTATGATTCACAGCTCGTGTGTTAACTAGCCG 499
QY 556 PheSerAsnAepLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPhe 605
DB 500 TTCTCTTATGACTCTTCAACAGAGTCTCTGAGGTATCAACCCCTGGAACAGCAATTC 559
QY 606 ThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIle 625
DB 560 ACGAGCTCTGCTGCTCCATCMACGATGATCTTACGGGATTTAAAGCACTGAAATA 619
QY 636 LeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerVal 645
DB 620 CTCACCTTCAGAAACGAAAGTGTGATCGTGAACAGCAAGTCCGGTTGCAAAAGCGGTA 679
QY 646 ProTyrAsnLeuThrLysAlaValAlaHisGlyValLeuGluAspPheArgSerAlaAla 665
DB 680 CCTTCAACCTCAGCCAGCGCGGTGCGGGGTCTTGAGAGATCTTCGGTCCACCCAGCT 739
QY 666 GlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAla 685
DB 740 CAAGGCTCATCTGGAATCGAAAGCTATCTCCCTCGACATTGAACCACTGATCAAGCG 799
QY 666 AepProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThr 705
DB 800 GATCCCTGCAAACTTCTAGACTGTGGCAAAATTGCCCGAGTGTAAAGAAATGAGTGAACA 859
QY 706 GlnGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeu 725
DB 860 GAGGAAGCAGAGTGTGCTGACAGAGGACATGAGAGCCAGGACCTTGACCTACACAG 919
QY 726 GlnProGlyLeuCysGlyProGlyThrLysGlyCysGlyValLeuGlnGlnLysGlyAla 745
DB 920 ACCCTGAACCTCTGCTCCCTGGA--AAGACTGTGTGCGCGCGCGCAACAGCAACT 976
QY 746 ProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPhe 765
DB 977 CCATGAGGCGCACAGATCATCTACAAACCAAGCTCAGGAACCTGGTGTAAAGACTA 1036
QY 766 GlnAsnGlnGlnAsnAsnLysValIleSerLysArgAsnSerGlnLeuLeuThrValGlu 785
DB 1037 -----CGTCAGCAAAATAGATGATCAAGAAACGAATTTCTAACTACAGCTATAGA 1090
QY 786 TyrGlnGluPheAsnHisGlnAspTyrGlnGlyAsn 797
DB 1091 TTTGAAAAATTTGAAAGACCAAGACTGGAGGAAAT 1126

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RESULT 8  
US-10-783-528-9

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; Sequence 9, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsaeha
; APPLICANT: Glash, Kurt
; APPLICANT: Wilson, Keith
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4165
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4076)..(4076)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (4091)..(4091)
; OTHER INFORMATION: n is a, c, g, or t
US-10-783-528-9

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Alignment Scores:  
Pred. No.: 9,79e-79 Length: 4165  
Score: 927.00 Matches: 297  
Percent Similarity: 39.71% Conservative: 145  
Best Local Similarity: 26.68% Mismatches: 267  
Query Match: 22.52% Indels: 405  
DB: 8 Gaps: 36

US-10-007-270-2 (1-797) x US-10-783-528-9 (1-4165)

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QY 2 TyrLeuGluThrArgArgAlaIlePheValPheThrIlePheLeuGlnValGlnGlyThr 21
DB 202 TTCTCTTTTGGGAAGATTTCTCTGAGTATTTTG-AATTTGCTCTGATGAAAGAGAC 260
QY 22 --LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro-- 39
DB 261 TTTCATATATTAAACGACAAACCTATCTATCT--ATAGAGAGATCCAAAGACCAAG 317
QY 40 -----ProArgAsnGluThr-----ThrGluSer 47
DB 318 AGTGCAGTTCTTTTCTCTGCTGAGAGATCAACAGACCTTCTCTAGCTACCAAAAAG 377
QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67
DB 378 AAACGCTCTGAGACCGAGAGAACTGAAGACAGTGCTTA-----ATCGAA 425
QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87
DB 426 AGCGGAGATCATATTCTGTTCTCTTAATGAGTGAAGAAATCTGCCAGATGAAGAGTGTGA 485
QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValIleTrp 107
DB 486 GAGGCTGTGGCAAAATCATGATGAAGTATTTAAAGCCAGAGTGTGCAGGAAGCTGTCTGG 545
QY 108 GlnAlaTyrArgGlyIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127
DB 546 GAAAGCTTCAGAGACTTTTGGATTCGACTTCTGCGCGCTGAGAAATCATCTACGTGATG 605
QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147
DB 606 AATTGTGTGAGAGATGAGTCAACAAGTATATTGAAATGGGACAAATTTTAGTAATCT 665
QY 148 GlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167
DB 666 GTGGAACATAGAGCTTAATCATGAAAGAACTGACTTAT-----GCAAAAG 710

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QY 168 AaPgluIleSerAlaGluThrLeuGluPro-----GlyGluThrIleVal 184  
 Db 711 GAACTGTAAAGAGCTCTGAA--CTGTCTTCTCCAGTTCCTGTGTGATCTTCAACA 767  
 QY 185 ILeSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200  
 Db 768 TTGGAGACACACTACTCAGTGTT-----CCACATCCAGAGGTGAGCGCTTGA 818  
 QY 201 -----ProAspAspThrIleuLeuGluIleuAsp 211  
 Db 819 GGTGCTCAGAGACAGCTTGGAAAGCCGAGAGAGATATTGATGCAATTAATTT--GAG 875  
 QY 212 AaPThrLeuAsnAspThrIleuSerProThrThrGluArgGluThrGluPheAlaValLeu 231  
 Db 876 AATGTGATGAAAGACCCACAAACACAGAGGTGAACAGATTGCACAAATTC----- 926  
 QY 232 GluGluGluArgValGluLeuSerValSerLeuValAsnGluIleuPheValGluLeu 251  
 Db 927 -----AGTATCCACCTTTGGGGAGCAGTACAGGGAAAGACTA 965  
 QY 252 AlaAspSerGlnSerProGlyTyrGlnGluLeuAlaGlyLysSerGlnLeuMetGln 271  
 Db 966 CAGGATTCCTCCAGCTTTCACCCACAGACCTTGAAGAAGAAATTATTTCAGAGGTTGA 1025  
 QY 272 LysIlePheLysLeuProGluPheLysValIleValLeuGlyPheArgProLys 291  
 Db 1026 AATGCATTAATCTGGGTGTACAGGCTACAGAAATTCGTGTACTTAATTTAGGTCCCC 1085  
 QY 292 LysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHis 311  
 Db 1086 AAGGAAATATGAC-----AGTGCCTGAAGTGTATTACTATGCAATTACCTTC 1130  
 QY 312 SerAlaGluAlaLysSerProAlaSer--AspLeuLeuSerPheAspSerAlaValIle 330  
 Db 1131 AATGTGAGAGCCCATCGCAATACCACTGGACCTTATAGCTTACCTTCACTCAACAAGTG 1190  
 QY 331 GluSerGluGluValLysIleGlyThrMetGluGluAspLysGluProGluIleTyrLeu 350  
 Db 1191 GAAAC-----CATGGCTTGTGAACTGATGATAAACCACTGTGTTTAT 1238  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerValIleGluGlu----- 365  
 Db 1239 ACAATCAGTAATCTCAGAGATTAATTTGCTGAGACATTGCAAGCAATTTTGTCTGGG 1298  
 QY 365 ----- 365  
 Db 1299 AACTCTTCTGTAATCAGATCCTGATTCCTGACAGTTAATGTAAGAGAGTTTG 1358  
 QY 366 ---GluGlnSerLeuAspVal-----GlyThrIleGlnPheThr--- 377  
 Db 1359 CCGTCAACAACTGAAGATCTAGTTTGAAACACCAAGTTCAAGTCTTACAGGCACGCCG 1418  
 QY 378 -----AspGluIleAla 381  
 Db 1419 TCATCTATTCTGATAATACTTTCAGTCGATGCGCTTCAGCAGATGAATCATCTACC 1478  
 QY 382 GlySerLeuPro-----AlaPheGlyProAspThr 391  
 Db 1479 ACAGATATTCCACACTGATATTTCAGCTGTGCTCCCTCAGCCACTGCGAGGAAATC 1538  
 QY 392 GlnSerGluLeuPro----- 396  
 Db 1539 TGGTCAAAAGTCTTGTGGATATTAGTGTACACACAAATTAGCTTTCCTGGAAG 1598  
 QY 396 ----- 396  
 Db 1599 ATGGGCTCAGCTCTTCCCAAGGTTTTAGAGGTTAGAGCTTGACTCTTCAATTCTGTC 1658  
 QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 Db 1659 ACCCCGAGAGTGTCTCAGACTGGCTGTGCTGTGGCTTCTGAGGAAGAAGCTTGTGATCT 1718  
 QY 411 GluLeuProProValGluProGluLeuGluThrValAspGlyAlaGlu----- 426

Db 1719 CACTTG-----GTGAAGATGATTAAGCCAAATGTTGAAGATCAGAAATTTCTTCT 1772  
 QY 427 ---HisGlyLeuProAspThrSerThrSerProProAlaMetAlaSerThr----- 442  
 Db 1773 ATTTGATTAATTCCTTCAAGTTCAATTCATCTCACTCAACCTGTGCCAAAGAAACAATACATCC 1832  
 QY 443 -----SerLeuSerGluAlaPro-----ProPhe 450  
 Db 1833 ATGGAAGACTGTGATGTGTCTTAAACATCTGTACCAATATGTGACCTTCTTATACCTTTT 1892  
 QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
 Db 1893 GCGTGAAGCTCTTGAATCTTCAAAAGTCAAAAGCAATTAATAAGAGCCCTTCTCGCA 1952  
 QY 471 AspGlnThrMet----- 474  
 Db 1953 GATGCATCCATGAAAAGAGTTAATAATTGACGGGTGTTTAGTTCAAGGTCTGGGCA 2012  
 QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
 Db 2013 AAGGTAGATCTGATTAATTCAGGTCATGAGTGAAGACTTCACTCA--GAGAAAGCGCCGA 2069  
 QY 495 GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyLysIleuAsp 514  
 Db 2070 CCACTGTCCAGCCGTGGCTTGAAGATGAATGATTAATCTTTTCCAGCTGAGATTGAAGAC 2129  
 QY 515 MetValArgHisLeu--AspGluMetAspLeuSerAsp----- 526  
 Db 2130 AAGAAATAGTTTGTGTTGACAAATGATTCACAGACCAAAATTAAGTAAGACTCAAA 2189  
 QY 527 -----ThrProAlaProSerGluValPro----- 534  
 Db 2190 TATGAACATGATGACAGATCCACACTTTCAGAGAAAGACCTTATAGTGGCTGTCT 2249  
 QY 535 -----GluLeuSerGluTyrValSerValProAspHisPhe 546  
 Db 2250 GTGCCCATCTTGCAGATATCTGACGTGAATCTGCGTCTTAACCTCCCAAGCAGATA 2309  
 QY 547 LeuGlu-----AspThr 550  
 Db 2310 TCAAGAAATACCTGTGTGATGATGATTGCTCAGTTACCAAGACCTTTATCTGACATCT 2369  
 QY 551 ThrProValSerAla----- 555  
 Db 2370 GTAGCAATCTGTGCTCTACTGATTAATTCAGATCAGCAGATGCATCTTAAGAGAGAT 2429  
 QY 556 LeuGlnTyrIleThrThrSerSer----- 563  
 Db 2430 ATGGAACAATTAATCGATCATCCAACTATGAATGTTTGACAGTAGGTTCAATGTGTA 2489  
 QY 564 -----MetThrIleAlaProLysGlyArgGlu----- 572  
 Db 2490 AAGCAGATATGCCAAACTTGTGACTATATTGCTCCAGAAATCAGAGAGATTGGACAA 2549  
 QY 572 ----- 572  
 Db 2550 ACTTCTCCCTAGAGAAATTGTCAGAGACATATTGGCAATGACACACAGAGTGTGAC 2609  
 QY 572 ----- 572  
 Db 2610 AGGCTGTGTTATCTGTGACACAGTCTCAAAATTGCTCCAAACAATTCACACCTTG 2669  
 QY 572 ----- 572  
 Db 2670 CTAGAGATGAAGTAATTAATGGGTGTACAGATATTGCTTAGAACTGAGCCGATAGGC 2729  
 QY 572 ----- 572  
 Db 2730 ACAGATTAATACAGCTGAGCAAGTCCAAAGACAAATGCAAGGTTGTAGTTATGNG 2789  
 QY 572 ----- 572

Db 2790 GAAATGTCAACAAGTGTTCATCCACAGAGATGTGTAGTGCTTGCCACAGAAAGA 2849  
Qy 573 -----LysVal1PhePheSerLeuArg 580  
Db 2850 GGAGATGACTGATTATACCCAGACTTACAGAGCTTGTTGTGTTTCTTCAGCCCTCGA 2909  
Qy 581 Val1AsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
Db 2910 GTGACTTAACATGATGTTTTCAGAGATCTGTTTAATATAAACTCCCTGGAGATATAAGCC 2969  
Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 2970 CTGGAGCAAAATCTTCAAGATTGCTGCTTCCTATCTCCAGTCAAAATCTCAGCGGCTTC 3029  
Qy 621 LysGlnLeuGluLysLeuAsnAspPheArgAsnLysSerVal1LeuValAsnSerLysMetLys 640  
Db 3030 CAGAACTTGAATCTCTCAACTTCAGAAATGGCAGCATTTGTGTGACAGTGAATGAAG 3089  
Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaVal1IleGlyVal1LeuGluAspPhe 660  
Db 3090 TTGGCAATCTGTCTCCCTCTCAACGTCAACAAATGGGTGTACATGATTTCTGGAAGCTTT 3149  
Qy 661 ArgSerAlaAlaIleGlnLeuLysIleGluGlu1LeuAspSerTyrSerLeuAsn1IleGlu 680  
Db 3150 TGTACCACTGCTCAACATACCAATGAACTTGCTATTGATTAATACTCTTGTATGTGAA 3209  
Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
Db 3210 TCAGGTGATGAAGCCCAAGCTTCAGAGCTTCGATGAATGAAATTTCAAGAGTGTCTG 3269  
Qy 701 LysAsnGluArgThrGlnGlu1IleGluCysArgCysLysProGlyTyrAspSerGln--- 719  
Db 3270 GTCAACCCCTGGAGTGAAGCAAGCAAGTGCAGATGCTTCCTGGATACCTGAGTGTGAA 3329  
Qy 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735  
Db 3330 GAACGGCCCTGTCAAGTCTCTGTGACCTACAGCCGACTTCTGCTTGAATGATGAAG 3389  
Qy 736 GluCysGluVal1LeuGlnGlyLysGlyAlaProCysArg 748  
Db 3390 ---TGTGACATTATGCTGTGGCAGCGGGCCATTGTAGG 3425

RESULT 9  
US-10-007-270-16  
Sequence 16, Application US/10007270  
Publication No. US20020160954A1  
GENERAL INFORMATION:  
APPLICANT: Hegeman, Gregory S.  
APPLICANT: Kuehn, Markus H.  
APPLICANT: University of Iowa Research Foundation  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
FILE REFERENCE: 020618-000120US  
CURRENT APPLICATION NUMBER: US/10/007,270  
CURRENT FILING DATE: 2001-11-08  
PRIOR APPLICATION NUMBER: US 09/430,195  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 09/183,972  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 4166  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human IPM 200 (Isoform A) cDNA  
US-10-007-270-16

Alignment Scores:  
Pred. No.: 9,8e-79 Length: 4166  
Score: 927.00 Matches: 297  
Percent Similarity: 39.71% Conservative: 145  
Best Local Similarity: 26.68% Mismatches: 267

Query Match: 22.52% Indel: 405  
DB: 5 Gaps: 36  
US-10-007-270-2 (1-797) x US-10-007-270-16 (1-4166)

Qy 2 TyrLeuGlnThrArgArgAla1IlePheVal1PheThr1IlePheLeuGlnVal1GlnGlyThr 21  
Db 202 TTCCCTCTTTGGGAAGATTCTCTGAGTATTTTG-ATATTGTCTGATGAAGAGAC 260  
Qy 22 ---LysAsp1IleSer1IleAsn1IleTyrHisSerGluThrLysAsp1IleAspAsnPro--- 39  
Db 261 TTTTCATCATTAACAGACAAACCTACTTATCT--ATAGAGAGATCCAGAAACCCAG 317  
Qy 40 -----ProArgAsnGluThr-----ThrGlnSer 47  
Db 318 AGTGCAGTTCTTTTCTCTGCTGCAAGATCAACAGACCTTCTCTACCTACCAAAAG 377  
Qy 48 ThrGluLysMetTyrLysMetSerThrMetArgArg1IlePheAspLeuAlaLysHisArg 67  
Db 378 AAACAGCCTCGAGCCGAGAGAACTGAAGACAGTGGTA-----ATCAGA 425  
Qy 68 ThrLysArgSerAlaPhePheProThrGlyVal1LysVal1CysProGlnLysSerMetLys 87  
Db 426 AGCGGAGATCTATTCTGTTCTTAATGAGTGAATACTGCCAGATGAAGAAGTGTGCA 485  
Qy 88 Gln1IleLeuAspSerLeuGlnAla1IleTyrTyrArgLeuArgVal1CysGlnGlu1IleVal1Trp 107  
Db 486 GAGCTGTGGCAATCATGTGAAGTATTTAAAGTCCAGAGTGTGACAGAACTGTCTGG 545  
Qy 108 GluAlaTyrArg1IlePheLeuAspArg1IleProAspThrGlyGluTyrGlnAspTrpVal 127  
Db 546 GAAGCTTCACAGACTTTTGGGATGATGACCTCTCGGCGCGTGAAGAAATCATTAATCGATG 605  
Qy 128 Ser1IleCysGlnGlnGlnThrPheCysLeuPheAsp1IleGlyLysAsnPheSerAsnSer 147  
Db 606 AATTGTGTGAGATGAGTGAAGTCAAGATATTTTGAAGGGCACAATTTTAAGTAATCT 665  
Qy 148 GlnGlnLysLeuAspLeuLeuGlnGlnArg1IleLysGlnArgSerPheProAspArgLys 167  
Db 666 GTGAAACATTAAGCTTAATCATGAAGAACTGACTTAT-----GCAAAG 710  
Qy 168 AspGlu1IleSerAlaGluLysThrLeuGlyGluPro-----GlyGluThrLysVal 184  
Db 711 GAACTGTAAAGAGCTTGAA---CTGTCTTCCAGTTCCTGTGGTGTGATCTTCAACA 767  
Qy 185 1IleSerThrAspVal1AlaAsnVal1SerLeuGlyProPheProLeuThr----- 200  
Db 768 TTGGAGACACTACTCTCAGTGT-----CCACATCCAGAGGTGAGCGCTATGAA 818  
Qy 201 -----ProAspAspThrLeuLeuAsnGlu1IleLeuAsp 211  
Db 819 GGTGCTCAGAGAGAGCTTGGAAGGCAAGAGAGATATTAGCAATGAATTT---GAG 875  
Qy 212 AsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaVal1Leu 231  
Db 876 AATGATATGAAGAACCAACAAACAGACAGTGAACAGATTGACGAATTC----- 926  
Qy 232 GluGlnGlnArgVal1GluLeuSerVal1SerLeuVal1AsnGlnLysPheLysAlaGluLeu 251  
Db 927 -----AGTATCCACCTTTGGGAGAGCACTATACAGGAAACACTA 965  
Qy 252 AlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGln 271  
Db 966 CAGGATTCCTCCAGCTTTCACACACAGCACTTGAAGAAATTTATTTCAGAGGTGAA 1025  
Qy 272 Lys1IlePheLysLysLeuProGlyPheLysLysIleHisVal1LeuGlyPheArgProLys 291  
Db 1026 AATGATTTACGGGTTCACAGGCTTACAAAGAAATTCGTGATCTGAATTTAGTCCCCC 1085  
Qy 292 LysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAla1IlePheLysArgHis 311  
Db 1086 AAGGAAATGTAC-----AGTGGCTGATGATGTTTACTATGACGATTACCTTC----- 1130

QY 312 SerAlaGluAlaIysSerProAlaSer---AspLeuSerPheAspSerAnlySile 330  
 Db 1131 ATGTGAGAGCCCTATGCAATACCACTGGACCTTAATGCTTCACTCAACAGGTG 1190  
 QY 331 GluSerGluGluValTyrHisGlyThrMetGluGluAspLysGluProGluIleTyrLeu 350  
 Db 1191 GAAAC-----CATGCTTGTGAACTGGATGATTAACCACTGTGTTAT 1238  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGlu- 365  
 Db 1239 ACAATCAGTAACCTTCAGATTAATATGCTGAGACATGACAGAAATTTTGTGCGG 1298  
 QY 365 ----- 365  
 Db 1299 AACTTCTCTGTAATCCAGATCTCTATCCCTGACCTTAATCAATGAGAGATTG 1358  
 QY 366 ---GluGlnSerLeuAspVal-----GlyThrIleGlnPheThr--- 377  
 Db 1359 CGTCAACCAACTGAATATCTAGTTTGGAACACCCAAAGTTCAAGTCTTCAGCAACGCG 1418  
 QY 378 -----AspGluIleAla 381  
 Db 1419 TCATCTATTCTGGATATACTCTTCAAGCTGACGCTGACAGATGATCATCAC 1478  
 QY 382 GlySerLeuPro-----AlaPheGlyProAspThr 391  
 Db 1479 AGCAGATTTCCACCACTGATTTACAGCTGTGCTCTCCCTCAAGCCACTGGACGAACTC 1538  
 QY 392 GlnSerGluLeuPro----- 396  
 Db 1539 TGTGTGAAGAGTCTTTGGGTGATTTAGTGTCAACACAAATAGCTTCCCTCGAAG 1598  
 QY 396 ----- 396  
 Db 1599 ATGCGCTCAGCTCTCCCAAGGTTTAAAGGTTAGCAGCTTGACTCTTCACTGTGTC 1658  
 QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 Db 1659 ACCCGGCGAGTCTTCAGACTGTGCTGCTGTGCTTGTGAGAAAGACTTCTGTGATCT 1718  
 QY 411 GluLeuProProValGluProGluLeuGluThrValAspGlyAlaGlu- 426  
 Db 1719 CACTTG-----GTAAAGATGATTAAGCAATGTTGAAGAGCAGAAATTTCTTCT 1772  
 QY 427 ---HisGlyLeuProAspThrSerTyrSerProProAlaMetAlaSerThr- 442  
 Db 1773 ATGTATTCATGCTTCAAGTTCATTCATCAACCTGTGCCAAAGAAACAAATACCATCC 1832  
 QY 443 -----SerLeuSerGluAlaPro-----ProPhe 450  
 Db 1833 ATGGAAGACTGTGATGTGCTTAAACATCTTCACCAATATGACCTTCTATACCTTT 1892  
 QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
 Db 1893 GCGTTGACTCTCTTACCTTCAAGTCAAGTCAAAAGCAATTAAGAGCCCTTCTGCCA 1952  
 QY 471 AspGlnThrMet----- 474  
 Db 1953 GATGATCCATGGAAGAAAGATTAAATTTGACCGGTGTTAGGTTGAGGCTGTGGCA 2012  
 QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
 Db 2013 AAGGATAGATCTGATTACTTGGCCATGAGTGAAGACTTCATCA---GAGAAGAGCCGCA 2069  
 QY 495 GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGluIleAsp 514  
 Db 2070 CCACCTTCCAAAGCCGCGCTGAAGATGATGATTCATTTGCGCACTGAGATTGAAGC 2129  
 QY 515 MetValArgHisLeu---AspGluMetAspLeuSerAsp----- 526  
 Db 2130 AAGAACTAGTTTATGTTGACAAATAATGATTCACAGACCAATATGTAAGACATCAAA 2189  
 QY 527 -----ThrProAlaProSerGluValPro----- 534

Db 2190 TATGAACATGATGACAGATTCACACATTTCCAGAGAAAGAGCTTTATGTGGCTGCT 2249  
 QY 535 -----GluLeuSerGluTyrValSerValProAspHisPhe 546  
 Db 2250 GTGCCATCTTGCAGATATCTGACGTGAATCTGGGTCTTAACCTCCCAAGACATTA 2309  
 QY 547 LeuGlu-----AspThr 550  
 Db 2310 TCAGAAAGTACTGTGTGTGATGATTTGCTCAGTTAACCAAGACCTTTATCTGACATCT 2369  
 QY 551 ThrProValSerAla----- 555  
 Db 2370 GTAGCAATCTCTGCTCTTAATGATTAATCAGATCAGGACAGATCCATCTTAAGAGAT 2429  
 QY 556 LeuGlnTyrIleThrThrSerSer----- 563  
 Db 2430 ATGGAACAAATTAATCAGATCAACAACTAATGATTTGACAGTGAAGTTCAATGTA 2489  
 QY 564 -----MetThrIleAlaProLysGlyArgGlu- 572  
 Db 2490 AAGCAGATATCAAACTTTGTGACTATATTGCCAGATCAGAGAGATTGACAAAGA 2549  
 QY 572 ----- 572  
 Db 2550 ACTTCTCCCTAAGAAATTTGCCAGAGACATATTTGGCAAGTACACACAGAGTGTGAC 2609  
 QY 572 ----- 572  
 Db 2610 AGGCTGTGTTATCTGTGACACAGTCTACCAATTTGCTCCCAACCAATCTCCACCTG 2669  
 QY 572 ----- 572  
 Db 2670 CTAGAGATGAATTAATATGGGTGTACAGATATTTGTTAGAACTGGACCGATAGGC 2729  
 QY 572 ----- 572  
 Db 2730 ACAGATTAATCACTGACCTGAGCAAGTCCAGAGCAAAATGGCAAGTTGTATATGTG 2789  
 QY 572 ----- 572  
 Db 2790 GAAATGTCAAAAGTTCATCTCCACAGAGATGTTAGTGTGCTGGCCACAGAAAGA 2849  
 QY 573 -----LeuValValPhePheSerLeuArg 580  
 Db 2850 CGAGATGACTGATTAATACCAAGACTTCAGAGGCTTTGTGTGTTCTTACGCTCCGA 2909  
 QY 581 ValAlaAspMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGlnTyrArgAla 600  
 Db 2910 GTGACTTAATCATGATGTTTCAAGAAATCTGTTTAATAAACTCTTGAAGTAAAGCC 2969  
 QY 601 LeuGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
 Db 2970 CTGGAGCAAAAGTTTGAATTTGCTGTGTTCCCTATCTCCATCAAACTTCACGGGGTTC 3029  
 QY 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
 Db 3030 CAGAACTTAAGAAATCTCAACTTCAGAAATGSCACATTTGTGTAAACAGTGAATGAAG 3089  
 QY 641 PheAlaLysSerValProTyrAsnLeuThrIleValIleGlyValIleGluAspPhe 660  
 Db 3090 TTTGCAATTTGTGCTCCCTCAACCTCAACAAATGCGGTGATCATATCTTGAAACATTT 3149  
 QY 661 ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680  
 Db 3150 TGTACACTGCTCAAAATCAATGAACTTGCTGCTTAATTAATCTCTTGAATGGA 3209  
 QY 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
 Db 3210 TCAAGTGTGAAGCAACCTTGCAAGTTTCAGGCTGTAAATGAATTTTCAGAGTGTCTG 3269  
 QY 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln--- 719

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Db      3270 GTCAACCCCTGGAGTGAGAACAAAGTCAGATGCTTCCCTGATACCTGAGTGGAA 3329
Qy      720 -----GlySerLeuAspGlyLeuGluProGlyLeuCyGlyProGlyThrIys 735
Db      3330 GAACGGCCCTGTCAAGGCTCTGTGACCTACAGCCTGACTTCTGCTTGAATGATGAAG 3389
Qy      736 GluCyGluValLeuGlnGlyLeuGlyAlaProCyAsp 748
Db      3390 ---TGTGACATTATGCTGGGCAAGGCGCATTTGTAG 3425

RESULT 10
US-10-007-270-14
/ Sequence 14, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ APPLICANT: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-000120US
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ PRIOR FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ PRIOR FILING DATE: 1998-10-29
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 555
/ TYPE: DNA
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Monkey IPM 150 cDNA (partial)
US-10-007-270-14
/ OTHER INFORMATION: Description of Unknown Organism: Monkey species
US-10-007-270-14

Alignment Scores:
Pred. No.: 5 676-76 Length: 555
Score: 885.00 Matches: 167
Percent Similarity: 95.65% Conservatve: 9
Best Local Similarity: 90.76% Mismatches: 8
Query Match: 21.50% Indels: 0
Gaps: 0
DB: 5

US-10-007-270-2 (1-797) x US-10-007-270-14 (1-555)
Qy      73 PhePheProThrGlyValIysValCyProGlnGluSerMetIysGlnIleLeuAspSer 92
Db      4 TTCTTCCGAAAGGGGTTAAAGTCTGTCCACAGAAATCCATGAACAGATTTTTACCACT 63
Qy      93 LeuGlnAlaIyrTyArgLeuArgValCyGlnGlnAlaValTTPGlnAlaTyArgIle 112
Db      64 CTTCAAGCTTATTATGATTGAGAGTGTGTCAAGAGCATATGGGAACATATCGCATC 123
Qy      113 PheLeuAspArgIleProAspThrGlyGluTyArgIleAspThrValSerIleCyGlnGln 132
Db      124 TTCTGGAATCGATCCCTCAACAGGGGAATACAGAGCTGGGTCTGCTTGGCCAGCG 183
Qy      133 GluThrPheCyLeuPheAspIleGlyIysAsnPheSerAsnSerGlnIleIleLeuAsp 152
Db      184 GAGACCTTCTGCTCTTGAACATCGCAAAACTTCAAGCATTTCCAGAGAGCACTGGAT 243
Qy      153 LeuLeuGlnGlnArgIleIysGlnIleArgSerPheProAspArgIysAspGlnIleSerAla 172
Db      244 CTTCTCCACAGAGAAATAAACAAGAGATTTCCCTGAGAGAAAGATGAATATCTACA 303
Qy      173 GluIysThrLeuGlnIysGluProGlyGluThrIleValIleSerThrAspValAlaAsnVal 192
Db      304 GAGAAACATTTGGAGAGCCTAGTGAACCATTTGTGTTCACAGATTTTGGCCGCTC 363
Qy      193 SerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsn 212

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Db      364 TCACCTGGGCTTTCCCTGTCATCTGTATGACACCCCTCCATATGAATTCGTGATAT 423
Qy      213 ThrLeuAsnAspThrIysMetProThrThrGluArgGluThrGluPheAlaValLeuGlu 232
Db      424 GCACCTCAACGACACCAATATGCTTACACAGAAAGAAAGAAAGAACTGCTGTCTAG 483
Qy      223 GluGlnArgValGluLeuSerValSerLeuValAsnGlnIysPheIysAlaGluLeuAla 252
Db      484 GAGCAGAGGTTGGAGCTGACATCTCTGTATTAACAGAGTTTCAAGGACAGACTCCCT 543
Qy      253 AspSerGlnSer 256
Db      544 GACCTCACTGCA 555

RESULT 11
US-10-007-270-18
/ Sequence 18, Application US/10007270
/ Publication No. US20020160954A1
/ GENERAL INFORMATION:
/ APPLICANT: Hageman, Gregory S.
/ APPLICANT: Kuehn, Markus H.
/ APPLICANT: University of Iowa Research Foundation
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
/ FILE REFERENCE: 020618-000120US
/ CURRENT APPLICATION NUMBER: US/10/007,270
/ PRIOR FILING DATE: 2001-11-08
/ PRIOR APPLICATION NUMBER: US 09/430,195
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 09/183,972
/ PRIOR FILING DATE: 1998-10-29
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 18
/ LENGTH: 2964
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Human IPM 200 cDNA sequence, isoform C
US-10-007-270-18

Alignment Scores:
Pred. No.: 3 896-71 Length: 2964
Score: 846.50 Matches: 274
Percent Similarity: 41.81% Conservatve: 142
Best Local Similarity: 27.54% Mismatches: 256
Query Match: 20.56% Indels: 325
DB: 5

US-10-007-270-2 (1-797) x US-10-007-270-18 (1-2964)
Qy      2 TyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnIleThr 21
Db      100 TTCCCTCTTTGGAGAAATTTCTGCGGTATTTG-ATAATGTCCTGATGAAGAGAGAC 158
Qy      22 ---LysAspIleSerIleAsnIleTyrIleSerGluThrIysAspIleAspAsnPro--- 39
Db      159 TTTCATCATTTACAGCAAAACCTACTTATCT---ATAGAGAGATTCAGAAACCCAG 215
Qy      40 -----ProArgAsnGluThr-----ThrGlnSer 47
Db      216 AGTGACGTTTCTTCTCCTGCTGAGAGATCAACAGACCTTCTGACTACCAAAAG 275
Qy      48 ThrGluIysMetTyrIysMetSerThrMetArgGlyIlePheAspLeuAlaIysIleArg 67
Db      276 AAACGCTCTGAGCCGAGAGAACTGAAGAGACGTGTTA-----ATCAGA 323
Qy      68 ThrIysArgSerAlaPhePheProThrGlyValIysValCyProGlnGlnIysMetIys 87
Db      324 AGCGGAAATCTATTCTGTTCTTAATGAGAGAAATCTGCCAGATGAAGTGTGCA 383
Qy      88 GlnIleAspSerLeuGlnAlaIyrTyArgLeuArgValCyGlnGlnIleValIleTyr 107

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Db 384 GAGCTGTGGCAAAATCATGTGAAGTATTTAAAGTCCGAGTGTGTGACGAGAGCTGTCTGG 443  
 Qy 108 GUAUATYAArGllleheleuAsparGlieProAspThrGlyGluTyrglnAspTrpVal 127  
 Db 444 GAAGCCTTGAGACCTTTTGGATCAGCTCTCGGCGGTGAGAAATATCATTAACCTGGANG 503  
 Qy 128 SerIleCyseGlnGlnGlnThrPheCyseuPheAspIleGlyLyseAsnheSerAsnSer 147  
 Db 504 AATTGTGTGAGAGAGAGAGTACACAGATATATTTGAAATGAGCAAAATTTTAgTGAATCT 563  
 Qy 148 GlnGlnHileuAspLeuLeuGlnGlnArgIleGlyGlnArgSerPheProAspArgLys 167  
 Db 564 GTGGAACATAGAAGCTTATATCATGAAGAAAGACTTAT-----GGAAG 608  
 Qy 168 AspGluIleSerAlaGluLysThrLeuGlyGluPro-----GlyGluThrIleVal 184  
 Db 609 GAATCTGTAAAGCAGCTGTAA--CTGTCTCTCCAGTTCGTGTGTGATATCTTCACAGA 665  
 Qy 185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200  
 Db 666 TTGGGAGACATCACTCTCACTGTT-----CCACATCCAGAGGTGACCGCTATGTAA 716  
 Qy 201 -----ProAspAspThrLeuLeuAsnGluIleLeuAsp 211  
 Db 717 GGTGCTCAGAGAGCAGCTTGGAAAGCCAGAGAGATTAAGCAATGAATTT---GAG 773  
 Qy 212 AsnThrLeuAsnAspThrIlySmetProThrThrGluArgGluThrGluPheAlaValLeu 231  
 Db 774 AATGTGATATGAAGAGCCACAAACCCAGAGGTGAACAGATTGCAGAAATTC----- 824  
 Qy 232 GlnGlnGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeu 251  
 Db 825 -----AGTATCCACCTTTTGGGAGAGAGTACAGGAGAAAGACTA 863  
 Qy 252 AlaAspSerGlnSerProTyTyrglnGlnLeuAlaGlyLysSerGlnLeuGlnMetGln 271  
 Db 864 CAGGATTCCTCCAGCTTTCACCAACAGCAGCCTTGAAGAAGAAATTTATTTCAAGGTTGA 923  
 Qy 272 LysIlePheLysLysLeuProGlyPheLysIleHisValLeuGlyLysArgProLys 291  
 Db 924 AATGCACTTAACTGGGTTTACAGGCTCAAGAAATTCGTGACTTGAATTTAGTCCGCC 983  
 Qy 292 LysGlnLysAspGlySerSerSerThrGlnMetGlnLeuThrAlaIlePheLysArgHis 311  
 Db 984 AAGGAATAATGAC-----AGTGGCGTGAATGTTTACTATGACGTTACCTTC----- 1028  
 Qy 312 SerAlaGlnAlaLysSerProAlaSer---AspLeuLeuSerPheAspSerAsnLysIle 330  
 Db 1029 AATGTGAGGCGCATACAGCAATACCACTGGAGCTCATTAAGCTTCACTCCAAACAGGTG 1088  
 Qy 331 GlnSerGlnGlnValTyriHisGlyThrMetGlnGlnAspLysGlnProGluIleTyriLeu 350  
 Db 1089 GAAAC-----CATGGCTTGTGGAACCTGATGATAAACCCACTGTTGTTTAT 1136  
 Qy 351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGlnGlnGlnSerLeu--- 369  
 Db 1137 ACAATCACTAATCTTCAAGATTAATATGCTGAGACATTCAGACAGAAATTTTGTCTGGGG 1196  
 Qy 370 -----AspValGlyThrIleGlnPhe----- 376  
 Db 1197 AACTCTCTTGAATCCAGATCTGATTCCTCGACGCTTATCATAGTGAAGAGAGTTTG 1256  
 Qy 377 -----ThrAspGluIle-----AlaGlySerLeuProAlaPheGly 388  
 Db 1257 CGTCAACCAACTGAATCTAGTTTGAACACCCAAAGTTCAAGTCTTCAAGCA---ACG 1313  
 Qy 389 ProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGlnAspAlaThrLeu 408  
 Db 1314 CGGTCACTCTAT-TCGTGCTTCAACTGCTGCTGCTGCTGCTTCAAGAAAGAGACTTCT 1372  
 Qy 409 SerProGluLeuProProValGlnProGlnLeuGluThrValAspGlyValGlu----- 426  
 Db 1373 GGATCTCACTTG-----GTAGAAGATGATTTAGCAATGTTGAAGAGTCAGAAAGTTT 1426

Qy 427 -----HisGlyLeuProAspThrSerTTPSerProProAlaMetAlaSerThr--- 442  
 Db 1427 CTTTCTATTGATTCAATGCTTCATTCCTTCACTTCAACCTGTGCCAAAGAAACAATA 1486  
 Qy 443 -----SerLeuSerGlnAlaPro----- 448  
 Db 1487 CCATCAGTGAAGAGACTGTCATGTGTCCTTACATCTTCCATATCTGACCTTCTTATA 1546  
 Qy 449 ProphePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMet 468  
 Db 1547 CTTTGTGGCTTGAGCTCTTGTGACCTCAAGTCAAAGACCAATTAAGTAGCCCTTTC 1606  
 Qy 469 AlaThrAspGlnThrMet----- 474  
 Db 1607 CTGCCAGATGACCTCATGAAAAAGATTAAATTTGACGGTGTATTAGTTCAAGGCTCT 1666  
 Qy 475 -----LeuValProGlyLeuThrIleProThrSerAspTySerAlaIleSerGlnLeu 492  
 Db 1667 GGGCAAAAGTATGATCTGATTTACTTGGCCATGAGTGAAGACTTCACTCA---GAGAAAGCC 1723  
 Qy 493 AlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAlaGlyGly 512  
 Db 1724 GCTGAACACATGTCCAGCGCGGTGAAATGATGATTCATTTTGCCACCTGAGATT 1783  
 Qy 513 GluAsp-----MetValArgHisLeuAspGlnMetAsp----- 523  
 Db 1784 GAAGCAAGAAACTAGTTTATGTTGACAAATGATTCACAGACCAATTAATGAAGCAC 1843  
 Qy 523 ----- 523  
 Db 1844 TCAGAAATATGAACATGATGACATCCATCACTTCCAGAGAAAGCCTTTAGTGGG 1903  
 Qy 524 -----LeuSerAspThrProAlaPro----- 530  
 Db 1904 CTTGCTGTGCCATCTTGCGACATATCTGAGCTGAATGCGCTCTTAACCTCCCAAG 1963  
 Qy 531 -----SerGlnValProGlnLeuSerGluTyriValSerValProAspHisPheLeuGlu 548  
 Db 1964 CACATATCAAGATGATCTCGGTGTGATGATTAATCACTGATTAACCAAGCAGCTCTTATACG 2023  
 Qy 549 AspThrThrProValSerAla----- 555  
 Db 2024 ACATCTGAGCAATCTGCGCTTACTGATTAATATGATCAGGAGAGTCCATCTTAAG 2083  
 Qy 556 -----LeuGlnTyriIleThrThrSerSer----- 563  
 Db 2084 GAGGATATGAACAATTAATTAAGTCAATCCAACTATGATGTTGACAGTGAAGTTTCA 2143  
 Qy 564 -----MetThrIleAlaProLysGlyArgGlu----- 572  
 Db 2144 ATGTAAAGCCAGATATGCAAACTTTGTGACTATATTTGCCAGAAATCAGAGAGATTGG 2203  
 Qy 572 ----- 572  
 Db 2204 ACAAGAACTTCTTCCCTAGAGAAATTTGCCAGAGACATATTTGGCAAGTACACACAGAGT 2263  
 Qy 572 ----- 572  
 Db 2264 GGTGACAGGCTGTGTTATCTGTGACAGAGTCAACAAATTGCTCAACACAAATCTCC 2323  
 Qy 572 ----- 572  
 Db 2324 ACCCTGTAGAGATGAAGTAATTAATGGGTGTAAGATATTTTGTGAACTGACCGG 2383  
 Qy 572 ----- 572  
 Db 2384 ATAGGACAGATTACTATCAGCTGAGCAAGTCCAAAGACAAATGSCAAGTGTGATCT 2443  
 Qy 572 ----- 572  
 Db 2444 TATGTGAATATGTCAACAAAGTGTCACTCCACAGAGATGTTAGTGTGGCTTGCCCA 2503

QY 573 -----LeuValValPhePheSer 578  
 Db 2504 GAAGAGAGATGATCTGATTATACCGAGACTTCAGAGCTTTGGTGTCTTTCTTCAGC 2563  
 QY 579 LeuValValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyr 598  
 Db 2564 CTCGAGGTACTCAACATGATGTTTTCAGAAAGATCTGTTTAATAAAACCTCTTGAGATAT 2623  
 QY 599 ATGAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuAspSerAsnLeuThr 618  
 Db 2624 AAAGCCTGAGAACAGATTTCTTGAATGTGGTTCCTATCTCCAGTCAAAATCTCAGC 2683  
 QY 619 GlyPheLysGlnLeuGluLysLeuAsnPheArgAsnGlySerValIleValAsnSerLys 638  
 Db 2684 GGGTTCGAACACTTGAATTCCTCAACTTCAGAAATGGCAGCATTTGGTGTGAACGTGA 2743  
 QY 639 MetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGlu 658  
 Db 2744 ATGAAGTTTGCATATCTGTCTCTCTCAACGTCAACATGCGGTGTATGATCTTGGA 2803  
 QY 659 AAPPheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluLysAspSerTyrSerLeuAsn 678  
 Db 2804 GACTTTGTACCACTGCTTCAATACCATGAACTTGCTTATGATTAATCTCTTGAT 2863  
 QY 679 IleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGln 698  
 Db 2864 GTGGAATCAGGTGATGAACCAACCTTCCAAAGTTTCAGGCTGTAAATGATTTTCAGAA 2923  
 QY 699 -CysValLysAsn-GluArgThrGluGlnAlaGluCysArg 711  
 Db 2924 GTGTCTGTCAACCCCTGAGAGTGAAGAAACAAAGTCAGAA 2964

## RESULT 12

us-10-007-270-23  
 / Sequence 23, Application US/10007270  
 / Publication No. US20020160954A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Hageman, Gregory S.  
 / APPLICANT: Kuehn, Markus H.  
 / APPLICANT: University of Iowa Research Foundation  
 / TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 / FILE REFERENCE: 020618-000120US  
 / CURRENT APPLICATION NUMBER: US/10/007,270  
 / CURRENT FILING DATE: 2001-11-08  
 / PRIOR APPLICATION NUMBER: US 09/430,195  
 / PRIOR FILING DATE: 1999-10-29  
 / PRIOR APPLICATION NUMBER: US 09/183,972  
 / NUMBER OF SEQ ID NOS: 37  
 / SOFTWARE: Patentin Ver. 2.1  
 / SEQ ID NO 23  
 / LENGTH: 4204  
 / TYPE: DNA  
 / ORGANISM: Mus sp.  
 / FEATURE:  
 / OTHER INFORMATION: Mouse IPM 200 cDNA sequence (partial)  
 / NAME/KEY: misc\_feature  
 / LOCATION: (1)..(4204)  
 / OTHER INFORMATION: n is a, c, g, or t.  
 / us-10-007-270-23

## Alignment Scores:

Pred. No.: 2,26e-70 Length: 4204  
 Score: 841.00 Matches: 261  
 Percent Similarity: 41.20% Conservative: 123  
 Best Local Similarity: 28.00% Mismatches: 238  
 Query Match: 20.43% Indels: 310  
 DB: 5 Gaps: 34

us-10-007-270-2 (1-797) x us-10-007-270-23 (1-4204)

QY 96 TTTTArgLeuArgValCysGlnGlnAlaValITrgLualatArgIlePheLeuAsp 115

Db 21 TATTTAAAGCCGAGTGTGCAGAGAACCATCTCGGAAGCCTTCAGACGTTTGGAT 80  
 QY 116 ArgIleProAspThrGlyGluTyrGlnAspTyrPylSerIleCysGlnGlnLthrPhe 135  
 Db 81 CGACTTCTGGCCGTGATGAATATCTGTCATCGAATGAATTTATGTGAGATGAGTCA 140  
 QY 136 CysLeuPheAspIleGlyLysAsnPheSerAsnSerGlnGlnAlaLeuAspLeuGln 155  
 Db 141 AGCTATTTGAATGGGCCCATTTTGTAGCTGTGTGGAACATGAAACCTTATCATG 200  
 QY 156 GlnArgIle-----LysGlnArgSerPheProAspArgLysAspGluLysSerAla 172  
 Db 201 AAGAAACCTGGCTTACACAAAGGAAGCTGAGACAGCTCTCGAAGATCAG---TCTGT 257  
 QY 173 GluLysThrLeuGlyLysPro-----GlyLysThrIleValIleSerThrAspVal 189  
 Db 258 GGGCCTGAGTTGTCTTTCAGTTCCTATTGTGTGAGCC-----TCAACCTGACA 308  
 QY 190 ALAAsnValSerLeuGlyProPhePro-----LeuThrPro 201  
 Db 309 GGTGCTGTCTCAGTCTTCTTATCCAGAGTTGGCTTGGAGAGCGCAGCTCAGC 368  
 QY 202 AspAspThrLeuLeuAsnGluLysLeuAspAsnThrLeuAsnAspThrLysPheProThr 221  
 Db 369 CAGAGAGATATCAGCAATGAATTT---GAGATGTGACAGAGAGCCACACCAACAGCT 425  
 QY 222 ThrGluArgGluThrGluPheAlaValLeuGluGlnGlnArgValGluLeuSerValSer 241  
 Db 426 GCTGAACAGATTGCGGAATTC-----AGCATTCAA 455  
 QY 242 LeuValAsnGlnLysPheLysAlaGluLeuLysAspSerGlnSerProTyrTyrGlnGlu 261  
 Db 456 CTTCTGGGAAAGCATATACATGAGAACTCGGGATTCCTCCAGCGCCCTTACCGGCTC 515  
 QY 262 LeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLys 281  
 Db 516 CTCGGGAAGAGATTATTTACAGAGGTGAAAAAGCATTCACAGGGTTACTCGGTACAAAG 575  
 QY 282 LysIleHisValLeuGlyPheArgProLysGlyLysAspGlySerSerSerThrGlu 301  
 Db 576 GGCATCCGCTGTTCTGGAATTCAGGGCCCCCGGAGAAATGACAGTGGATGATGTTGAC 635  
 QY 302 MetGlnLeuThrAlaIlePheLysArgHisSerAlaGlnAlaLysSerProLysSer--- 320  
 Db 636 TATGAGATTACC-----TTCAATGCGAAGCATACAGAAATCCACTCGG 680  
 QY 321 AspLeuLeuSerPheAspSerAsnLysIleGlnSerGlnGluValTyrHisGlyThrMet 340  
 Db 681 GACCTCATTAAGCTTCACTCCACCAAGGTAGAAAC-----CATGGCTTGTGA 728  
 QY 341 GlnGluAspLysGlnProGluLysTyrLeuThrAlaThrAspLeuLysArgLeuLysSer 360  
 Db 729 GAGATGATGATTAACCCACCTGCTGTATACATTAATTAATTAATTAATTAATTCCT 788  
 QY 361 LysAlaLeuGluGlnGlu-----GlnSerLeuAspVal----- 366  
 Db 789 GAGACGCTGCACCAAGAACTTTTGAATGGAAATTCCTTTGATCCAGATCCCAAGCT 848  
 QY 367 -----GlnSerLeuAspVal----- 371  
 Db 849 CTCGACATCATCATATGTAGAGAGATTGTTGCTCCGCCCAACAGAAAGACATGTTGGAAC 908  
 QY 372 -----GlyThrIleGlnPheThrAspGluLysIleGlySerLeuProAlaPheGly 388  
 Db 909 ACCCAAGTTCAAGTCTCAGGTGACA-----ACATCTCTATTATTTGTTGCTTGA 959  
 QY 389 ProAsp-----ThrGlnSerGlnLeuProThrPhePheAlaValIleThrGluAspAla 406  
 Db 960 CTTGACCTGCTGCTGCTCTGAGGAAAGACTCTTGATCTGATCTTATTAAGATGGG 1019  
 QY 407 ThrLeuSerProGlu----- 411

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Db 1020 TTAGCAGACCTGAGAAATTAGAACTACTCTGATTGATGATGTGGCTTCAAGCCATTAA 1079
QY 412 -----LeuProValGlu----- 416
Db 1080 ATTCAACCTGTGCCAAMAGAAACAGTACCACTATGAGAACTGTGACACGGCTCTCTTG 1139
QY 417 -----ProGlnLeuGlu-----ThrValAsp---GlyAlaGlu 426
Db 1140 TCCACACCAACATCTGACCTCTTCTGTCTATAGAAACCTTACTAAGACATAGAGACACT 1199
QY 427 HisGlyLeu----- 429
Db 1200 TCTGGCTTGAGTCCCTGTGGCTTCAAAACATCTGACACCAAGTGGAGTATCCCATGCTTT 1259
QY 430 ProAspThrSer----- 433
Db 1260 CCAGACACCTCTGTGGAAAAAGACTTCAATTTTGAAGTGGCTTGGGTTCTGGGCTGGG 1319
QY 434 -----TrpSerProAlaMetAlaSerThr----- 442
Db 1320 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1379
QY 443 -----SerLeuSerGlnAlaPro----- 448
Db 1380 CCACGTCAAAAGTCAATGCTCTGAAGAACAGATGACATTAACCACTGAGGCTAGAGAA 1439
QY 448 ----- 448
Db 1440 AAATTACATATAGATGACAGAGTATGATCCACAGAACAAATTATTGAATCATCAGAACAT 1499
QY 448 ----- 448
Db 1500 AGATATGAGATAGAGCCCATACATTTATAGAGAAAGANTCCCATGTTAGATCTACTATA 1559
QY 449 ProPheMetAlaSerSer-----LeuPheSer-----LeuThr 460
Db 1560 CCCATCTTGTAGAGTCCGCAACTCCACCTACATCTCCATCTTTTCAAAAACACTTCA 1619
QY 461 AapGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValPro---GlyLeu 479
Db 1620 GATGTACACAGACATTTGATTTACTTACCTACCAAAACACCCCTTCTTACCGGTAATA 1679
QY 480 ThrIleProThrSerAspThrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499
Db 1680 GCAATCCCTGCTTCCATTAAGAAAACAGATGAGTATCTTAAGAGAAATATGTTACATACA 1739
QY 500 ProAlaSerSerAsp-----AspSerArgSerSerAlaGlyGlyIleAspMet--- 515
Db 1740 GAATCATCTCACTCAAAAGAACTTGACAGTGAAGTTCACAGTGTCAAGGCCAATATGACG 1799
QY 516 -----ValArg 517
Db 1800 CCTGTGTGACCATGTGTGCCAGAAATCAGATACAGTTTGGACAAGAACTTCTCTTAAAGG 1859
QY 518 HisIleAspGlnMetAspLeuSerAspThrPro----- 528
Db 1860 AAATGTGTCAGAGACACATTTGGCAGATACACAGAGAGACATGACAGACTCTGTGGAAA 1919
QY 529 -----AlaProSerGlnValPro-----GlnLeuSerGln 538
Db 1920 GCTTCCATGACACAGTCCACTGATATGCTTCAACCAACCCACTCCACCCAGCTAGAGAG 1979
QY 539 TyrValSerVal----- 542
Db 1980 GAAGTAATAATAGCGGTCCAGATATTTCAATTAGAACTAGATCAGGTAGGCACAGATTAT 2039
QY 543 -----ProAspHisPheLeuGlnAspThr 550
Db 2040 TATCAGTCCGAGCTAATGAGAACAAACATGCGCAAGCTGACATATGTGGAATATGCTCT 2099
QY 551 ThrProValSerAlaLeuGlnIleThrThrThrSerSerMetThrIleAlaProGlyGly 570
Db 2100 ACCAGTGT-----CACTACACAGAGATGCTTATTTGTGCTCTGCCCAAAAAGAA 2150

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QY 571 -----ArgGlnLeuValValPhePheSerLeuArgVal 581
Db 2151 GGTGTTCTGAGTACACACCAGACCTGACAGAGCAGTGGTGTCTTCTTCAAGCTCCGCGG 2210
QY 582 AlaAsnMetAlaPheSerAsnAspLeuPheAsnIleValSerSerLeuGluIleTyrArgAlaLeu 601
Db 2211 ACMAACATGTTGTTTTCAGAAAGACTTGTTTTAAACAAAACCTCTTGGAAATATTAAGCCCTG 2270
QY 602 GlnGlnGlnPheThrGlnLeuLeuValProTyrLeuAspGlnSerAsnLeuThrGlyPheIys 621
Db 2271 GAACAAAGATCTTATGAACCTGCTGCTCCATCTCCAGTCAAAATCTGACAGGTTCCAG 2330
QY 622 GlnLeuGlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerIleMetIysPhe 641
Db 2331 AACCTGAAGAAATCTGAGTTTCAGAAACGGACGACATGTGTGTGAACAGCCGAGTGAAGTTC 2390
QY 642 AlaIysSerValProTyrAsnLeuThrIysAlaValHisGlyValLeuGlnAspPheArg 661
Db 2391 GCCGAGTCTGCCCTCTTAATGTCAACAAAGCCATGTATAGGATTTCTGAAAGACTTTTGT 2450
QY 662 SerAlaAlaAlaGlnGlnLeuHisIleLeuGlnIleAspSerTyrSerLeuAsnIleGlnPro 681
Db 2451 ACCACTGCTTACCAAAACCATGACATCTGATATGATTAAGTACTCCCTGAGCGTGAATCA 2510
QY 682 AlaAspGlnAlaAspProCysIysPheLeuAlaCysGlyGlnPheAlaGlnCysValIys 701
Db 2511 GGTGTAGAGGCCAACCTTGGCAAGTTTCAGCTGTATATGAATTTCTGAGGTGTGGTA 2570
QY 702 AsnGlnIleGlnGlnIleGlnIleCysArgCysIysProGlyTyrAspSerGlnIle--- 720
Db 2571 AATCCATGAGTGAAGGAAAGCAAAAGTCAACCTCGGTATACCTGATGTGATGA 2630
QY 721 -----SerLeuAspGlyLeuGlnIlePheCysGlyProGlyThrIysGln 736
Db 2631 CTGCTTGTCAAAAGCTCTGTGATCTTACAGCTGACTCTGTGTTAAGATGAAG---- 2687
QY 737 CysGlnValLeuGlnGlyIysGlyAlaProCysArg 748
Db 2688 TGTGACATTAATGCTGTGGCAGATGAGCCATTTGTAGA 2723

RESULT 13
US-10-972-079-61156/C
/ Sequence 61156, Application US/10972079
/ Publication No. US2005015317A1
/ GENERAL INFORMATION:
/ APPLICANT: MWI GENOMICS, INC.
/ APPLICANT: DENIS, Sue K.
/ APPLICANT: ROSENFELD, David
/ APPLICANT: KERR, Richard
/ APPLICANT: BATES, Stephen
/ APPLICANT: HOLM, Tom
/ TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEP
/ FILE REFERENCE: MW1110-2
/ CURRENT APPLICATION NUMBER: US/10/972, 079
/ CURRENT FILING DATE: 2004-10-22
/ PRIOR APPLICATION NUMBER: US 60/514,333
/ PRIOR FILING DATE: 2003-10-24
/ NUMBER OF SEQ ID NOS: 96631
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 61156
/ LENGTH: 592
/ TYPE: DNA
/ ORGANISM: Chicken 19866894321451_5
US-10-972-079-61156

Alignment Scores:
Pred. No.: 4,39e-14 Length: 592
Score: 248.50 Matches: 51
Percent Similarity: 69.89% Conservative: 14
Best Local Similarity: 54.84% Mismatches: 23
Query Match: 6.04% Indels: 5

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DB:          9          Gaps:          1
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QY 603 GlnGlnPheThrGlnLeu-----LeuValProTyrLeuArgSerAnLeu 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 CAAGCTTTCTGTCATTTGCCCTTGTTGTGCAGCTGTACCTTACCTTCAAGCAATCTA 224
QY 618 ThrGlyPheLysGlnLeuGlnIleLeuAnPheArgAnGlySerValIleValAnSer 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 223 ACAGGCTTCCGAATCTGGAATCCCTGAACTTCGAAATGCGAAGATGCTGTAACAGT 164
QY 638 LysMetLysPheAlaLysSerValProTyrAnLeuThrLysAlaValIleGlyValLeu 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 163 CGAATGAATTTGCCAAACCTGTRCTGAAATGTCACCAACGCTGTATATGATCTCTG 104
QY 658 GluAspPheArgSerAlaAlaIleGlnLeuHisLeuGlnIleAspSerTyrSerLeu 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 103 GAAGACTTCTGCACACCTGCMATATCACACCATGAACCTGCGCATTAATACTCTCTG 44
QY 678 AsnIleGluProAlaAspGlnAlaAspProCysLysPhe 690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 43 GATGTGAATCAAGTTAAAGATGCGAGGAAAGTACGGTTT 5
RESULT 14
US-10-972-079-61152/c
; Sequence 61152, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61152
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Chicken 19866894321451_1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(5)
; OTHER INFORMATION: n is any nucleotide
US-10-972-079-61152
Alignment Scores:
Pred. No.: 4,47e-14      Length: 599
Score: 248.50           Matches: 51
Percent Similarity: 69.89%      Conservative: 14
Best Local Similarity: 54.84%      Mismatches: 23
Query Match: 6.04%           Indels: 5
DB:          9          Gaps:          1
US-10-007-270-2 (1-797) x US-10-972-079-61152 (1-599)
QY 603 GlnGlnPheThrGlnLeu-----LeuValProTyrLeuArgSerAnLeu 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500 CAAGCTTTCTGTCATTTGCCCTTGTTGTGCAGCTGTACCTTACCTTCAAGCAATCTA 441
QY 618 ThrGlyPheLysGlnLeuGlnIleLeuAnPheArgAnGlySerValIleValAnSer 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 440 ACAGGCTTCCGAATCTGGAATCCCTGAACTTCGAAATGCGAAGATGCTGTAACAGT 381
QY 638 LysMetLysPheAlaLysSerValProTyrAnLeuThrLysAlaValIleGlyValLeu 657
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DB 380 CGAATGAATTTGCCAAACCTGTRCTGAAATGTCACCAACGCTGTATATGATCTCTG 321
QY 658 GluAspPheArgSerAlaAlaIleGlnLeuHisLeuGlnIleAspSerTyrSerLeu 677
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DB 320 GAAGACTTCTGCACACCTGCMATATCACACCATGAACCTGCGCATTAATACTCTCTG 261
QY 678 AsnIleGluProAlaAspGlnAlaAspProCysLysPhe 690
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DB 260 GATGTGAATCAAGTTAAAGATGCGAGGAAAGTACGGTTT 222
RESULT 15
US-10-972-079-61153/c
; Sequence 61153, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61153
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894321451_2
US-10-972-079-61153
Alignment Scores:
Pred. No.: 4,48e-14      Length: 600
Score: 248.50           Matches: 51
Percent Similarity: 69.89%      Conservative: 14
Best Local Similarity: 54.84%      Mismatches: 23
Query Match: 6.04%           Indels: 5
DB:          9          Gaps:          1
US-10-007-270-2 (1-797) x US-10-972-079-61153 (1-600)
QY 603 GlnGlnPheThrGlnLeu-----LeuValProTyrLeuArgSerAnLeu 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 443 CAAGCTTTCTGTCATTTGCCCTTGTTGTGCAGCTGTACCTTACCTTCAAGCAATCTA 384
QY 618 ThrGlyPheLysGlnLeuGlnIleLeuAnPheArgAnGlySerValIleValAnSer 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 ACAGGCTTCCGAATCTGGAATCCCTGAACTTCGAAATGCGAAGATGCTGTAACAGT 324
QY 638 LysMetLysPheAlaLysSerValProTyrAnLeuThrLysAlaValIleGlyValLeu 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 CGAATGAATTTGCCAAACCTGTRCTGAAATGTCACCAACGCTGTATATGATCTCTG 264
QY 658 GluAspPheArgSerAlaAlaIleGlnLeuHisLeuGlnIleAspSerTyrSerLeu 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 GAAGACTTCTGCACACCTGCMATATCACACCATGAACCTGCGCATTAATACTCTCTG 204
QY 678 AsnIleGluProAlaAspGlnAlaAspProCysLysPhe 690
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DB 203 GATGTGAATCAAGTTAAAGATGCGAGGAAAGTACGGTTT 165
Search completed: January 15, 2006, 07:35:33
Job time : 1642 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2006, 04:07:16 ; Search time 350 Seconds

(without alignments)  
1843.002 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117  
Sequence: 1 MYLERRAIFWVIFLQVQV.....NSELLTVEYEFHNDWEN 797

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-CGN2\_1/USPTO.spo1/US10007270/runat.11012006.110807.10791/app.query.fasta.1.967  
-DB=Published Applications NA New -OPMT=fastcap -SUPFIX=trnbn -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USRR=US10007270.0CGN.1.122.0/runat.11012006.110807.10791  
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-LONGLOG -DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

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10: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	6.2	1219	6	US-10-750-185-30474
2	257	6.2	1219	6	US-10-750-623-30474
3	188.5	4.6	6245	6	US-10-401-3868-61
4	168	4.1	1288	6	US-10-750-185-46240
5	168	4.1	1288	6	US-10-750-623-46240
6	162	3.9	554	6	US-10-750-185-30481
7	162	3.9	554	6	US-10-750-623-30481
8	143.5	3.5	3741	7	US-11-044-899-1

9	140.5	3.4	2358	6	US-10-995-561-485	Sequence 485, App
10	140.5	3.4	2338	6	US-10-995-561-483	Sequence 483, App
11	140.5	3.4	3207	6	US-10-995-561-487	Sequence 487, App
12	140.5	3.4	3303	6	US-10-995-561-486	Sequence 486, App
13	140.5	3.4	3373	6	US-10-995-561-481	Sequence 481, App
14	140.5	3.4	3442	6	US-10-995-561-480	Sequence 480, App
15	140.5	3.4	3538	6	US-10-995-561-484	Sequence 484, App
16	138	3.4	10170	7	US-11-136-527-1817	Sequence 1817, App
17	137.5	3.3	2156	7	US-11-000-688-1488	Sequence 1488, App
18	136.5	3.3	2244	6	US-10-467-657-7103	Sequence 7103, App
19	136.5	3.3	2244	6	US-10-467-657-8035	Sequence 8035, App
20	135.5	3.3	2748	6	US-10-821-234-662	Sequence 662, App
21	133	3.2	4834	7	US-11-077-712-1	Sequence 1, Appl
22	133	3.2	9286	7	US-11-136-527-578	Sequence 578, App
23	131.5	3.2	7748	7	US-11-136-527-3397	Sequence 3397, App
24	131.5	3.2	7872	7	US-11-136-527-2235	Sequence 2235, App
25	130.5	3.2	5506	6	US-10-821-234-277	Sequence 277, App
26	130.5	3.2	5510	7	US-11-150-406-1	Sequence 1, Appl
27	129.5	3.1	5286	6	US-10-955-054A-61	Sequence 61, Appl
28	128.5	3.1	5085	7	US-11-052-554A-467	Sequence 467, Appl
29	128.5	3.1	921	6	US-10-401-386B-30	Sequence 30, Appl
30	127.5	3.1	3343	6	US-10-401-386B-32	Sequence 32, Appl
31	127	3.1	5795	7	US-11-136-527-3157	Sequence 3157, App
32	126.5	3.1	14770	6	US-10-821-234-268	Sequence 268, App
33	126	3.1	10211	7	US-11-000-688-98	Sequence 98, Appl
34	125.5	3.0	3656	6	US-10-947-249-138	Sequence 138, App
35	125	3.0	5054	6	US-10-821-234-123	Sequence 123, App
36	123	3.0	4070	7	US-11-000-688-134	Sequence 134, App
37	123	3.0	6900	7	US-11-000-688-1142	Sequence 1142, App
38	123	3.0	8512	7	US-11-124-368A-46	Sequence 46, Appl
39	123	3.0	10300	6	US-10-947-249-122	Sequence 122, App
40	122	3.0	6266	6	US-10-955-054A-24	Sequence 24, Appl
41	121	2.9	6035	7	US-11-136-527-3751	Sequence 3751, App
42	121	2.9	11598	7	US-11-124-368A-137	Sequence 137, App
43	121	2.9	11602	7	US-11-124-368A-136	Sequence 136, App
44	121	2.9	12678	7	US-11-124-368A-135	Sequence 135, App
45	120.5	2.9	3644	7	US-11-136-527-2438	Sequence 2438, App

#### ALIGNMENTS

RESULT 1  
US-10-750-185-30474  
; Sequence 30474, Application US/10750185  
; Publication No. US2005026063A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: PANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750.185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 30474  
; LENGTH: 1219  
; TYPE: DNA  
; ORGANISM: Bovine 19868880607526  
US-10-750-185-30474  
Alignment Scores:  
Pred. No.: 1.38e-13  
Score: 257.00  
Percent Similarity: 96.00%  
Best Local Similarity: 90.00%  
Query Match: 6.24%  
Length: 1219  
Matches: 45  
Conservative: 3  
Mismatches: 2  
Indels: 0

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QY 99 LeuAaGValCyGgInGUaLaVaITpGluAaITpAaGIllePheLeuAaPaArgIlePro 118
DB 1070 CTTCCAGTGTGCAGAGAGCGGTGTGGAGGCTTACCGGATCTTCTGGATGCTCCCT 1129
QY 119 AaPThrGluTyrGlnAspTrpValSerIleCyGgInGUaLThrPheCysLeuPhe 138
DB 1130 GAGCCGGGGGAATCCAGAGACTGGGTGACGCTTGTCCAGAGAGACCTTCTGCTCTTT 1189
QY 139 AaPileGlyLysAsnAspSerAsnSerGln 148
DB 1190 GACATCGGAAAAATTTCAGCAACTCCAG 1219

RESULT 2
US-10-750-623-30474
/ Sequence 30474, Application US/10750623
/ Publication No. US2005028751A1
/ GENERAL INFORMATION:
/ APPLICANT: MMT GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: M11100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30474
/ LENGTH: 1219
/ TYPE: DNA
/ ORGANISM: Bovine 1986680607526
US-10-750-623-30474

Alignment Scores:
Pred. No.: 1,38e-13 Length: 1219
Score: 257.00 Matches: 45
Percent Similarity: 96.00% Conservative: 3
Best Local Similarity: 90.00% Mismatches: 2
Query Match: 6.24% Indels: 0
DB: 6 Gaps: 0

US-10-007-270-2 (1-797) x US-10-750-623-30474 (1-1219)
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DB 1070 CTTCCAGTGTGCAGAGAGCGGTGTGGAGGCTTACCGGATCTTCTGGATGCTCCCT 1129
QY 119 AaPThrGluTyrGlnAspTrpValSerIleCyGgInGUaLThrPheCysLeuPhe 138
DB 1130 GAGCCGGGGGAATCCAGAGACTGGGTGACGCTTGTCCAGAGAGACCTTCTGCTCTTT 1189
QY 139 AaPileGlyLysAsnAspSerAsnSerGln 148
DB 1190 GACATCGGAAAAATTTCAGCAACTCCAG 1219

RESULT 3
US-10-401-386B-61
/ Sequence 61, Application US/10401386B
/ Publication No. US2005026121A1
/ GENERAL INFORMATION:
/ APPLICANT: Patrick Branigan
/ APPLICANT: Theresa J Goletz
/ APPLICANT: David M Knight
/ APPLICANT: Stephen G McCarthy
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/ APPLICANT: Bernard J Scallion
/ APPLICANT: Linda A Snyder
/ TITLE OF INVENTION: Nucleic Acid Compositions and Methods
/ TITLE OF INVENTION: for Use
/ FILE REFERENCE: GEN 310C1P
/ CURRENT APPLICATION NUMBER: US/10/401,386B
/ CURRENT FILING DATE: 2003-03-28
/ PRIOR APPLICATION NUMBER: 10/247,203
/ PRIOR FILING DATE: 2002-09-19
/ PRIOR APPLICATION NUMBER: 60/328,371
/ PRIOR FILING DATE: 2001-10-10
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 61
/ LENGTH: 6245
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (2767)...(3521)
/ OTHER INFORMATION: HCMV\ promoter
/ FEATURE:
/ NAME/KEY: polyA_signal
/ LOCATION: (47)...(241)
/ OTHER INFORMATION: SV40 PolyA
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (3525)...(4422)
/ OTHER INFORMATION: HCMV\IE\Introna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (4453)...(6241)
/ OTHER INFORMATION: MUC1\CDNA
/ FEATURE:
/ NAME/KEY: rep origin
/ LOCATION: (1589)...(2540)
/ OTHER INFORMATION: ori1
US-10-401-386B-61

Alignment Scores:
Pred. No.: 3.74e-06 Length: 6245
Score: 188.50 Matches: 85
Percent Similarity: 40.84% Conservative: 51
Best Local Similarity: 25.53% Mismatches: 126
Query Match: 4.58% Indels: 71
DB: 6 Gaps: 16

US-10-007-270-2 (1-797) x US-10-401-386B-61 (1-6245)
QY 385 ProAaPheGly-----ProAaPThrGlnSerGluLeuProThrSerPheAa 400
DB 4753 CCAAGCCAGGAGTGTACCTCGGCGCCGAGACACAGG---CCGCGCCCGGCTCCACCGCC 4809
QY 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProPro-----ValGlu 416
DB 4810 CCCCAGCCAGCGGTGTACCTCGGCGCCGAGACACAGCGCGCGCGGTCTCCACCGAA 4869
QY 417 ProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAaPThrSerTrpSerPro 436
DB 4870 CCCCAGCCAGCGGTGTACCTCGGCG-----CCGAGACACAGCGCGCGCGCG 4917
QY 437 -----ProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMetAla 453
DB 4918 GGCTTCACCCCGGCGCGCGCGCTCCAC-----GCCCGCCCA-----GCC 4956
QY 454 SerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThr 473
DB 4957 CACGGTGTCACTCGGCGCGCGAC-----ACC 4983
QY 474 MetLeuValProGlyLeuThrIleProThrSer-----AspTyrSerAlaIleSer 490
DB 4984 AGCGCGCGCGGCTTCACCGCGCCCGCCAGCCATGTGTCACTCGGCGCGCGCAAC 5043
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Db      94 GACATCATGCTGTGACATGGCGCATTTGTAG 62
RESULT 6
US-10-750-185-30481/C
/ Sequence 30481, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: BATES, Stephen
/ APPLICANT: HOLM, Tom
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30481
/ LENGTH: 554
/ TYPE: DNA
/ ORGANISM: Bovine 19866881169584
US-10-750-185-30481
Alignment Scores:
Pred. No.: 2,88e-05 Length: 554
Score: 162.00 Matches: 35
Percent Similarity: 75.00% Conservative: 7
Best Local Similarity: 62.50% Mismatches: 10
Query Match: 3.93% Indels: 4
DB: 6 Gaps: 1
US-10-007-270-2 (1-797) x US-10-750-185-30481 (1-554)
QY      221 ThrThrgluArgGluThrGluPhaAlaValLeuGlu-----GluGlnArgVal 236
DB      416 ACACAGGAAAGAAAATAATGAATTCACGAGATGCTGCTGACAGATGCACTGAGCAGAAAGTA 357
QY      237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256
DB      356 GAGCTAAGTATCTCTCTGCGAAACCGAAGTTCAAGTCAAGCTGATTAATCCAGTCC 297
QY      257 ProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLys 272
DB      296 CCGTATTACCGAGAGGTCCAGCCAAAGTCTCAGCTTCAGGTGAGCAAA 249
RESULT 7
US-10-750-623-30481/C
/ Sequence 30481, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 30481
/ LENGTH: 554
/ TYPE: DNA

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/ ORGANISM: Bovine 19866881169584
US-10-750-623-30481
Alignment Scores:
Pred. No.: 2,88e-05 Length: 554
Score: 162.00 Matches: 35
Percent Similarity: 75.00% Conservative: 7
Best Local Similarity: 62.50% Mismatches: 10
Query Match: 3.93% Indels: 4
DB: 6 Gaps: 1
US-10-007-270-2 (1-797) x US-10-750-623-30481 (1-554)
QY      221 ThrThrgluArgGluThrGluPhaAlaValLeuGlu-----GluGlnArgVal 236
DB      416 ACACAGGAAAGAAAATAATGAATTCACGAGATGCTGCTGACAGATGCACTGAGCAGAAAGTA 357
QY      237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256
DB      356 GAGCTAAGTATCTCTCTGCGAAACCGAAGTTCAAGTCAAGCTGATTAATCCAGTCC 297
QY      257 ProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLys 272
DB      296 CCGTATTACCGAGAGGTCCAGCCAAAGTCTCAGCTTCAGGTGAGCAAA 249
RESULT 8
US-11-044-899-1
/ Sequence 1, Application US/11044899
/ Publication No. US20050260616A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, M.
/ APPLICANT: Schwab, M.
/ TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
/ FILE REFERENCE: 10200-017-999
/ CURRENT FILING DATE: 2005-01-26
/ PRIOR APPLICATION NUMBER: US/11/044,899
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: 09/830,972
/ PRIOR FILING DATE: 1999-11-05
/ PRIOR APPLICATION NUMBER: PCT/US99/26160
/ PRIOR FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1
/ LENGTH: 3741
/ TYPE: DNA
/ ORGANISM: Rattus sp.
/ NAME/KEY: CDS
/ LOCATION: (253)...(3741)
US-11-044-899-1
Alignment Scores:
Pred. No.: 0.0265 Length: 3741
Score: 143.50 Matches: 158
Percent Similarity: 35.17% Conservative: 123
Best Local Similarity: 19.77% Mismatches: 283
Query Match: 3.49% Indels: 236
DB: 7 Gaps: 41
US-10-007-270-2 (1-797) x US-11-044-899-1 (1-3741)
QY      139 AsplleGlyLysAsnPhaSerAsnSerGlnGlu---HisLeuAspLeuLeuGlnGlnArg 157
DB      1111 GAAATGGATCATCTTTAAAGGCTCCCAAAAGAGAGTCAAGCATATTAGTAGAAAC 1170
QY      158 IleLysGlnArgSerPheProAspArgLysAsp-----GluLisSerAlaGluLysThr 175
DB      1171 ACTAAGAGAAAGTAATGTGTGAGAGTAAAGCAAGAGATTGTGTGATGTCAGCC 1230
QY      176 LeuGlyGluProGlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGly 195

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Db      1231 CTTGACAGTCCACAGAAATCACCTGTGGTAAAGAACAGAGT----- 1275
Qy      196  ProPheProLeuThrProAspAphThrLeuLeuAenGluLeuAenAphThrLeuAen 215
Db      1276 -----GTCTCTCCAGAAAAACAATG-----GACATTTTAAATCAATGACAGATG 1320
Qy      216  AepThrLyMetProThrThrGluArgGluThrGluPheAlaValLeuGlu----- 232
Db      1321 TCAGTAGTAGACACCTGTGAGGAGAGTAGACAGCTTTAAACCTTTGAACAAACATG 1380
Qy      233 -----GluGlnArgValGluLeuSerValSerLeuValAenGlnLys 246
Db      1381 GAAGTAAAGATACCTTATGAGGAGTAGGAGTAGGATGCTGCTGCTAGAGCTAATGTGAA 1440
Qy      247  PheLyValGlu-----LeuAlaAspSerGlnSerProTyrrGlnGluLeuAla 263
Db      1441 AGTAAAGTCGACGAAAAATGCTTGGAAGATAGC----- 1473
Qy      264  GlyLysSerGlnLeuGlnMetGlnLysIlePheLyValLeuProGlyPheLyValIle 283
Db      1474 -----CTGAGACAAAAAGCTCTGGAAAGATAGTGAAGCGCAAAATGAGAT 1521
Qy      284  HisValLeuGlyPheArgProLyValGlyLysAspGlySer----- 297
Db      1522 GCTTCTTTCCCAAGTACCAGAACCTGTGAAGGACAGCTCCAGAGCATATTAACCTGT 1581
Qy      298 -----SerSerThrGlnMetGlnLeuThrAlaIlePheLyValArg 310
Db      1582 GCTTCTTTTACTCAGCAACCGAAAGCACACAGCAAAACATTTCTCTTTGTTAGAAAT 1641
Qy      311  HisSerAlaGluAlaLysSerProAlaSerAsePheLeuSerPheAspSerAenLyValIle 330
Db      1642 CATACTTCGAAATTAACA-----GATGAAAAAAATA 1677
Qy      331  GluSerGlnLys-----ValTyrrHisGlyThrMetGlnGluAspArgGlnProGlu 347
Db      1678 GAAAGAAAGAGAGGCCCAATTTATACAGAGAAAGATGAGCCCAAAACGTCAAAATCTTTC 1737
Qy      348  Ile-----TyrLeuThrAlaThrAspLeuLyValArg--- 357
Db      1738 CTTGAGCAGTAGACGATTTCTGAGGACAGATGATGTTACAAAGATACCTTCAAAAGTG 1797
Qy      358 -----LeuIleSerLyVala 362
Db      1798 ACTGAGGACAGCTGTCAAAACATGCTGAGAGGTCTGAGCCGACAGATTGATGACAGAGCA 1857
Qy      363  LeuGlnGluGlnSerLeuAspValaGlyThr----- 373
Db      1858 TGTGAAGTGAATGAAATGAACCCACAGGTACAAAGATTGCTTATGAACAAAGTGAGAC 1917
Qy      374  ---IleGlnPheThrAspGluIleAlaGlySerLeu---ProAlaPheGlyProAspThr 391
Db      1918 TTGGTCAAAACATCAGAGCTATACAGATCATTTACCCACA----- 1962
Qy      392  GlnSerGlnLeuProThrSerPheAlaValIleThrGluAsePheAlaThrLeuSerProGlu 411
Db      1963 ---GCACAGCTTTGCCATCATTTGAG-----GAGCTGAAGCAACCTCCGTCACAGATT 2013
Qy      412  LeuProValaGluProGlnLeuGluThrValaArgValaGlnHisGlyLeuProAsp 431
Db      2014 TTGCTGTGATTT-----GTTATGGAAGACCACTTAATATCTCTCTTCCA 2058
Qy      432  ThrSerTyPseProProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePhe 451
Db      2059 AGCGCTGGGCTTCTGTAGTGACAGCTGATCCCACTGAGAGCACTCT----- 2112
Qy      452  MetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAsp 471
Db      2113 -----CCAGTTAGTTATGAC 2127
Qy      472  GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrrSerAlaIleSerGln 491

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Db      2128 AGTATAAGCTTGAGCTGAAGAACCCCCACCATATGAAAGACCATGATGATGACCTA 2187
Qy      492  LeuAlaLeu-----GlyTyrIleSerHisProProAlaSerSerAspAspSerArg 507
Db      2188 AAAGCTTTGGACAAAGAAAGAAATAAAGACCT-----GAAAGTTT 2232
Qy      508  SerSerAlaGlyGlyGlu-----AspMetValArg 517
Db      2233 AATGACGCTGTTCAGGAAACAGAAAGCTCTTATATATTCATTCATGCTGCTGATTTAATAA 2292
Qy      518  HisLeuAspGlnMetAspLeuSerAspThrProAlaPro-----SerGlnValaProGlu 535
Db      2293 -----GAAACAAAGCTCTCCACGTGAGCAAGTCAGATTCTTATATTACAGA 2343
Qy      536  LeuSerGlnTyrr---ValSerValProAspHis-----PheLeuGluAsePThrThrPro 552
Db      2344 ATAGCAAAATTCGAGAAAGTCCGTCGCCCAACACCTGAGTACGTAGTGCAGAGATTCCTCACCT 2403
Qy      553  ValSer---AlaLeuGlnTyrrIleThrThrSerSerMetThrIleAlaProLyValArg 571
Db      2404 GAATCTGAACAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCACAAACACAA 2463
Qy      572  GluLeuValValPhePheSerLeuArgValaIlaAspMetAlaPheSerAspAspLeuPhe 591
Db      2464 GAGGAGCGCTG-----ATGCTCATGAAGAGAGAGTCTCACT 2499
Qy      592  AsnLysSerSerLeuGlnTyrrArgAlaLeuGlnGlnPheThr-----Gln 607
Db      2500 GAAGTGTCTGACAGATGAGCCACACAAAGAGAGAGACTTAGTGCCTCAGCTCAGAGAG 2559
Qy      608  LeuLeuValProTyrrLeuArgSer-----AsnLeuThrGlyPheLyVal----- 621
Db      2560 CTAGGAAAGCCATTTTGAAGTCTTTTCAGCCCAATTTACATGACAAAGATGCTGCA 2619
Qy      622 -----GlnLeuGluIleLeu 626
Db      2620 TCTATATGACATTCACACATTCGCAAAAGAGAAATTTCTTGCAATGGAAGAGTTT 2679
Qy      627  Asn-----PheArgAsnGlySerValIleValAsnSerLyMetLyPheAlaLys 643
Db      2680 AATAGTCGAATTTATTCAAATGATGATGACTTACTTCTTCAAGAAACAAATTAAGAA 2739
Qy      644  SerValProTyrrAsnLeuThrLyValAlaValHisGlyValaLeuGluAsePheAspSer--- 662
Db      2740 AGTAAACATTTTCAGATCATCTCCGATTTGAG---ATAAATGATGAATTTTCCACGTTT 2796
Qy      663 -----AlaAlaIlaGlnGlnLeuHisLeuGlnIleAsp 673
Db      2797 GTGAGTGTAAAGATGATTTCTCTTAATTTAGCCAAAGAGTACACTGATCTGAAGTATCC 2856
Qy      674  SerTyrrSer-----LeuAsnIleGluProAlaAspGlnAlaAspProCyValAspPheLeu 691
Db      2857 GACAAAGTGAATTTGCAATATATCCAAAGCGGGCAGATTCATTCCTGCTTGAAATTTG 2916
Qy      692  AlaCyseGly---GluPheAlaGlnCyse-----ValLyPheAsnGlu 703
Db      2917 CCCGTGACCTTTCTTCMAAATATATATATCTTAAGATGAATGATGATTTTCAGATTA 2976
Qy      704  ArgThrGlnGluAlaGlnCyseArgCyseLyAspProGlyTyrrAspSerGlnGlySerLeuAsp 723
Db      2977 TTCTCCAAATATAGTCCAGTGTATCTTAAGGCAATCCAT---TGCCTTCAAAAGTCTCT 3033
Qy      724  GlyLeuGlnProGlyLeuCyseGlyProGlyTyrrLyGluCyseGlnValaLeuGlnGlyLys 743
Db      3034 GCTTTGGA-----CTTCAGACAGAAATGGCAGACATAGTTAAATCCAAA 3078
Qy      744  Gly-----AlaProCyseArgLeuProAspHisSerSerGlnAenGlnAlaTyrrLys 759
Db      3079 TCACCTTAGAAAGAGAGAAATAAATCTTCTTCTGACAGAGAAA----- 3126
Qy      760  ThrSerValLyValPheGlnAenGlnAenAsnLyValIleSerLyValArgAsnSer 779
Db      3127 -----GAGGACAGATCCCTGTACAGTGTATTTGTCTACAGAGACTGAGT 3168

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/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 483
/ LENGTH: 3138
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-483

Alignment Scores:
Pred. No.: 0.0387 Length: 3138
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conservative: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
DB: Gaps: 19

US-10-007-270-2 (1-797) x US-10-995-561-483 (1-3138)

QY 171 SerAlaGluLeuThrLeuGluProGluGluThrIleValIleSerThrAspValAla 190
DB 173 ACTGGGATCTCCAGAAAGAACCGACGAG-----CTAAGGCGCAGCGATGGCG 226
QY 191 AsnValSerLeuGluProPheProLeuThrProAspAspThrLeuLeuGluLeu 210
DB 227 GACGAGGCTTACCTGAGGCTG-----GATGAGGAGCCCTTCGAAAGCTG 274
QY 211 AspAspThrLeuAsnAspThrIleuMetProThrThrGluArgGluThrGluPheAlaVal 230
DB 275 GAGGTACGACGACATGTGGACAG-----CGGCGGCGCATCCGCTCAGCCATC 322
QY 231 LeuGluGluGlnArgValGluLeu-----SerValSerLeuValGlnGlnPhe 247
DB 323 CGGAACTGACGAGCGAGCTGAGCGCGAGAGAGCCCTTCGATCCAAAGCTTTC 382
QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyr-----GlnGluLeuAlaGlyLys 265
DB 383 CTTGCCAGCGGACGACACACAGAGAACTGCTCCTCAGCTCAGCGGAGGCTGAG 442
QY 266 SerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGluPheLysIleIleVal 285
DB 443 CAGCGGCTGCTCCGACGCGCTGCGAGGAGCTGAGTCCATGAACATTCGAGGAA 502
QY 286 LeuGluPheArgProLysLysGluLysAspGlySerSerSerThrGluMetGlnLeuThr 305
DB 503 TTG-----ACTGCACTGTTGCGAAGCGCTGAGTATGAGAGCGCAAGCTGATCCGA 556
QY 306 AlaIlePheLysArgIleSerAla-----GluAlaLysSerProAlaSerAspLeu 322
DB 557 GCTGCCATCCGCGGTACGGCTCAGAGATTTAGAGGCTGCCCTTGGCTGGAGTTG 616
QY 323 LeuSerPheAspSerAsnLysIleGlnSerGluGluValTyrHisGlyThrMetGlnGlu 342
DB 617 TACAGCGGCGCTCCCAAGT-----CGCTCAGAGAGAGAC 652
QY 343 AspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeu-----IleSerLys 361
DB 653 AGCAAGCGG-----CTAGCGGACACAGGCTGAAACAGTGAAGTGCAGAG 700
QY 362 AlaLeuGluGluGlnSerLeuAspVal-----GlyThr 373
DB 701 CGAGAGAAACAGGACAGGAGGATTTCMAAGCAACCCCAACCCCTGAAAGGACCC 760
QY 374 IleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSer 393
DB 761 AGCGAAGATGTACACACAGTACATCCCTGCGAGCC-----CAACTGGAGACATCC 817
QY 394 GluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuPro 413
DB 818 AGTCACTGCTCCCTACCCAGCAAGTTCAACCAACCCCTGCTCTGAGCTCATATTGAG 877
QY 414 ProValGluProGlnLeuGluThrValaAspGlyAlaGlnHisGlyLeuProAspThrSer 433
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DB 878 CCTGCGAGGCGCCATGCTTACAGTGA-----GTTCCAGGAGCCCAAGCAACCC 931
QY 434 TrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPheMetAla 453
DB 932 CCCAGCCCAACCAAGACACACAGCCCTGAGCTCAGAGTCTCCA----- 976
QY 454 SerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThr 473
DB 976 ----- 976
QY 474 MetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAla 493
DB 977 -----ACGCTCCCAAGCATGAGGCGCAKGTGTACAAGCTTTCG 1018
QY 494 LeuGlyIleSerHisProProAlaSer-----SerAspAspSer 506
DB 1019 TCTGGCCCCAAGAGACCCCTGCTGCCAGAGCCCAACCAAGAGCCCTGTACACCAAG 1078
QY 507 ArgSerSer---AlaGlyGlyLysAspMetValArgHisLeuAspGluMet----- 522
DB 1079 AAGAGACAGTGGCTGAGACCCCAAGCTCCCAAGCTCCCTGCTGAGTGTACGCCCCGC 1138
QY 523 -----AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu 538
DB 1139 CAACCAAGCCCAAGACCGAGATCCACCCCTTGGCAGCGACCTTCTCATTTCCAGCGG 1198
QY 539 TyrValSerValProAspHisPhe----- 546
DB 1199 GCTGCTGTGCGGAGTCGTGTCCCAAGTTACATGTGATTTCTATGCTGTAGG 1258
QY 547 LeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIle 566
DB 1259 CTCCAGATATGGACACCCCAAGCTGCTTAATGCTCGAACCCCGCAAGGCTC---CTG 1315
QY 567 AlaProLysGlyArgGluLeuValAlaPhePheSerLeuArgValAlaAsnMetAlaPhe 586
DB 1316 GGCCTCTCCCTACCAAGACCAACCCCTGCTCTCTTCCAGGAGGCTCTCTGCGGAGC 1375
QY 587 SerAsnAspLeuPheAsnLysSerSerLeuGlnTyrTyrAlaLeuGlnGlnPheThr 606
DB 1376 CCGAGTGAATACCTCTCCCGGTTTCAGAAAGAGCAAGAGTGAAGCCACCTTGAGC 1435
QY 607 GlnLeu 608
DB 1436 CAGCTT 1441

RESULT 11
US-10-995-561-487
/ Sequence 487, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CLO01559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 487
/ LENGTH: 3207
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-487

Alignment Scores:
Pred. No.: 0.04 Length: 3207
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conservative: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
DB: Gaps: 19
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US-10-007-270-2 (1-797) x US-10-995-561-487 (1-3207)
QY 171 SerAlaGluValThrLeuGluValProGluGluThrIleValIleSerThrAspValAla 190
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 ACTGGGAGATCTCCAGAAAGAACCGACGAG-----CTAGAGGCCAGCAGATGGCG 226
QY 191 AsnValSerLeuGluProPheProLeuThrProAspAspThrLeuLeuAsnGluIleLeu 210
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 GACGAGGCTTACCTGAGGCTG-----GATGAGGAGGCCCTTGGAAGCTGAGTGG 274
QY 211 AspAsnThrLeuAsnAspThrIlePheMetProThrThrGluArgGluThrGluPheAlaVal 230
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 GAGGTCAACAGCATCTGGCAGAG-----CGCGCGGAGATCCGCTCAGCAGCATC 322
QY 231 LeuGluGluGlnArgValGluLeu-----SerValSerLeuValAsnGluIlePhe 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 CGGGAAGTCCAGCGGAGAGCTGGAGCGCAGAGAGAGGCCCTGCGCATCCAGGCGTTTC 382
QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyr-----GlnGluLeuAlaGlyLys 265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 CCGTCCGAGCGGAGAGACAAACAGAACTGGCTGCACTCTCAGCAGCGGAGAGCTGAG 442
QY 266 SerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleVal 285
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 CAGCGGCGTGGCTGGCAGCGCTGGCAGGAGCTGAGTCCATGAGAAGATGGAGAGA 502
QY 286 LeuGlyPheArgProLysLysLeuLysValAspGlySerSerSerThrGluMetGlnLeuThr 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 503 TTG-----ACTGCACTGTGGCAAGCCGCTGGTGAATGATAGAGAGCGCACTGCCA 556
QY 306 AlaIlePheLysArgIleSerAla-----GluAlaLysSerProAlaSerAspLeu 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 GCTGCCATCCGCGGTACGGGCTCAGGAGATTTAGAGGCTGCCCATCTGGCTGGAGCTTG 616
QY 323 LeuSerPheAspSerAsnLysIleGlnSerGluGluValTyrHisGlyThrMetGlnGlu 342
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 617 TACAGCGGGCGTCCCAACAGT-----GGCTCAAGAGAGAGAC 652
QY 343 AspLysGlnProGluIleTyrIleuThrAlaThrAspLeuLysArgLeu---IleSerLys 361
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 653 AGCAAGAGGG-----CTAGCGGAGACAGAGCTGGAAACAGTGTGAGCTGCAGAG 700
QY 362 AlaLeuGluGluGlnSerLeuSerVal-----GlyThr 373
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 701 CAGAGAGAAACAGAAACAGAGCAAGGATTTCAAAACCAACCCCACTTAAAGGACAC 760
QY 374 IleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSer 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 761 AGCCAGGATGTGACCAAGTGAACATCTGCTGCGAGCC---CAACTGGAGACATCC 817
QY 394 GluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuPro 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 818 AGCTCACTGCTGCTCACCAGCAGATTCAACCCCTGCTCTCTGAGCTCCATCTGAG 877
QY 414 ProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSer 433
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 878 CTGCGGAGGCCAGTGCCTTACAGCTGAG-----GTTCCAGGACGCCCAAGGCCACCC 931
QY 434 TrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPheMetAla 453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 932 CCCAGGCCAACCAAGACCAAGCCCTGAGGCTCAGAGATGTTCA----- 976
QY 454 SerSerIlePheSerLeuThrAspGlnGlyThrAspThrMetAlaThrAspGlnThr 473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 976 ----- 976
QY 474 MetLeuValProLysLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAla 493
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 977 -----AGCTCCCAAGCACTGAGGCGCAGTGTGTCAACAGCTTCTG 1018
QY 494 LeuGlyIleSerThrAspProAlaSer-----SerAspAspSer 506
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 1019 TCTGCCCCCAAGAGACCTCTGCTGCCAGAGCCCAACABAGGCCCTGTGACACCAAG 1078
QY 507 ArgSerSer---AlaGlyGlyGluAspMetValArgHisLeuAspGluMet----- 522
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1079 AGAGAGAGCTGTGGAGTGGACCCCAAGCCCTGCCAAGCTCTCTGTGTGAGTCAAGCCCCGC 1138
QY 523 -----AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu 538
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1139 CAACCAAGCCCAAGAACCAAGATCCACCCCTTGCAGAGGACCTTCTCATTCAGAGCG 1198
QY 539 TyrValSerValProAspPhePhe----- 546
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1199 GCTGCTCTGTGGAGGATCGTGTCCACAAATTACATCTGATTCCTATGAGCTGTAGG 1258
QY 547 LeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIle 566
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1259 CTCAGAGTGGACACCCCAAGCTGCTTAAGTCCCTGACGCCCGCAAGGCTC---CTG 1315
QY 567 AlaProLysGlyArgGluLeuValAlaPhePheSerLeuArgValAlaAsnMetAlaPhe 586
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1316 GAGCCCTCTCCACCAAGACCAACCCCTGCTCTCTCCAGCGGCTCTCTCTGCGGCGC 1375
QY 587 SerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPheThr 606
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1376 CCAGTGAATACCTCTCTCCGCTTCAAGAGAGCAAGAGATGACCAAGCCCTGCGC 1435
QY 607 GlnLeu 608
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1436 CAGCTT 1441

RESULT 12
US-10-995-561-486
/ Sequence 486, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: C1001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 486
/ LENGTH: 3303
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-995-561-486

Alignment Scores:
Pred. No.: 0.0418 Length: 3303
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conservative: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
Gaps: 19

US-10-007-270-2 (1-797) x US-10-995-561-486 (1-3203)
QY 171 SerAlaGluValThrLeuGluValProGluGluThrIleValIleSerThrAspValAla 190
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 ACTGGGAGATCTCCAGAAAGAACCGACGAG-----CTAGAGGCCAGCAGATGGCG 226
QY 191 AsnValSerLeuGluProPheProLeuThrProAspAspThrLeuLeuAsnGluIleLeu 210
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 GACGAGGCTTACCTGAGGCTG-----GATGAGGAGGCCCTTGGAAGCTGAGTGG 274
QY 211 AspAsnThrLeuAsnAspThrIlePheMetProThrThrGluArgGluThrGluPheAlaVal 230
   ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 GAGGTCAACAGCATCTGGCAGAG-----CGCGCGGAGATCCGCTCAGCAGCATC 322
QY 231 LeuGluGluGlnArgValGluLeu-----SerValSerLeuValAsnGluIlePhe 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db      323 CGGAACTGACGGGCGACGCTGACCGCGGAGAGAGGCCCTTGACATCAAGCCTTC 382
Qy      248 LysAlaGluLeuAlaApsSerGlnSerProTyTyTyr-----GlnGluLeuAlaGlyLys 265
Db      383 CGTGGCGAGCGGCGACCAACAGAGAACTGCTGACTCTCAGCAGCGGAAAGCTGAG 442
Qy      266 SerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyLysIleLysVal 285
Db      443 CAGCGGCGCTCCCTGCGACGCTGGCGACGCGACCTGATCCATGAACGATGCGAGAA 502
Qy      286 LeuGlyPheArgProLysLysGlnLysApsGlySerSerSerThrGlnMetGlnLeuThr 305
Db      503 TTG-----ACTGCACCTGTCGACGAGCGCTGAGATGATGAGAGCGCAAGCTGATCCGA 556
Qy      306 AlaIlePheLysArgHisSerAla-----GlnAlaLysSerProAlaSerApsLeu 322
Db      557 GCTGCATCCGCGCTGACGCGCTGACGAGATTCAGGCTGCCACCTTGCGTGGAGGTTG 616
Qy      323 LeuSerPheApsSerSerLysIleGlnSerGlnLysValTyHisGlyThrMetGlnLys 342
Db      617 TACAGCGGCGCTCCCAACAGT-----GGCTCAAGAGAGAGAC 652
Qy      343 ApsLysGlnProGlnLysLeuTyLeuThrAlaThrApsLeuLysArgLeu---IleSerLys 361
Db      653 AGCAAGGG-----CTAGCGCGACACAGCGCTGAGACATGTGAGTGCCAGAG 700
Qy      362 AlaLeuGlnGlnGlnSerLysLeuApsVal-----GlyThr 373
Db      701 CGAGAGAAACAGAAACAGCAGCAGAGAGATTCAAGCAACCCCAAGCTGAAAGGACCC 760
Qy      374 IleGlnPheThrApsGlnLysIleAlaGlySerLeuProAlaPheGlyProApsThrGlnSer 393
Db      761 AGCCAGAGATGTGACCAACAGTGAACATCTGCTGCGAGCC---CCACCTGGAGACACATCC 817
Qy      394 GlnLeuProThrSerPheAlaValIleThrGlnApsAlaThrApsLeuSerProGlnLeuPro 413
Db      818 AGCTACCTGCTCCTACCCAGCACTTCAACCCAGCTGCTCTCTTCAAGCTCCATTCAGAG 877
Qy      414 ProValGlnProGlnLeuGlnThrValApsGlyAlaGlnHisGlyLeuProApsThrSer 433
Db      878 CTGCGCAGGCGCCAGTGCCTTACAGCTGAG-----GTTCCAGAGCAGCCAGAGCCACCC 931
Qy      434 TrpSerProProAlaMetAlaSerThrSerLeuSerGlnAlaProProPhePheMetAla 453
Db      932 CCCAGGCCACCCCAAGACCAACAGCCTGAGCCTCAGAGATCTCA----- 976
Qy      454 SerSerIlePheSerLeuThrApsGlnGlyThrThrApsThrMetAlaThrApsGlnThr 473
Db      976 ----- 976
Qy      474 MetLeuValProGlyLeuThrIleProThrSerApsTySerAlaIleSerGlnLeuAla 493
Db      977 -----ACGCTCCCAAGACTGAGAGGCCAGTGTCAACAAGCTTCG 1018
Qy      494 LeuGlyIleSerHisProProAlaSer-----SerApsApsSer 506
Db      1019 TCTGGCCCAAGAGAGACCCCTGCTGCCAGAGCCCAACAGAGCCCTCTGACCAAG 1078
Qy      507 ArgSerSer---AlaGlyGlyLysMetValArgHisLeuApsGlnMet----- 522
Db      1079 AGAGCAGACGTGCTGACACCCAGCCTGCAACGCTCCCTGCGTGTCTCAGGCCCCCG 1138
Qy      523 -----ApsLeuSerApsThrProAlaProSerGlnValProGlnLeuSerGln 538
Db      1139 CAACAGCCCAAGAACCGAGAGTCAACCCCTTGCAAGAGGACCTTCATTCAGCGG 1198
Qy      539 TyrValSerValProApsHisPhe----- 546
Db      1199 GCTGCGTCTGTGGGATGCTGTCCAAAGTTCAATTCATTCCTATGCTGTGCTAG 1258
Qy      547 LeuGlnApsThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIle 566

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Db      1259 CTCACGATGACGACACCCAGGCTGCTTAAGTCCCTTAAGTCCCGCAAGCTC---CTG 1315
Qy      567 AlaProLysGlyArgGlnLeuValValPhePheSerLeuArgValAlaApsMetAlaPhe 586
Db      1316 GGCCTCTCCCTCAACAGCAGACCAACCCCTGCTCTCTCTCCAGGAGCTCTCTCTCGGGG 1375
Qy      587 SerApsApsLeuPheApsLysSerSerLeuGlnTyTyArgAlaLeuGlnGlnPheThr 606
Db      1376 CCCAGTAACTCTCTCCGTTTCAGCAAGAGACAGAGATGACCCAGCCCTGACC 1435
Qy      607 GlnLeu 608
Db      1436 CAGCTT 1441

RESULT 13
US-10-995-561-481
; Sequence 481, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARILIL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 3373
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-481

Alignment Scores:
Pred. No.: 0.0431 Length: 3373
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conservative: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
DB: Gaps: 19

US-10-007-270-2 (1-797) x US-10-995-561-481 (1-3373)
Qy      171 SerAlaGlnLysThrLeuGlnLysProGlnGlnThrIleValIleSerThrApsValAla 190
Db      408 ACTGGGAGATCTCACCAAGAAAGAACGACGAG-----CTAGRGCCACGAGATGGG 461
Qy      191 ApsValSerLeuGlyProPheProLeuThrProApsApsThrLeuLeuApsGlnLysLeu 210
Db      462 GACGAGGCTTATGCTGCGCTG-----GATGAGGAGAGCCCTTCGAAAGCTGATG 509
Qy      211 ApsApsThrLeuApsApsPheThrLysMetProThrThrGlnArgGlnThrGlnLysValAla 230
Db      510 GAGGTCAACAGACACTGTGCAAG-----CGCGCGCAGATCCGCTCAGCCATC 557
Qy      231 LeuGlnGlnGlnArgValGlnLeu-----SerValSerLeuValApsGlnLysPhe 247
Db      558 CGGAACTGACGCGGACGAGAGCTGAGCGCGAGAGAGGCCCTTGCAATCCAGCCTTC 617
Qy      248 LysAlaGlnLeuAlaApsSerGlnSerProTyTyTyr-----GlnGlnLeuAlaGlyLys 265
Db      618 CGTGCCGAGCGGACAGACCAACAGAGAACTGCTGCACTCTCACAGCGGAGACTGAG 677
Qy      266 SerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyLysValLysValIleHisVal 285
Db      678 CAGCGGCGCTGCTGCGACGCTGCGACGAGCTGAGTCCATGAAGATGAGAGAA 737
Qy      286 LeuGlyPheArgProLysLysGlnLysApsGlySerSerSerThrGlnMetGlnLeuThr 305
Db      738 TTG-----ACTGCACCTGTCGACGCGCTGATGATGAGAGCGGAGCTGATCCGA 791
Qy      306 AlaIlePheLysArgHisSerAla-----GlnAlaLysSerProAlaSerApsLeu 322

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Db      996 AGCAGAGATGTGACACAGTACACTCTGCTGCGAGCC---CCACTCGGAGACATCC 1052
Qy      394 G|L|E|U|E|P|R|O|T|H|S|E|P|H|E|A|L|A|V|A|I|E|T|H|G|L|U|A|P|A|L|T|H|L|E|U|S|E|P|R|O|G|L|U|E|P|P|R|O 413
Db      1053 AGCTCACTGCTCCCTACCCAGCACTTCAACCCACCCCTGCTCTCTGAGCTCCATTCATGGAG 1112
Qy      414 P|R|O|V|A|L|G|U|P|R|O|G|L|U|E|G|U|T|H|P|H|E|A|L|A|V|A|I|E|T|H|G|L|U|A|P|A|L|T|H|L|E|U|S|E|P|R|O|G|L|U|E|P|P|R|O 433
Db      1113 CTGCGGAGGCCCTAGGCTTACAGCTAG---GTTCCAGAGGCCCGGAGGCCACCC 1166
Qy      434 T|P|S|E|P|P|R|O|L|A|E|T|A|S|E|T|H|S|E|L|U|S|E|S|E|G|U|A|L|E|U|G|I|N|G|I|N|P|H|E|T|A| 453
Db      1167 CCCAGGCCACCCAGACACACACACCCCTGAGCCCTCAGAGCTTCA----- 1211
Qy      454 S|E|S|E|T|L|E|P|H|E|S|E|L|U|T|H|A|P|G|I|N|G|I|N|T|H|A|P|T|H|E|T|A|L|A|T|H|A|P|G|I|N|T|H| 473
Db      1211 ----- 1211
Qy      474 M|E|L|L|E|U|V|A|P|R|O|G|L|U|E|T|H|L|E|P|R|O|T|H|S|E|A|P|T|Y|S|E|R|A|L|L|E|S|E|G|I|N|L|E|U|A| 493
Db      1212 -----ACGCTCCCGACACTGAGGCGCAGTGGTCAACAGCTTCTG 1253
Qy      494 L|E|U|G|I|L|E|S|E|T|H|A|P|P|R|O|L|A|S|E|-----S|E|A|P|A|P|S|E| 506
Db      1254 TCTGGCCCCAAGAGACCCCTGCTGCGCAGAGGCCCAACAGAGCCCTCTGACACCAAG 1313
Qy      507 A|P|G|S|E|S|E|-----A|A|G|I|G|L|G|U|A|P|M|E|T|V|A|A|H|G|I|A|E|U|A|P|G|L|U|E|T|----- 522
Db      1314 AAGAGCAGAGCTGCTGAGCCCGACCCCTGCGCAACGCTCCCTGCGGTGCTCAGCCCCCG 1373
Qy      523 -----A|P|L|E|U|S|E|A|P|T|H|P|R|O|L|A|P|R|O|S|E|G|I|U|A|P|R|O|G|L|U|E|S|E|G|I|U| 538
Db      1374 CAACAGCCCAAGAACGAGAGTCAACCCCTTGCAGCGGACCTTCTCATTCACGCG 1433
Qy      539 T|Y|V|A|S|E|T|H|A|P|R|A|P|H|E|----- 546
Db      1434 GCTGGCTCTGCTGGGATGCTGTCACAAAGTTCAATCTGATTCCTGCTGCTAGG 1493
Qy      547 L|E|U|G|U|A|P|T|H|P|R|O|V|A|L|S|E|A|L|E|U|G|I|N|T|Y|L|E|T|H|T|H|S|E|S|E|T|H|L|E| 566
Db      1494 CTCACGATGACACACCCAGGCTGCTTAAGTCCCTGACCCCGCAGGCTC---CTG 1550
Qy      567 A|A|P|R|O|L|G|I|A|P|G|I|U|E|U|A|I|A|P|H|E|S|E|L|U|A|A|A|A|E|T|A|A|A|E|T|A|A|P|H|E 586
Db      1551 GGCCTCTCCCTCAACAGACCAACCCCTGCTCTCTCCAGCGGCTCTCTCTCGGCGC 1610
Qy      587 S|E|A|A|P|L|E|U|P|H|E|A|N|L|Y|S|E|S|E|T|H|G|U|T|Y|A|I|A|L|E|U|G|I|N|G|I|N|P|H|E|T|H| 606
Db      1611 CCCAGTATACCTCTCCGCTTCAAGAAAGACAAAGAGTACCCGAGCCCTGCGCC 1670
Qy      607 G|I|N|L|E|U| 608
Db      1671 CAGCTT 1676

```

```

RESULT 15
US-10-995-561-484
; Sequence 484, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE. METHODS OF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 484
; LENGTH: 3538
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

US-10-995-561-484
Alignment Scores:
Pred. No.: 0.0463 Length: 3538
Score: 140.50 Matches: 103
Percent Similarity: 36.51% Conserved: 73
Best Local Similarity: 21.37% Mismatches: 203
Query Match: 3.41% Indels: 103
DB: 6 Gaps: 19

US-10-007-270-2 (1-797) x US-10-995-561-484 (1-3538)
Qy      171 S|E|A|L|G|U|T|H|L|E|U|G|I|U|P|P|R|O|G|L|U|T|H|L|E|A|L|L|E|S|E|T|H|A|P|V|A|A| 190
Db      408 A|C|T|G|G|A|G|A|T|C|A|C|A|G|A|A|G|A|C|C|G|A|G|-----C|T|A|G|G|C|C|A|G|A|G|G|G| 461
Qy      191 A|E|N|V|A|S|E|L|E|U|G|I|P|R|O|P|H|E|P|R|O|L|U|T|H|P|R|A|P|S|T|H|L|E|U|A|N|G|I|L|E|U| 210
Db      462 G|A|C|A|G|G|C|T|T|A|G|C|T|G|G|G|C|T|G|-----G|A|T|A|G|G|A|G|C|C|T|T|C|G|A|A|G|C|T|G| 509
Qy      211 A|A|P|A|N|T|H|L|E|U|A|N|A|P|T|H|L|Y|S|E|T|P|R|O|T|H|T|H|G|U|A|G|I|N|T|H|G|I|U|P|H|E|A|L|A|V|A| 230
Db      510 G|A|G|T|C|A|C|A|G|A|G|A|T|G|G|C|A|G|-----C|G|C|G|G|C|G|A|T|C|C|G|T|C|A|G|C|A|T|C| 557
Qy      231 L|E|U|G|I|U|G|I|A|P|V|A|G|I|U|E|U|-----S|E|A|L|S|E|L|E|U|A|A|N|G|I|N|L|Y|S|E| 247
Db      558 C|G|G|A|A|C|T|G|C|A|G|G|C|G|A|G|A|G|C|T|G|A|G|C|G|C|G|A|G|A|G|C|C|T|G|C|A|T|C|C|A|A|G|C|T|T|C| 617
Qy      248 I|Y|A|I|A|G|I|U|E|U|A|A|P|S|E|S|E|I|N|S|E|P|R|O|T|Y|T|Y|-----G|I|N|L|U|E|U|A|G|I|L|Y|S| 265
Db      618 C|G|T|G|C|G|A|G|C|G|C|A|G|A|C|A|C|A|G|A|A|A|C|T|G|C|T|G|C|A|C|T|C|A|C|A|G|C|G|G|A|G|C|T|G|A| 677
Qy      266 S|E|G|I|N|L|E|U|G|I|M|E|T|G|I|L|Y|L|E|P|H|E|U|Y|L|E|U|P|P|R|O|G|I|P|H|E|Y|L|L|E|I|L|E|V|A| 285
Db      678 C|A|G|C|G|G|C|C|C|T|G|C|A|C|G|C|G|C|G|C|A|G|G|C|A|G|C|T|G|A|T|C|C|A|T|A|A|C|A|G|A|T|G|A|G|A| 737
Qy      286 L|E|U|G|I|P|H|E|A|P|P|R|O|L|Y|L|E|U|Y|L|E|U|Y|A|P|G|I|Y|S|E|S|E|T|H|G|I|U|E|T|G|I|N|L|E|U|T|H| 305
Db      738 T|T|G|-----A|T|G|C|A|C|T|G|T|G|C|G|A|A|C|G|C|T|G|T|A|G|T|A|G|A|G|G|C|A|G|C|T|G|A|T|C|C|A| 791
Qy      306 A|A|I|E|P|H|E|Y|A|H|I|S|E|R|A|-----G|U|A|A|L|Y|S|E|P|R|O|L|A|S|E|A|P|L|E| 322
Db      792 G|C|T|G|C|A|T|C|G|C|G|G|T|A|C|G|G|C|T|C|A|G|A|G|A|T|T|A|G|G|C|G|C|C|A|C|C|T|G|C|T|G|G|A|G|T|T|G| 851
Qy      323 L|E|U|S|E|P|H|E|A|P|S|E|A|N|L|Y|L|E|U|S|E|G|I|U|A|I|T|Y|H|I|G|I|T|H|T|E|T|G|I|U|G|I| 342
Db      852 T|A|C|A|G|C|G|G|C|G|C|C|A|A|C|A|G|T|-----G|G|C|T|C|A|A|G|A|G|A|G|A|C| 887
Qy      343 A|E|P|Y|S|G|I|N|P|R|O|G|I|U|L|E|T|Y|T|E|U|T|H|A|L|A|T|H|A|P|L|E|U|Y|A|A|G|L|E|U|-----I|L|E|S|E|T|Y|S| 361
Db      888 A|G|C|A|A|G|G|G|-----C|T|A|G|C|G|C|A|C|A|G|C|T|G|A|A|C|A|G|T|G|A|G|T|G|C|C|A|G|A|G| 935
Qy      362 A|A|L|E|U|G|I|U|G|I|N|S|E|L|E|U|A|V|A|-----G|I|T|H| 373
Db      936 C|G|A|G|A|G|A|C|A|G|A|C|A|G|A|G|C|A|G|A|G|T|T|A|A|A|G|C|C|A|C|C|C|C|C|T|G|A|G|G|C|A|C| 995
Qy      374 I|L|E|I|N|P|H|E|T|H|A|P|G|I|U|L|E|A|A|G|I|S|E|T|E|U|P|R|O|A|L|A|P|H|E|G|I|P|R|O|A|P|T|H|G|I|N|S|E| 393
Db      996 A|C|C|A|G|A|G|A|T|G|T|A|C|A|C|A|G|A|C|A|C|T|C|T|G|C|G|A|G|C|-----C|C|A|C|T|G|A|G|C|A|C|A|T|C|C| 1052
Qy      394 G|U|L|E|U|P|R|O|T|H|S|E|P|H|E|A|L|A|V|A|I|E|T|H|G|L|U|A|P|A|L|T|H|L|E|U|S|E|P|R|O|G|L|U|E|P|P|R|O 413
Db      1053 A|G|T|C|A|C|T|G|C|T|C|C|C|A|G|C|A|G|T|T|C|A|C|C|A|C|C|C|T|G|C|T|G|A|G|C|T|C|A|T|T|G|A|G| 1112
Qy      414 P|R|O|V|A|L|G|U|P|R|O|G|L|U|E|G|U|T|H|P|H|E|A|L|A|V|A|I|E|T|H|G|L|U|A|P|A|L|T|H|L|E|U|S|E|P|R|O|G|L|U|E|P|P|R|O 433
Db      1113 C|T|G|C|G|A|G|G|C|C|A|G|C|C|T|T|A|C|A|G|T|A|G|-----G|T|T|C|A|G|G|A|G|C|C|C|A|G|C|C|A|C|C| 1166
Qy      434 T|P|S|E|P|P|R|O|L|A|E|T|A|S|E|T|H|S|E|L|U|S|E|S|E|G|U|A|L|E|U|G|I|N|G|I|N|P|H|E|T|A| 453
Db      1167 C|C|A|G|C|C|C|A|C|C|A|A|G|C|A|C|A|G|C|C|T|G|A|G|C|T|G|A|G|A|G|T|T|C|C|A|----- 1211
Qy      454 S|E|S|E|T|L|E|P|H|E|S|E|L|U|T|H|A|P|G|I|N|G|I|N|T|H|A|P|T|H|E|T|A|L|A|T|H|A|P|G|I|N|T|H| 473

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Db      1211 ----- 1211
QY      474 MetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAla 493
Db      1212 -----ACGGTCCCGCAGCAGCTGAGGGCCAGTGGTCAACAAGCTTCG 1253
QY      494 LeuGlyIleSerHisProProAlaSer-----SerAspAspSer 506
Db      1254 TCTGGCCCCAAGAAGACCCCTGCTGCTGCCAGAGCCCAACAGAGCCCTCTGACACCAAG 1313
QY      507 ArgSerSer--AlaGlyGlyGluAspMetValArgHisLeuAspGluMet----- 522
Db      1314 AAGAGCAGAGCTGGCTGAGACCCCGACCTGCAACGCTCCCTGCGGTCTCAGCCCCGCG 1373
QY      523 -----AspLeuSerAspThrProAlaProSerGluValProGlyLeuSerGlu 538
Db      1374 CAACCAGCCGAGAACCGAGAGTCCACCCCTTGGCCAGCGACTTCCTCATTCACGCGG 1433
QY      539 TyrValSerValProAspHisPhe----- 546
Db      1434 GCTGGCTCTGTGCGGGATGTCCTCCACAAGTTCACATCTGATTCTATGGCTGCTAGG 1493
QY      547 LeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIle 566
Db      1494 CTCGAGGATGGCACACCCCGAGGCTGCTAGTCCCTGACCCCGCAAGGCTC---CTG 1550
QY      567 AlaProIysGlyArgGlnLeuValAlaPheSerLeuArgValAlaAsnMetAlaPhe 586
Db      1551 GGCCCTCCCTCACCAGCACCACCCTGCTCTCTCCAGCGGCTCTCTCGGGGCG 1610
QY      587 SerAsnAspLeuPheAsnIysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThr 606
Db      1611 CCCAGTGAATACCTCTCCCGGTTCCAGCAAGAGCAACAGAGTGAAGCCCGCTGGCC 1670
QY      607 GlnLeu 608
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Search completed: January 15, 2006, 07:40:26  
Job time : 401 secs



XX 08-NOV-2001; 2001US-00077270.  
 PR (IOWA ) UNIV IOWA RES FOUND.  
 PA Hageman GS, Kuehn MH;  
 PI WPI: 2003-441440/41.  
 XX P-PSDB; ABR42342.  
 DR  
 XX New interphotoreceptor matrix proteins and polynucleotides, useful for  
 PT treating or preventing photoreceptor death or retinal detachment, or for  
 PT creating ocular disorders.  
 XX  
 XX Claim 1; Page 77; 105dp; English.

XX The present sequence is that of cDNA encoding isoform A of novel human  
 CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
 CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
 CC is located on chromosome 6q13-q15, a region that also contains loci for  
 CC progressive bilateral choroidretinal atrophy, autosomal dominant Stargardt's  
 CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
 CC disease. Members of the IPMC gene family have been identified in humans,  
 CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
 CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
 CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
 CC antibodies that specifically bind the polypeptides, and vectors  
 CC comprising the polynucleotides. A claimed method of treating or  
 CC preventing photoreceptor death or retinal detachment involves  
 CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
 CC claimed is a method for identifying a compound capable of modulating IPMC  
 CC gene expression

XX Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 0 Length: 3330  
 Score: 4073.00 Matches: 796  
 Percent Similarity: 97.31% Conservative: 0  
 Best Local Similarity: 97.31% Mismatches: 1  
 Query Match: 98.93% Indels: 22  
 DB: 9 Gaps: 1

US-10-007-270-2 (1-797) x ACC57946 (1-3330)

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 DB 131 ATGTATTGGAAGCTAAGAGAGCTATTTGTTTGGATTGTTCTCCAAAGTCAAGGA 190  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 DB 191 ACCAAGATATCTCCATTACATATACATCTCTGAAATCAAAAGACATACATACATCCCA 250  
 QY 41 ArgAsnGluThrThrgIuSerThrgIuLysMetTyrLysMetSerThrMetArgArgIle 60  
 DB 251 AGAAATGAAGAACAACGAAAGTACTGAAAAATGTACAAAATGCACTATGAGAGCAATTA 310  
 QY 61 PheAspLeuAlaIleHisArgThrLysArgSerAlaPhePheProThrGlyValIleVal 80  
 DB 311 TTCGATTGGAAGATGAAACMAAATCCGCAATTTTCCCAACGGGGGTAAAGTC 370  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaIleTyrTrpArgLeuArg 100  
 DB 371 TGTCCACAGAAATCCATGAACAGATTTTAGACAGCTTCAAGCTTATTAAGATTGACA 430  
 QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 431 GGTGTCAAGGAAGCAATATGGAGCAATCCGATCTTTCTGGATCGATCCCTGACACA 490  
 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 491 GGGGATATACAGATCGGGTCAAGCATCTCCAGCAGAGAGACCTTTCCTTTGACATT 550

QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgIleLeuGln 160  
 DB 551 GAAAAAATCTTACCAATTTCCCAAGAGCAGCTGGATCTTCTCCAGCAGAGATTAACAG 610  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluIleTrpLeuGlyGluProGly 180  
 DB 611 AGAAGTTTCCCTGACAGAAAAAGATGAAATATCTCGACAGAGAGACATTGGAGAGCTGGT 670  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 671 GAAACCATTTGCAATTTCAAC-AGCAATCTACATTTCAAGAAGCTTGGCGATATTCTAAGA 729  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 730 AAACCTCAGAGAGCAAAATTCAGATGTTCCCAAGCTCTCACTTGGGCTTTCCCTTC 789  
 QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
 DB 790 ACTCCTGATGACACCTCTCTCAATGAATTTCTCGATTAATACATCAACGACACCAAGATG 849  
 QY 220 ProThrTrpGluArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSer 239  
 DB 850 CTTACCAACAGAAAGAGAAACGAATTCGCTGTGGAGAGCAGAGGGTGAAGCTCAAGC 909  
 QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
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 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
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 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
 DB 1390 GCTGTTATAACAGAGAGATGCTTACTTGAAGTCAGAACTTCTCTGTTGAACCCAGCTT 1449  
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 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
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 QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
 DB 1570 ACTGATCAAGGACACACAGATACAAATGACCTGACCAAGAAATGCTAGTACCAAGGCTC 1629  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499

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Qy      520  AspGluMetAspLeuSerSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539
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Qy      540  ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559
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Db      1930 CTTGTTGCTAACATGGCTTCTTCCACAGACTGTTCACAAAGAGCTCTCGAGTACCGA 1989
Qy      600  AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAspLeuThrGly 619
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Qy      620  PheGlyGlnLeuGlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerIleMet 639
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Qy      640  LysPheAlaLysSerValProTyrAsnLeuThrValAlaHisGlyValLeuGluLeuAsp 659
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Qy      660  PheArgSerAlaAlaAlaGlnGlnLeuHisLeuGlnIleAspSerTyrSerLeuAsnIle 679
Db      2170 TTTGCTTGTGCGAGGCCCAACAATCTCCATCTGAAATATGACAGCTACTCTCAACAT 2229
Qy      680  GluProAlaAspGlnAlaAspProCysGlyPheLeuAlaCysGlyGluPheAlaGlnCys 699
Db      2230 GAACCAAGCTGATCAAGCAGATCCCTGCAAGTCTCTGGCCTGGCGGAATTTGCCAATGT 2289
Qy      700  ValLysAsnGluArgThrGlnGlnIleAlaGluCysArgCysLysProGlyTyrAspSerGln 719
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Qy      720  GlySerLeuAspGlyLeuGluProGlyLeuGlySerGlyProGlyThrLysGluCysGluVal 739
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Qy      740  LeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerSerGluAsnGlnAlaTyrLys 759
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Qy      760  ThrSerValLysLysPheGlnAsnGlnGlnAsnAlaValIleSerLysArgAsnSer 779
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KW      es; gene; human; IPMC 150 isoform A; gene therapy; disorder;
KW      interphotoreceptor matrix component; IPMC; ocular disorder;
KW      macular degeneration; photoreceptor death; retinal detachment.
OS      Homo sapiens.
Key      Location/Qualifiers
FT      CDS
FT      131..2586
FT      /tag= b
FT      /product= "IPMC 150 isoform A"
FT      /transl_except= (pos:689..756,aa:Thr-Asp)
FT      sig_peptide
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FT      /tag= c
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FT      misc_feature
FT      692..753
FT      /tag= d
FT      /note= "This region could represent intronic sequence not
FT      removed from the cDNA sequence."
PN      US2002160954-A1.
XX      31-OCT-2002.
PF      08-NOV-2001; 2001US-00007270.
XX      29-OCT-1998; 98US-00183972.
PR      29-OCT-1999; 99US-00430195.
XX      (IOWA ) UNIV IOWA RES FOUND.
XX      Hageman GS, Kuehn MH;
XX      WPI, 2003-238235/23.
DR      P-PsDB; ADA14841.
XX      PT      New isolated or recombinant interphotoreceptor matrix component
XX      PT      polynucleotide and polypeptide, useful for diagnosing, preventing,
XX      PT      treating or prognosticating ocular disorders, e.g. macular degeneration
XX      PT      or retinal detachment.
XX      PS      Claim 3; Page 29-30; 76pp; English.
XX      CC      The invention relates to an isolated or recombinant interphotoreceptor
XX      CC      matrix component (IPMC) polynucleotide. Also disclosed is a vector
XX      CC      comprising a promoter of an interphotoreceptor matrix component (IPMC)
XX      CC      gene operatively linked to the IPMC polynucleotide. The IPMC
XX      CC      polynucleotides, polypeptides and antibodies are useful for diagnosing,
XX      CC      preventing, treating or prognosticating ocular disorders, e.g. macular
XX      CC      degeneration, photoreceptor death or retinal detachment. They are also
XX      CC      useful for identifying a compound capable of modulating IPMC gene
XX      CC      expression in a cell. The present sequence represents cDNA encoding human
XX      CC      interphotoreceptor matrix component, IPMC, 150 isoform A.
SQ      Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 3330
Score: 4073.00 Matches: 796
Percent Similarity: 97.31% Conservative: 0
Best Local Similarity: 97.31% Mismatches: 1
Query Match: 98.93% Indels: 22
DB: 10 Gaps: 1
US-10-007-270-2 (1-797) x ADA14840 (1-3330)
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Qy      21  ThrLysAspLysSerLysLeuHisLeuTyrHisSerGluThrLysAspAlaAspAsnProPro 40

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Db 251 AGAAATGAAACAACGAAAGTACTGAAAAATGTCAAAATGTCAACTATGAGAGAAATA 310  
Qy 61 PheAPLeuAlaLyHhIeArgThrlyrsArgSerAlaPhePheProThrGlyValLyseVal 80  
Db 311 TTCGATTGGCAACATCGACATCAAAAGATCCGCATTTTCCCAACGGGGTTAAAGTC 370  
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Db 431 GTGTGTCAGGAAGACGTATGGAGCATATCGAATCTTCTGGATTCGCATCCCTGACACA 490  
Qy 121 GlyGluTyrgInApsTrpValserIleCysGInGInGluThrPheCysLeuPheApsIle 140  
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Qy 161 ArgSerPheProApsArglyAsnArgIleSerAlaGluLyseThrLeuGlyGluProGly 180  
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Qy 181 GluThrIleValIleSerThr----- 187  
Db 671 GAACCATTTGCTATTCAAC-AGCAATCTACATTTCAAGACTTGGGCGATTTCTAAGA 729  
Qy 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
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Qy 400 AlaValIleThrGluApsAlaIleThrLeuSerProGluLeuProProValGluProGlnLeu 419  
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Qy 500 ProAlaSerSerApsApsSerArgSerSerAlaGlyGlyAlaApsMetValArgHhIeLeu 519  
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Qy 620 PheLyseGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLyseMet 639  
Db 2050 TTTAAAGCACTTGAATACTTAATTCAGAAACGGAGATGTGATGTGAATAGCAAAATG 2109  
Qy 640 LysPheAlaLyseSerValProTyTyAsnLeuThrLyseAlaValHhIeGlyValLeuGluAps 659  
Db 2110 AAGTTTGTATAGTGTGTGCCATTAACCTTCAACCAAGCTGTGTGACGGGCTCTGAGGAT 2169  
Qy 660 PheArgSerAlaAlaIleGlnGlnLeuHhIeLeuGluIleApsSerTyTySerLeuAsnIle 679  
Db 2170 TTTCTGTTCTGCTGACGCCCAACTCCATCTGGAATATGACAGCTACTCTCTCAACTT 2229  
Qy 680 GluProAlaApsGlnAlaApsProCysLysePheLeuAlaCysGlyGluPheAlaGlnCys 699  
Db 2230 GAACCAAGCTGATCAAGCAGATCTCTGCAAGTCTCTGGGAGGAAATTTGGCCAAATGT 2289  
Qy 700 ValLyseAsnGluArgThrGluGluAlaGluCysArgCysLyseProGlyTyTyApsSerGln 719  
Db 2290 GTTAAAGAACGAAACGACATGAGGAAGCGAGTGTGCTGTCAAAACGATATGACAGCCAG 2349  
Qy 720 GlySerLeuApsGlyLeuGluProGlyLeuCysGlyTyProGlyThrLyseGluCysGlyVal 739  
Db 2350 GGGAGCTGTGACGGTCTGAAACAGAGCTCTGTGTGCTCTGACCAAAAGAAATGCGAGGTC 2409

Oy	740	LeuGInGlyLyvGGlyAlaProCYSAaGleuProAspHisSerGluabengInAlaYLyS	759
Db	2410	CTCCAGGGAGAAAGGAGCTCATGCAAGGTGGCCAGATCACTTGAAATATCAAGCATACAA	246
Oy	760	ThrsSerValLyLyvAspHegInaengInGInaAsnAsnLyvAlIleSerLySAaGAsnSer	779
Db	2470	ACTAGTGTAAAAAGTTCGAAATCAACAAATTAACAGGTAAATCGATTAAAAAAATTCT	2522
Oy	780	GIuLeuLeuThrValGInuTYrGInGInuIupheAsnHisGInaSPTrpGInuIyaen	797
Db	2530	GAATTACTGACCGGTAGATATGAAATGAATTTAAACATCAAGATTGGAGAGAAAT	2583
RESULT 3			
AAAA6205	ID	AAAA6205 standard; cDNA; 3263 BP.	
XX	AC	AAAA6205;	
XX	DT	04-SEP-2000 (first entry)	
DE		cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).	
XX	KW	Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;	
KW		chromosome 6q13-q15; ocular disease; retinal detachment;	
KW		chorioretinal degeneration; retinal degeneration; cone degeneration;	
KW		age related macular degeneration; photoreceptor degeneration;	
XX		retinal pigment epithelium degeneration; mucopolysaccharidosis;	
XX		rod- cone dystrophy; cone-rod dystrophy; ss.	
OS		Homo sapiens.	
XX			
FH	Key	Location/Qualifiers	
FT	CDS	128..2444	
FT		/*tag= a	
FT		/transl_except= (pos: 2411..2414, aa: Lys)	
FT		/product= "interphotoreceptor matrix proteoglycan IPM150"	
PN		WO200026367-A2.	
XX			
PD		11-MAY-2000.	
XX			
PF		29-OCT-1999; 99WO-US025440.	
XX			
PR		29-OCT-1998; 98US-00183972.	
XX			
PA		(IOWA ) UNITV IOWA RES FOUND.	
XX			
PI		Hageman GS, Kuehn MH;	
XX			
DR		WPI: 2000-365616/31.	
XX		P-PEDB; AAY93336.	
PT			
PT		Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for	
PT		preventing, diagnosing and treating ocular disorders such as retinal	
XX		detachment and chorioretinal degeneration.	
PS		Claim 2; Fig 3; 183pp; English.	
XX			
CC		The present sequence encodes an interphotoreceptor matrix (IPM)	
CC		proteoglycan, designated IPM150. The protein is an IPM component (IPMC).	
CC		Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene	
CC		is located on chromosome 6q13-q15, between markers CHLC.GAT11F10 and	
CC		D6S384. The IPM proteins may be used to supplement a patient's own	
CC		production of the protein or to rectify alterations in their nucleic	
CC		acids that result in expression of an inactive protein. The IPM nucleic	
CC		acids may be used in this way to treat ocular diseases such as retinal	
CC		detachment, chorioretinal degeneration, retinal degeneration, age related	
CC		macular degeneration, photoreceptor degeneration, RPE (retinal pigment	
CC		epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-	
CC		cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may	
CC		also be used to assay for other modulators of IPM proteoglycan expression	
CC		and activity that may be used to treat ocular diseases. The nucleic acids	

CC	and proteins may also be used as diagnostic reagents to detect the
CC	presence of 17M nucleic acids and their products in samples from patients
CC	according to standard methodologies
XX	
XX	
Sequence 3263 BP; 1040 A; 721 C; 663 G; 838 T; 0 U; 1 Other;	
Alignment Scores:	
Pred. No.:	4,92e-317 Length: 3263
Score:	4039.50 Matches: 794
Percent Similarity:	99.62% Conservative: 1
Best Local Similarity:	99.50% Mismatches: 2
Query Match:	98.12% Indels: 3
DB:	3 Gaps: 0
US-10-007-270-2 (1-797) x AAA46205 (1-3263)	
QY	1 MetTyrLeuGluThrArgArgAlaIlePheValIlePheThrIlePheLeuGlnValGlnGly 20
Db	128 ATGATTTTGGAACTTGAAGAGCTATTTTGTGTTTGGATTTTCTCCAAGTTCAAGCA 187
QY	21 ThrIlyAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
Db	188 ACTAAAGATATCTCCATTATACATATACCATTTGAAACCTAAAGACATATAGCATCCCCA 247
QY	41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60
Db	248 AGAAATGAACAACATGAAGAGTACTGAAAAAATGTCAAAATGTCAACTATAGACGATAT 307
QY	61 PheAspLeuAlaLysHisArgThrTyrValArgSerAlaPhePheProThrGlyValLysVal 80
Db	308 TTGCAATTTGGCAACACATCGAACAAAAAGATCCGATTTTCCCAACGGGGGTTAAAGTC 367
QY	81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
Db	368 TGTCACAGAGATCCATGAAACAGATTTTAAACAGCTTTCAAGCTTATATATGATTTAGA 427
QY	101 ValCysGlnGluAlaValIleTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
Db	428 GTGATCTCAGAAAGCATATGGGAAACATATCGATCTTTCTGATCGCATCCCTGACACA 487
QY	121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
Db	488 GGGGAATATCGAGACTGGGTGACATCTGCCAGCAGGAACCTTTCGCTCTTGTGACAT 547
QY	141 GlyLysAsnPheSerAsnSerGlnGlnIleLysLeuAspLeuGlnGlnArgIleLysGln 160
Db	548 GGAATAAACTTACGACATTTCCCGAGACACTTGATCTTCTCAGCAGGAATATAAACG 607
QY	161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGluGluProGly 180
Db	608 AGAGTTTCCCTGACAGAAAGATGAATATTTGCGAGAAACATTTGGAGAGCCTGGT 667
QY	181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db	668 GAAACCATATGTCATTTCAACAGATGTGCCAACGTCCTCACTTGCGCTTCCCTCCACT 727
QY	201 ProAspAspThrIleLeuAsnGluIleLeuAspAsnThrIleAsnAspThrLysMetPro 220
Db	728 CCTATATGACCCCTCTCTCAATGAATTTCTCGATATATACCTCAACAGACCAAGAGCCCT 787
QY	221 ThrThrGluArgGluThrGluPheAlaValLeuGlnGluGlnArgValGluLeuSerVal 240
Db	788 ACAACAGAAAGAAACAGAAATTCGCTGTGTGGAGAGACAGAGGTGAGCTCAGCGTC 847
QY	241 SerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGln 260
Db	848 TCTCTGGTAAACAGAAAGTTCAAGGCAAGCTCGCTGACTCCCAAGTCCCATATATACAG 907
QY	261 GluLeuValAsnGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPhe 280
Db	908 GAGCTAGAGAGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAACTTCACAGATTC 967
QY	281 LysLysIleHisValLeuGluPheArgProLysGluLysAspGluSerSerSerThr 300



CC newly identified interphotoreceptor matrix component (IPMC) gene family.  
 CC The cDNA was isolated from a human retinal cDNA library. The IMP 150 gene  
 CC is located on chromosome 6q13-q15, a region that also contains loci for  
 CC progressive bilateral chorioretinal atrophy, autosomal dominant Stargard's  
 CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
 CC disease. Members of the IPMC gene family have been identified in humans,  
 CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat [PM. 2  
 CC Subfamilies are designated IMP 150 (or IMPG1) and IMP 200 (or IMPG2). The  
 CC invention provides IMP 150 and IMP 200 polynucleotides and polypeptides,  
 CC antibodies that specifically bind the polypeptides, and vectors  
 CC comprising the polynucleotides. A claimed method of treating or  
 CC preventing photoreceptor death or retinal detachment involves  
 CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
 CC claimed is a method for identifying a compound capable of modulating IPMC  
 CC gene expression

XX Sequence 3261 BP, 1039 A, 721 C, 663 G, 837 T, 0 U, 1 Other;

## Alignment Scores:

Pred. No.:	6,896-316	Length:	3261
Score:	4024.50	Matches:	793
Percent Similarity:	99.62%	Conservative:	1
Best Local Similarity:	99.50%	Mismatches:	3
Query Match:	97.75%	Indels:	3
DB:	9	Gaps:	0

US-10-007-270-2 (1-797) x ACCS7960 (1-3261)

QY 1 MetTyrLeuGluThrArgAlaIlePheValIlePheThrIlePheLeuGlnValGlnGly 20  
 DB 128 ATGTAATTCGAAACATGAAAGAGCTATTTGTTTTTGATTTTCTCCAAATTCAGAGA 187  
 QY 21 ThrIleAspIleSerIleAsnIleTyrIleSerGluThrIleAspIleAspAsnProPro 40  
 DB 188 ACTAAAGATATCTCATTAACATATACCATCTCGAAACTAAAGACATGACATCCCCCA 247  
 QY 41 ArgAsnGluThrThrGluSerThrGluIleMetTyrIleMetSerThrMetArgArgIle 60  
 DB 248 AGAAATGAAACACTGAAAGTACTGAAAGAAATGTAACAAATCTCAACTATGAGAGAAATA 307  
 QY 61 PheAspLeuAlaIleValIleAspThrIleAspSerAlaPhePheProThrGlyValIleVal 80  
 DB 308 TTCGATTTGGCAAGACATCGAACAABAAAGATCCGATTTTCCCAACGGGGTTAAAGTC 367  
 QY 81 CysPProGlnGluSerMetIleGlnIleLeuAspSerLeuGlnAlaIleTyrIleArgLeuArg 100  
 DB 368 TGTCCACAGGAAATCATGAAACAGATTTAGACAGCTTCAAGCTTATATAGATTGAGA 427  
 QY 101 ValCysGlnGluValIleTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 428 GTGTCTCAGGAAGCAGTATGGAGACATATCGAATCTTCTGATCGCATCCCTGACACA 487  
 QY 121 GlyGluTyrGlnAspIlePheValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 488 GGGGAATTCAGGAGATGGGCTGAGCATCTGCCAGCAGAGACCTTCTGCTTTTACATT 547  
 QY 141 GlyIleAsnPheSerAsnSerGlnIleIleLeuAspLeuLeuGlnIleArgIleIleGln 160  
 DB 548 GGAATAAACTTCAGCAATTCCTCCAGAGACCTCGATCTTCTCCACAGAAATAAACAAG 607  
 QY 161 ArgSerPheProAspArgIleAspGluIleSerAlaGluIleThrLeuGlnGluProGly 180  
 DB 608 AGAATCTTCCTCCAGCAAGAAAGATGAATATCTGAGAGAAACATTTGGAGAGGCTGAT 667  
 QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 DB 668 GAAACCATTTGCTTCAACAGATGTTGCCACGCTCACTTGGGCTTTTCCCTTCACT 727  
 QY 201 ProAspAspThrIleLeuAsnGluIleLeuAspAsnThrIleAsnAspThrIleMetPro 220  
 DB 728 CCTGTATGACACCTCTCTCAATGAATATCTCGATTAATACCTCAAGACCAACAGATGCT 787  
 QY 221 ThrThrIleArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerVal 240

DB 768 ACAACGAAAGAAAGAAACGAATTCCTGTGTTGGAGGACAGAGGTGAGCTCAGCGTC 847  
 QY 241 SerLeuValIleGlnIlePheIleValIleGluLeuAlaAspSerGlnSerProTyrTyrGln 260  
 DB 848 TCTGTGTAAACCAAGAAATTCAGAGGACAGGCTCGCTGACTCCCACTTCCCATATTAACAG 907  
 QY 261 GluLeuAlaGlyIleSerGlnIleGlnIleMetGlnIleIlePheIleValLeuProGlyPhe 280  
 DB 908 GAGCTGAGAGGAAAGATCCCACTTCAGATGCAAAAGATATTTAAACATTCACAGATTC 967  
 QY 281 LysIleIleIleIleValIleGluIlePheArgProIleIleGluIleValIleAspGlyIleSerSerThr 300  
 DB 968 AAAAAATCCATGTCTTGTGATTTAGACCAAGAAAGAAAGAAAGATGCTCAAGCTCCACA 1027  
 QY 301 GluMetGlnLeuThrAlaIlePheIleValIleIleSerAlaGluAlaIleValIleSerProAlaSer 320  
 DB 1028 GAGATGCAACTTACCGGCATCTTTAAAGAGACACAGTCAGAAAGCAAAAGCCCTGCAAGT 1087  
 QY 321 AspLeuLeuSerPheAspSerAsnIleIleGluSerGluGluValIleTyrIleGlyThrMet 340  
 DB 1088 GACCTCCGTCTTTGATTCACAAAGAAATGAAAGTGAAGATCTATCATGGAACCAATG 1147  
 QY 341 GluGluAspIleGlnProGluIleIleTyrLeuThrAlaThrAspLeuIleValIleSer 360  
 DB 1148 GAGAGGACAGCAACCAAGAAATCTATCTCACAGTCAAGACCTCAAAAGGCTGATCAGC 1207  
 QY 361 LysAlaLeuGluGluGluGlnIleSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
 DB 1208 AAAGCATAGAGGAAGAAACAATCTTGATGTGGGGAACAATTCAGTTCACGTATGAATTT 1267  
 QY 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
 DB 1268 GCTGATATCACTGCCAGCTTTGGTCTCGACACCAATCAGAGCTGCCACATCTTTTCT 1327  
 QY 401 ValIleThrGluAspAlaIleThrLeuSerProGluLeuProProValGluProGluLeuGlu 420  
 DB 1328 GTTATACAGAGATGCTACTTGTAGTTCAGAACTTCTCTGTTGAAACCCAGCTTAG 1387  
 QY 421 ThrValAspGlyAlaGluIleGlyLeuProAspThrSerTyrSerProProAlaMetAla 440  
 DB 1388 ACAGTGAGCGAGGACAGCAATGCTATCTACCTACCTTGTGCTCCACCTGCTATGCC 1447  
 QY 441 SerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThr 460  
 DB 1448 TCTACTCTCCGTGAGAGAGCTCCACCTTCTTATGCGATCAAGCATCTTCTCTGACT 1507  
 QY 461 AspGlnGluThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThr 480  
 DB 1508 GATCAAGGACACACAGATACAAATGCGCACTGACAGAAATGCTAAGCCAGGGCTCAC 1567  
 QY 481 IleProThrSerAspIleValIleSerGlnIleValIleSerGlnIleSerIleProPro 500  
 DB 1568 ATCCCAACCATGATATATCTTCTGCAATCAGCCAACTGGCTCGGAATTTCACTCACT 1627  
 QY 501 AlaSerSerAspAspSerArgSerSerAlaGlyGlyIleAspMetValIleArgIleLeuAsp 520  
 DB 1628 GCATCTTCAGATGACAGCGCATCAAGTCAGAGTGGCGAAATATATGTCAGACACCTAAT 1687  
 QY 521 GluMetAspLeuSerAspThrProAlaProSerGluValIleProGluLeuSerGluTyrVal 540  
 DB 1688 GAAATGAGATCTGTGACACTCTGCCCATCTGAGTACAGAGCTCAGGAAATATATTT 1747  
 QY 541 SerValProAspIlePheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560  
 DB 1748 TCTGTCCAGATCATTTCTTGGAGATACCACTCTGCTCAGCTTTACATATATCAACC 1807  
 QY 561 ThrSerSerMetThrIleAlaProIleGlyIleArgGluLeuValIlePhePheSerLeuArg 580  
 DB 1808 ACTAGTTCTATGACCATTTGCCCCCAAGGGCGAGAGGCTGTGATGTTCTTCACTGTGCT 1867  
 QY 581 ValAlaAsnMetAlaPheSerAspAspLeuPheAsnIleValIleSerIleGluTyrArgAla 600

Db 1868 GTTGCTAACATGCGCTTCTCCACGACCTGTTCACAAAGCTCTGTGAGTACCGAGCT 1927  
QY LeuGlInglInpThrGluLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 1928 CTGGGCAACATTCACACAGCTGTGTTCCATTCATCGATCCCAATCTTACAGGATTT 1987  
QY LysGlnLeuGlnIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
Db 1988 AAGCAACTTGAATTAATTACTTACATTGAGAAACGGGAGTGTGATGTGAATAGCAAAATGAAG 2047  
QY PheAlaLysSerValProTyrAsnLeuThrLysAlaValHleGlyValLeuGlnAspPhe 660  
Db 2048 TTTCGTAGTGTGTGCTGCTGATTAACCTCACCAAGGCTGTGACGGGGCTTTGAGAGATTTT 2107  
QY ArgSerAlaAlaGlnGlnLeuHleuGlnIleAspSerTyrSerLeuAsnIleGln 680  
Db 2108 GATTGTGCTGACGCCCAACACTCCATCTGGAAATGACAGCTACTCTCTCAACATTGAA 2167  
QY ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGlnPheAlaGlnCysVal 700  
Db 2168 CCAAGCTGATCAAGCAGATCCCTCCGAAAGTTCCTGGCTCGCGGAGATTGGCCAAATGTGTA 2227  
QY LysAsnGlnLysGlnGlnGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 720  
Db 2228 AAGAAGCAACGGAAGTGAAGGAGGAGGAGTGTGCTGCAAAACAGATATGACAGCGAGGG 2287  
QY SerLeuAspGlyLeuGlnProGlyLeuCysGlyProGlyThrLysGlnCysGlnValLeu 740  
Db 2288 AGCCTGACAGCTGTGAAACAGGCTGTGTGG-CTGGGCAAAAGAAATGCGAGGTCTTC 2346  
QY GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGlnLysGlnAlaTyrLysThr 760  
Db 2347 CAGGGAAGGAGGCTCCATGCG--GTTCAGATCACTCGAAATCAAGCAATCAAAAAT 2404  
QY SerValLysLysPheGlnAsnGlnIleAsnAsnLysValIleSerLysArgAsnSerGln 780  
Db 2405 AGCTGTTAA-AGTCCAAATATCAACAAATATCAAGGTATATCAATAAAGAAATCTGAA 2463  
QY LeuLeuThrValGlnTyrGlnGlnPheAsnHisGlnAspTyrGlnGlyAsn 797  
Db 2464 TTACTGACCGTGAATATGAAATTTTAAACATCAAGATTGGGAAAGAAAT 2514  
RESULT 5  
ID ADA14866 standard; cDNA; 3261 BP.  
XX ADA14866;  
AC ADA14866;  
DT 06-NOV-2003 (first entry)  
XX  
XX Human cDNA encoding variant IPMC 150 isoform A.  
DE  
XX  
XX 88; gene; human; IPMC 150 isoform A; gene therapy;  
KW interphotoreceptor matrix component; IPMC; ocular disorder;  
KW macular degeneration; photoreceptor death; retinal detachment.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 128..2443  
FT CDS /tag= a  
FT /product= "Variant IPMC 150 isoform A"  
XX  
XX US2002160954-A1.  
XX  
XX 31-OCT-2002.  
XX  
XX 08-NOV-2001, 2001US-00007270.  
XX  
XX 29-OCT-1998, 98US-00183972.  
XX 29-OCT-1999, 99US-004310195.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;  
PI WPI: 2003-238235/23.  
DR P-PSDB; ADA14867.  
XX  
XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.  
XX  
XX Claim 3; Page 63-66; 76pp; English.  
XX  
XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding  
CC variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
XX  
SQ Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;  
Alignment Scores:  
Pred. No.: 6,896-316 Length: 3261  
Score: 4024.50 Matches: 793  
Percent Similarity: 99.62% Conservative: 1  
Best Local Similarity: 99.50% Mismatches: 3  
Query Match: 97.75% Indels: 3  
DB: 10 Gaps: 0  
US-10-007-270-2 (1-797) x ADA14866 (1-3261)  
QY 1 MetTyrLeuGlnThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
Db 128 ATGATTTTGGAAATCAAGAGAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGGA 187  
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
Db 188 ACTAAAGATATCTCATTTAATATACATACCATCTGAAATCAAGATGACATGACATCCCCCA 247  
QY 41 ArgAsnGlnThrTrpGlnGlnSerThrGlnLysMetTyrLysMetSerThrMetArgArgIle 60  
Db 248 AGAAATGAAACACTGAAAGTACTGAAAGAAATGTCAAATATGTCATATAGAGCAATTA 307  
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
Db 308 TTCCATTTGGCAAGAGCATCGAAACAAAGATCCGCATTTTCCCAAGGGGTTTAAATC 367  
QY 81 CysProGlnGlnSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
Db 368 TGTCACAGCAATCATGAAACAGATTTTAAACAGTCTTCAAGCTTATTATAGATTGAGA 427  
QY 101 ValCysGlnGlnLysAlaValTyrGlnLysArgIlePheLeuAspArgIleProAspPhe 120  
Db 428 GTGTGTCAAGAGCAAGTATGGAAGCATATGATCTTTCGAGTCCGATCCGATCCGACACA 487  
QY 121 GlyGlnTyrGlnAspTyrValSerIleCysGlnGlnGlnLysThrPheCysLeuPheAspIle 140  
Db 488 GGGGAAATTCAGAGCTGGGTGATCGATCTGCCAGCAGAGACCTTCTGCTTTTGACATT 547  
QY 141 GlyLysAsnPheSerAsnSerGlnGlnIleLeuAspLeuLeuGlnGlnArgIleLysGln 160  
Db 548 GGAATAAACTTCAGCAATTCCTCAAGAGCACTCGATCTTCTCCAGCAAGATAAAACAG 607  
QY 161 ArgSerPheProAspArgLysAspGlnIleSerAlaGlnLysThrLeuGlnGlnProGly 180  
Db 608 AGAAGTTTCCCTGACAGAAAGATGAAATATCTGCAAGAAAGACATTTGGAGAGCTTGT 667  
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200

Db	668	GAACCATGTCATTTCAACAGATGTTGCCAGCTCTCACTTGGGCTTCCCTCTCACT	727	Db	1748	TCTGTCCAGATCATTTCTTGAGAGATACCACTCCTGTCTCAGCTTTACAGTATATACCC	1807
Qy	201	ProAspAspThrLeuLeuAnglu11eLeuAspAspThrLeuAspThrLyMetPro	220	Qy	561	ThrSerSerMetThrIleAlaProLyArgLyArgLyLeuValValPhePheSerLeuArg	580
Db	728	CTGATGACACCTCTCTCAATGAAATTCGTATTAATCACTCAACGACACCAAGATGCTT	787	Db	1808	ACTAGTCTTATGACCATTTGCCCAAGGGCCGAGAGCTGTGTGTCTTCACTGCTGCGT	1867
Qy	221	ThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerVal	240	Qy	581	ValIleAspMetAlaPheSerSerAspLeuPheAsnLySerSerLeuGluTrpArgAla	600
Db	788	ACAAAGAAAGAAACAGAAATTCGCTGTGTGGAGACAGAGGGTGGAGCTCACCGCTC	847	Db	1868	GTTCCTAACATGCGCTTCTCCAAAGCAGCTGTTCACAGAGCTCTGGAGATCCGAGCT	1927
Qy	241	SerLeuValAsnGluNlyPheLyAlaGluLeuAlaAspSerGlnSerProLyTrpGln	260	Qy	601	LeuGluGlnGlnPheThrGluNleuLeuValProLyTrpLeuArgSerAsnLeuThrGlyPhe	620
Db	848	TCTCTGTAAACAGAAAGTTCAAGGACAGCTGCTGACTCCAGTCCCAATTTATCCAG	907	Db	1928	CTGGAGCAACAATTTACACAGCTGCTGGTTCCATTTACAGATCCAAATTTACAGGATTT	1987
Qy	261	GluLeuAlaGlyLySerSerGluNleuGlnMetGlnLyIlePheLyAlaLeuProGlyPhe	280	Qy	621	LyGluNleuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLyMetLyS	640
Db	908	GAGCTGACGAGAAAGTCCCAACTTCAGATGCAAAAGATTTTAAAGAACTTCAGGATTC	967	Db	1988	AAGCACTTGAATATCTTAATCTTGAAACGGGAGTGATGTAATGGCAAAATGGAAG	2047
Qy	281	LySlyValIleHisValLeuGlyPheArgProLySlyGluLyArgGlySerSerThr	300	Qy	641	PheAlaLySerValProLyTrpAsnLeuThrLyValAlaHisGlyValLeuGluAspPhe	660
Db	968	AAAAAATCATGTGTGTAGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACA	1027	Db	2048	TTTGCTTAAGTGTGTCGCTATTAACCTCAACAGGCTGTGACAGGGGTCTTGAGGATTTT	2107
Qy	301	GluMetGlnLeuThrAlaIlePheLyAspArgHisSerAlaGluAlaLySerProAlaSer	320	Qy	661	ArgSerAlaAlaAlaGlnGluNleuHisLeuGluIleAspSerTrpSerLeuAsnIleGlu	680
Db	1028	GAGATGCACACTTAAGGCAATCTTTAAGACACAGCTGCAGAGCAAAAGCCCTGCAGT	1087	Db	2108	CTTCTGCTGACGCCCAACAATCCATCTTGAAATAGACAGCTTCTCTCAACATTTGA	2167
Qy	321	AspLeuLeuSerPheAspSerAsnLyIleGluSerGluGluValTyriArgLyThrMet	340	Qy	681	ProAlaAspGluAlaAspProCySlyPheLeuAlaCyGlyGluPheAlaGlnCyVal	700
Db	1088	GACCTCCTGTCTTTTGAATCCAAACAAATTTGAAAGTGAAGATCATATGGAACCAAG	1147	Db	2168	CCAGCTGATCAAGAGAGATCCCTGCAAGTTCCGTGCGCTCGGGGATTTGCCAATGTGA	2227
Qy	341	GluGluAspLyGlnProGluIleTyLeuThrAlaThrAspLeuLyArgLeuIleSer	360	Qy	701	LyAsnGluArgThrGluGluAlaGluCyArgCySlyPProGlyTyTrpAspSerGlnGly	720
Db	1148	GAGGAGGACAAACCAACAGAAATCTATCTCACAGCTACAGACCTCAAAAGGCTGATCACG	1207	Db	2228	AAGAACGAACGACGAGAGAAAGCGAGTGTGCTGTCCAACCAAGATATGACAGCCAGGG	2287
Qy	361	LySAlaLeuGluGluGluGlnSerLeuAspValGlyThrIleGluPheThrAspGluIle	380	Qy	721	SerLeuAspGlyLyLeuGluProGlyLyLeuCySlyPProGlyTyThrLySlyGlyValLeu	740
Db	1208	AAAGACATAGAGAGAAACAAATCTTTGAGATGTGGGACAAATCACTGATGTAAGAAAT	1267	Db	2288	AGCTTGGACGCTTGTGAACAGGCTCTGTGTG-CTTGGCAAAAGAAATGCGAGGCTCTC	2346
Qy	381	AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla	400	Qy	741	GlnGlyLyArgLyAlaProCySlyPheLeuProAspHisSerGluAsnGluAlaTyriLyThr	760
Db	1268	GCTGATCACTGCCAGCTTTGTGCTGTGACACCAATCAGAGCTGCCCATCTTTTGTCT	1327	Db	2347	CAGGAAAGGGAGGCTCCATGGG--GTTCCAGATCACTCGAAATCAAGCATACAAAATCT	2404
Qy	401	ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu	420	Qy	761	SerValLySlyPheGlnAsnGlnGlnAsnAsnLyValIleSerLyArgAsnSerGlu	780
Db	1328	GTTATTAACAGAGAGATGCTACTTGTAGTCCAGAACTTCTCTGTGAAACCCAGCTTGAG	1387	Db	2405	AGTGTAA-AGTTCCAAATATCAAAATATCAAGTAAATCAATAAAGAAATTCGTGA	2463
Qy	421	ThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProProAlaMetAla	440	Qy	781	LeuLeuThrValGluTyriGluGluPheAsnHisGlnAspTrpGluGlyAsn	797
Db	1388	ACAGTGGACGAGACAGAGCATGCTCACTGACACTTCTTGTGCTTCCACTCTCTATGGCC	1447	Db	2464	TTACTGACCGTATGAAATATGAAGATTTAACCATCAAGATTTGGAAAGAAAT	2514
Qy	441	SerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThr	460	RESULT 6			
Db	1448	TCTACTCTCCCTGTCAAGAGCTCACTTCTTTATGGCATCAAGCATCTTCTCTGACT	1507	ID ACCT57947 standard; cDNA; 2887 BP.			
Qy	461	AspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThr	480	AC ACCT57947;			
Db	1508	GATCAAGGACACACAGATCAATGCGACCTGACACGACAAATCTAGTACAGAGGCTCACCC	1567	11-AUG-2003 (first entry)			
Qy	481	IleProThrSerAspTrpSerAlaIleSerGlnLeuAlaLeuGluTyriLeSerHisProPro	500	Human interphotoreceptor matrix IPM 150, isoform B, cDNA.			
Db	1568	ATCCCCACAGATGATTAATCTCAATCAACCACTGGCTCTGGAAATTTCAATCCACT	1627	Human, interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;			
Qy	501	AlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAsp	520	receptor; ophthalmological, gene therapy; gene; ss.			
Db	1628	GCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGGAGAAATGTGTCAGACACTAGAT	1687	Homo sapiens.			
Qy	521	GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyriVal	540	Key Location/Qualifiers			
Db	1688	GAAATGGAATCTGTGACACTCTGCTGCCATCTGAGGTACAGAGCTCAGCGAATATGTT	1747	CDS 2..2143			
Qy	541	SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyriIleThr	560	FT /tag= a			
				FT /product= "IPM 150"			
				FT /partial			
				FT /note= "No start codon"			
				XX XX			
				PN			
				W02003039346-A2.			

XX 15-MAY-2003.  
PD 08-NOV-2002; 2002MO-US036090.  
XX 08-NOV-2001; 2001US-00077270.  
PR (IOWA ) UNIV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
XX WPI; 2003-441440/41.  
DR New interphotoreceptor matrix proteins and polynucleotides, useful for  
PT treating or preventing photoreceptor death or retinal detachment, or for  
PT treating ocular disorders.  
XX Claim 1; Page 78-79; 105BP; English.  
XX The present sequence is that of cDNA encoding isoform B of novel human  
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bilateral chorioretinal atrophy, autosomal dominant Stargardt's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IMPG1) and IPM 200 (or IMPG2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polypeptides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression  
XX  
XX Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 4,22e-283 Length: 2887  
Score: 3619.00 Matches: 711  
Percent Similarity: 90.00% Conservative: 0  
Best Local Similarity: 90.00% Mismatches: 1  
Query Match: 87.90% Indels: 78  
DB: Gaps: 1  
US-10-007-270-2 (1-797) x ACC57947 (1-2887)  
QY 8 AlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThrIleAspIleSerIleAsn 27  
DB 5 GCTATTTTGTGTTTGGATTTTCTCCAGATTCAAGAAACCA----- 49  
QY 28 IleTyrlHisSerGluThrIleAspIleAspAsnProProArgAsnGluThrThrGluSer 47  
DB 49 ----- 49  
QY 48 ThrGluIleMetTyrIleMetSerThrMetArgArgIlePheAspLeuAlaIleHisArg 67  
DB 49 ----- 49  
QY 68 ThrIleArgSerAlaPhePheProThrGluValIleCysProGlnGluSerMetIle 87  
DB 49 ----- 49  
QY 88 GlnIleLeuAspSerIleGlnAlaIleTyrTyrArgLeuArgValCysGlnGlnAlaValTrp 107  
DB 50 -----GTGTCAGAGAAACAGATCG 70  
QY 108 GlnAlaTyrArgIlePheLeuAspArgIleProAspThrGluGluTyrGlnAspTrpVal 127  
DB 71 GAAGCATATCGAATCTTCTGATCGCATCCCTGACACAGGGAAATATCAGGACTGGGTC 130  
QY 128 SerIleCysGlnGlnIleThrPheCysLeuPheAspIleGlyIleAsnPheSerAsnSer 147

DB 131 AGCATTCGCAGACGAGAGACTTCGCTCTTTGACATGTGAAAAAACTTCAGCAATTCC 190  
QY 148 GlnGluIleIleAspLeuLeuGlnGlnIleArgIleIleGlnIleAspPheProAspArgIle 167  
DB 191 CAGAGCACCCTGGATCTTCTCCAGACGAATTAACAGAAAGTTTCCCTGACAGAA 250  
QY 168 AspGluIleSerAlaGluIleThrLeuGluValGluProGluGluThrIleValIleSerThr 187  
DB 251 GATGAATATCTCCAGAGAAACATTTGGAGAGCTGTGTAAACCATTTGTATTCACCA 310  
QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
DB 311 GATGTGGCAACGTCTGACTTGAGGCTTTCCCTCTCACTCTGATGACACCTCTCAT 370  
QY 208 GlnIleLeuAspAsnThrIleAsnAspThrIleTyrMetProThrThrGluArgIleThrGlu 227  
DB 371 GAAATTCGATTAATACCTCAAGCACCAAGATGCTTACACAGAAAGAAACAGAA 430  
QY 228 PheAlaValIleGluGluGlnArgValGluIleAspSerValSerLeuValAsnGluIlePhe 247  
DB 431 TTCCTGTGTTGGAGAGACAGAGGTGAGCTCAGCTCTCTGTGTAACCAAGATTC 490  
QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnIleLeuAlaGlyIleSerGln 267  
DB 491 AAGCAGAGCTCGCTGACTCCAGTCCCATATTACAGAGCTAGCAGAAAGTCCCA 550  
QY 268 LeuGlnMetGlnIlePheIleIleLeuProGluPheIleIleIleValLeuGly 287  
DB 551 CTTGAGAGCAAAAGATATTTAAAGAACTTCAGAGATTCAAAAATTCATGTTTACGA 610  
QY 288 PheArgProLysIleGluIleAspGlySerSerSerThrGluMetGlnLeuThrAlaIle 307  
DB 611 TTTAGACCAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCACTTACGGCCTTC 670  
QY 308 PheIleArgHisSerAlaGluAlaIleIleSerProAlaSerAspLeuLeuSerPheAspSer 327  
DB 671 TTTAAGAGACACAGTGAGAAAGCAAAAGCCCTGCAAGTCACTCTGTTTATTC 730  
QY 328 AsnIleIleGluSerGluGluValIleTyrHisGluThrMetGluGluAspIleProGlu 347  
DB 731 AACCAAAATTTGAAGTGAAGAAAGTCTATATGAAACCAAGAGAGAGAACCAACAA 790  
QY 348 IleTyrlleuThrAlaThrAspLeuIleArgLeuIleSerIleValLeuGluGluGln 367  
DB 791 ATCTATCTCAAGCTTACAGACTCCAAAGGCTGATCAGCAAGCATAGAGAAACAA 850  
QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
DB 851 TCTTTGATGATGAGGAGCAATTCAGTTCACTGATGAATTTGCTGATCACTCCAGCTTT 910  
QY 388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
DB 911 GGTCTGACACCAATCAAGACTGCTGCCACATCTTGTCTGTTAATAAGAGAGATCTCTCT 970  
QY 408 LeuSerProGluIleProProValGluProGlnIleGluThrValAspGlyValaGluHis 427  
DB 971 TTGAGTCCAGAACTTCTCTCTGTTGAACCCAGCTTGAGACAGTGAAGAGACAGCAT 1030  
QY 428 GlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAla 447  
DB 1031 GGTCTACCTGACACTTCTTGATCTCCACCTGATAGGCTTACCTCCCTGACAAAGCT 1090  
QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467  
DB 1091 CCACCTTCTTATGAGCATCAAGCATCTTCTCTGATGATCAAGAGACCAACATTCAC 1150  
QY 468 MetAlaThrAspGlnThrMetLeuValProGluIleuThrIleProThrSerAspTrpSer 487  
DB 1151 ATGGCCTGACCAAGACATGCTAGTACAGGGCTCAACATCCCAACAGATTAATCT 1210  
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArg 507

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Db      1211 GCAATCAGCCAACTGCGCTGGGAATTTCACATCCATCTTCAGATGACAGCCGA 1270
Qy      508 SerSerAlaGlyGlyGluSerMetValArgHisLeuAspGluMetCysLeuSerAspThr 527
Db      1271 TCAGATGCGAGGTGGCCAGATATATGTCAGACACCTGAATGAAATGATCTGCTGCACT 1330
Qy      528 ProAlaProSerGluValProGluLeuSerGluTyValSerValProAspHisPheLeu 547
Db      1331 CCGCCCCCATCTGAGGTACCAAGGCTCAGCGAATACGATTTCTGTCCAGATCAATTTCTTG 1390
Qy      548 GluAspThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAla 567
Db      1391 GAGGATACCACTCTGCTGCTCAGCTTACAGTATATACCACTAGTCTTATGACCAATTGGC 1450
Qy      568 ProValGlyValArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db      1451 CCCAAGGCGCGAAGCTGTGATGTCTTCAGTCTCGTGTCTTAACTAGGCTTCTCC 1510
Qy      588 AsnAspLeuPheAsnLysSerSerLeuGluTyArgAlaLeuGlnGlnPheThrGln 607
Db      1511 AACGACCTGTTCAACAAGAGCTCTTGAGATACCGAGCTCTGGAGCAACATTCACACAG 1570
Qy      608 LeuLeuValProTyLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
Db      1571 CTGCTGCTTCCATATCTACGATCCATCTTACAGATTTAAGCACTTGAAATCTTAAC 1630
Qy      628 PheArgAsnGlySerValIleValIleAsnSerLysMetLysPheAlaLysSerValProTy 647
Db      1631 TTCAGAAACCGGAGTGTGATTGTGAATACCAAAATAGATTGCTAAGCTGCGCGTAT 1690
Qy      648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaIleAlaGlnGln 667
Db      1691 AACCTCACCAGAGCTGTGACCGGGGCTTGAGAGATTTCGTCTGCTGAGCCCAACAA 1750
Qy      668 LeuHisLeuGluIleAspSerTyTyrSerLeuAsnIleGluProAlaAspGlnIleAspPro 687
Db      1751 CTCGATCTGGAAATATACACGCTACTCTCTCAATTTGAACCAAGCTATCAAGCAAGATCCC 1810
Qy      688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValIleLysAsnGluArgThrGlnGlu 707
Db      1811 TCCAGATTCCTGGCTCGCGCGCAATTGCGCCAAATGTGTAAAGAACGACGAGCTGAGGAA 1870
Qy      708 AlaGluCysArgCysLysProGlyTyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
Db      1871 GCGGAATGTGCGTGGCAACCGAGATATGACAGCGAGGAGCTTGACGCTGGAACCA 1930
Qy      728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db      1931 GGCCTCTGTGGCCCTGGCACAAAGAAATGCGAGTCTCTCAGGGAAGGAGGCTCCATGC 1990
Qy      748 ArgLeuProAspHisSerGluAsnGlnAlaTyIleThrSerValLysLysPheGlnAsn 767
Db      1991 AGGTGCGCAGATCACTCTGAAATCAAGCATACAAACCTAAGTGTAAAAAGTTCCAAAT 2050
Qy      768 GlnGlnAsnAsnLysValIleSerLysValArgAsnSerGluLeuLeuThrValGluTyGlu 787
Db      2051 CAACAAAATAAACAAAGGTAAATCGATAAAAGAAATTCGAATTACTGACCGTAGAATATGAA 2110
Qy      788 GluPheAsnHisGlnAspTyrGluGlyAsn 797
Db      2111 GAATTTAACCATCAAGATTGGAGGAAAT 2140

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RESULT 7
ADA14842
ID      ADA14842 standard; cDNA; 2887 BP.
XX
AC      ADA14842;
XX
DT      06-NOV-2003 (first entry)
XX
DE      Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.
XX
KW      ss; gene; human; IPMC 150 isoform B; gene therapy;

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KW      interphotoreceptor matrix component; IPMC; ocular disorder;
KW      macular degeneration; photoreceptor death; retinal detachment.
OS      Homo sapiens.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      5..2143
FT              /tag=a
FT              /partial
FT              /product= "IPMC 150 isoform B"
FT              /note= "No start codon given. Encodes residues 8-719 of
FT              {seqid:4}"
PN      US2002160954-A1.
XX
XX      31-OCT-2002.
XX
PF      08-NOV-2001; 2001US-00007270.
XX
PR      29-OCT-1998; 98US-00183972.
PR      29-OCT-1999; 99US-00430195.
XX
PA      (IOWA ) UNIV IOWA RES FOUND.
XX
PI      Hageman GS, Kuehn MH;
XX
PI      WPI; 2003-238235/23.
DR      P-PSDB; ADA14843.
XX
PT      New isolated or recombinant interphotoreceptor matrix component
PT      polynucleotide and polypeptide, useful for diagnosing, preventing,
PT      treating or prognosticating ocular disorders, e.g. macular degeneration
PT      or retinal detachment.
XX
PS      Claim 3; Page 33-34; 76pp; English.
XX
CC      The invention relates to an isolated or recombinant interphotoreceptor
CC      matrix component (IPMC) polynucleotide. Also disclosed is a vector
CC      comprising a promoter of an interphotoreceptor matrix component (IPMC)
CC      gene operatively linked to the IPMC polynucleotide. The IPMC
CC      polynucleotides, polypeptides and antibodies are useful for diagnosing,
CC      preventing, treating or prognosticating ocular disorders, e.g. macular
CC      degeneration, photoreceptor death or retinal detachment. They are also
CC      useful for identifying a compound capable of modulating IPMC gene
CC      expression in a cell. The present sequence represents cDNA encoding human
CC      interphotoreceptor matrix component, IPMC, 150 isoform B.
XX
SQ      Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.:      4,22e-283      Length:      2887
Score:          3619.00      Matches:      711
Percent Similarity: 90.00%      Conservative: 0
Best Local Similarity: 90.00%      Mismatches: 1
Query Match:      87.90%      Indels:      78
DB:              10      Gaps:      1

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US-10-007-270-2 (1-797) x ADA14842 (1-2887)
Qy      8 AlaIlePheValPheThrPhePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27
Db      5 GCTATTTTGTGTTTGTGATTTTCTCCAAAGTTCAAGAACCAAA----- 49
Qy      28 IleTyHisSerGluThrLysAspIleAspAsnProAspArgAsnGluThrThrGluSer 47
Db      49 ----- 49
Qy      48 ThrGluLysMetTyLysMetSerThrMetArgAlaIlePheAspLeuAlaLysHisArg 67
Db      49 ----- 49
Qy      68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysPProGlnGlnLysMetLys 87

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Db 49 ----- 49  
 QY 88 GlnIleuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGlnAlaValTyr 107  
 Db 50 ----- 70  
 QY 108 GlnAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTyrVal 127  
 Db 71 GAAGCATATCGATCTTTCTGATCGCATCCTGACACAGGGGAATATACAGACCTGGGTC 130  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheserAsnSer 147  
 Db 121 AGCATCTGGCCAGACAGACTTCTGCTTGTGACATTGGAAAAAATTCAGCAATTC 190  
 QY 148 GlnGlnIleuAspLeuGlnGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
 Db 191 CAGGAGCACCTGATCTCTCCAGCAGAGAAATAAAACAGAGAAATTTCCCTGACAGAAA 250  
 QY 168 AspGlnIleSerAlaGlyLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
 Db 251 GATGAAATATCTGCAGAGAAAGACATTGGAGAGCCTGGGAAACCATTTCTCATTTCAACA 310  
 QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
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 QY 208 GlnIleLeuAspAsnThrLeuAspAspThrLysMetProThrThrGlnArgGluThrGlu 227  
 Db 371 GAAATTTCTCGATTAATCACTCAACAGACACAAAGATGCTTACAAAGAAAAGAAAACAGAA 430  
 QY 228 PheAlaValLeuGlnGlnGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
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 Db 491 AAGGCGAGAGCTCGCTGACCTCCAGTCCCATTTACACAGAGCTGAGAGAAAGTCCCA 550  
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 QY 308 PheLysArgIleSerAlaGlnAlaLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
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 QY 328 AsnLysIleGlnSerGlnGlnValTyrIleGlyThrMetGlnGlnAspLysGlnProGlu 347  
 Db 731 AACAAATTTGAAAGAGAGAGAGCTATCATGGAACCATGAGAGAGACAAAGAACAGAA 790  
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 QY 388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGlnAspAlaThr 407  
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 QY 408 LeuSerProGluLeuProProValGluProGlnLeuGlnThrValAspGlnAlaGlnIle 427  
 Db 971 TTGAGTCCAGAACTTCTCTCTGTTGAACCCACCTTGAACAGTGAACGAGAGAGCAT 1030  
 QY 428 GlyLeuProAspThrSerTyrSerProProAlaMetAlaSerThrSerLeuSerGlnAla 447  
 Db 1031 GGTCCTACCTGACACTTCTTGCTCTCACTGCTATAGGCTCTTACCTCCCTGTCAGAAAGCT 1090

QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467  
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 QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
 Db 1151 ATGGCACTGACAGACAAATCTAGTACAGAGGCTCAACATCCCAACAGATTAATCT 1210  
 QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerIleProProAlaSerSerAspAspSerArg 507  
 Db 1211 GCATTCAGCCAACTGGCTCTGGAAATTCATCATCACTGATCTTCAGATGACAGCCGA 1270  
 QY 508 SerSerAlaGlyGlyGluAspMetValArgIleLeuAspGlnMetAspLeuSerAspThr 527  
 Db 1271 TCAGTGCAGGTGGCGAAGATATGTGCAGACACTTAATGATAATGATCTTCTGACACT 1330  
 QY 528 ProAlaProSerGlnValProGluLeuSerGlyTyrValSerValProAspIlePheLeu 547  
 Db 1331 CCGTCCCATCTGAGGTATCCAGGGCTCAGCAATATAGTTTCTGTCACGATCATTTCTTG 1390  
 QY 548 GlnAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567  
 Db 1391 GAGGATACCACTCTCTGCTCAGCTTACAGTATATCACACTAGTTCATATGACCATTTGCC 1450  
 QY 568 ProLysGlyArgGlnLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587  
 Db 1451 CCAAGGGCCAGAGCTGGTATGTGTTCTTCAGTCTGCTGCTGCTTACATAGCCCTTCCC 1510  
 QY 588 AsnAspLeuPheAsnLysSerSerLeuGlnTyrTyrArgAlaLeuGlnGlnGlnPheThrGln 607  
 Db 1511 AACGACCTGTTCAACAAGAGCTCTTGAGATACCAAGCTCTGAGCAACAATTCACAG 1570  
 QY 608 LeuLeuValProTyrTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGlnIleLeuAsn 627  
 Db 1571 CTGCTGTTCCATATCTACAGATTCATCAATCTTACAGATTTAAGCACTTGAATATCTTAAC 1630  
 QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647  
 Db 1631 TTCAGAAACGGAGTGTATGTGATATGCAAAATGAAGTTTCTTAATCTGTGCCGAT 1690  
 QY 648 AsnLeuThrLysAlaValIleGlyValLeuGlnAspPheArgSerAlaAlaGlnGln 667  
 Db 1691 AACCTCAACAAGGCTGTGACAGGGCTTGAGAGATTTCTGTTCTGTCAGCCCAACAA 1750  
 QY 668 LeuHleGlnGlnIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687  
 Db 1751 CTCCATCTGGAATATAGACAGCTACTCTCTCAACATTGAACAGCTGATCAAGCAGATCC 1810  
 QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGlnArgThrGlnGlu 707  
 Db 1811 TGCAGTTCCTGGCTGGCGGGAATTTCCCAATGTGTAAGAACGAAACGAGATGAGAA 1870  
 QY 708 AlaGlnCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727  
 Db 1871 GCGAGTCTCCCTGTAACAGATATGACAGCCAGGGAGCTGAGCGTCTGGAACCA 1930  
 QY 728 GlyLeuCysGlyProGlyThrLysGlnCysGlyValLeuGlnGlnLysGlyValProCys 747  
 Db 1931 GGCTCTGTGGCCCTGCGACAAAGAAATGCAAGGTCTTCCAGGGAAAGAGAGCTCAATGC 1990  
 QY 748 ArgLeuProAspPheSerGlnGlnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767  
 Db 1991 AGTTGCCAGATCACTCGAAATATCAACATACAAACCTAGTTTAAAGTTCCAAAT 2050  
 QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGlnLeuLeuThrValGluTyrGlu 787  
 Db 2051 CAACAATAATACAGATATCATGAATAAATAATTGTAATTACTGACCGTGAATATGA 2110  
 QY 788 GlnPheAsnIleGlnAspTyrGlnGlnLys 797  
 Db 2111 GAATTTAACATCAAGATTTGGGAAGAAAT 2140

RESULT 8  
 ID AAA46328  
 AC AAA46328; standard; DNA; 2966 BP.  
 DT 04-SEP-2000 (first entry)  
 DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.  
 XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 KW chromosome 6q33-q35; ocular disease; retinal detachment;  
 KW choriorretinal degeneration; retinal degeneration; cone degeneration;  
 KW age related macular degeneration; photoreceptor degeneration;  
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KW rod-cone dystrophy; cone-rod dystrophy; ss.  
 OS Homo sapiens.  
 XX MO200026367-A2.  
 PN 11-MAY-2000.  
 PD 29-OCT-1999; 99WO-US025440.  
 PF 29-OCT-1998; 98US-00183972.  
 PR 29-OCT-1998; 98US-00183972.  
 PA (IOWA) UNIV IOWA RES FOUND.  
 XX Hageman GS, Kuehn MH,  
 PI MPI; 2000-365616/31.  
 DR Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 PT preventing, diagnosing and treating ocular disorders such as retinal  
 PT detachment and choriorretinal degeneration.  
 XX Claim 3; Fig 18; 183pp; English.  
 PS The present sequence represents a splice variant of an interphotoreceptor  
 CC matrix (IPM) proteoglycan, designated IPM150. The sequence is missing  
 CC exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs,  
 CC IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome  
 CC 6q33-q35, between markers CHC.GAT11F10 and DS6284. The IPM proteins may  
 CC be used to supplement a patient's own production of the protein or to  
 CC rectify alterations in their nucleic acids that result in expression of  
 CC an inactive protein. The IPM nucleic acids may be used in this way to  
 CC treat ocular diseases such as retinal detachment, choriorretinal  
 CC degeneration, retinal degeneration, age related macular degeneration,  
 CC photoreceptor degeneration, RPS (retinal pigment epithelium)  
 CC degeneration, cone degeneration, mucopolysaccharidosis, rod-cone  
 CC dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also  
 CC be used to assay for other modulators of IPM proteoglycan expression and  
 CC activity that may be used to treat ocular diseases. The nucleic acids and  
 CC proteins may also be used as diagnostic reagents to detect the presence  
 CC of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies  
 XX  
 SQ Sequence 2966 BP; 918 A; 687 C; 624 G; 737 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,386-275 Length: 2966  
 Score: 3526.50 Matches: 707  
 Percent Similarity: 89.62% Conservative: 1  
 Best Local Similarity: 89.49% Mismatches: 4  
 Query Match: 85.66% Indels: 81  
 DB: 3 Gaps: 1  
 US-10-007-270-2 (1-797) x AAA46328 (1-2966)  
 QY 8 AlailephevalPheTrpIlePheLeuGlnValGlnGlyThrLeuAspIleSerIleAsn 27  
 DB 5 GCTATTGTTGTTTGGATTCTTCTCCAGTTCCAGGAAACCA----- 49

QY 28 IleTyrlHisSerGluThrLysAspIleAspAsnProProArgAsnGluThrThrLuser 47  
 DB 49 ----- 49  
 QY 48 ThrGluYMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67  
 DB 49 ----- 49  
 QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGlnuserMetLys 87  
 DB 49 ----- 49  
 QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGlnAlaValTyrp 107  
 DB 50 -----GTCGTCCAGAGACAGTAAATG 70  
 QY 108 GlnAlaTyrArgIlePheLeuAspArgIleProAspThrGlnGlnTyrGlnAspTrpVal 127  
 DB 71 GAAGCATATCGAATCTTCTGATCGCATCCCTGACACAGAGGAAATATCAGGACTGGGTC 130  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
 DB 131 AGCATCTCCAGACAGAGACCTTCGCTCTTGACATTGAAAAAACTTCAGCAATTC 190  
 QY 148 GlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
 DB 191 CAGGACACCTGGATCTTCTCCAGACAGAAATAAACAGAGAAATGTTCCCTGACAGAAA 250  
 QY 168 AspGluIleSerAlaGluLysThrLeuGlnGlnLysProGlnGlnTyrIleValIleSerThr 187  
 DB 251 GATGAATAATCTGCAGAGAGACACATTGGAGAGCTGTGGAACCATTTGATTCATTCACCA 310  
 QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
 DB 311 GATGTGCAACGCTCACTCTGGGCTTCCCTCTCACTCTGATGACACCTCTCAAT 370  
 QY 208 GlnIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGlnArgGluThrGln 227  
 DB 371 GAAATTCGTGATTAATACCTCAACGACACCAAGATGCTTCAACAGAAAGAAACAGAA 430  
 QY 228 PheAlaValLeuGlnGlnArgValGlnLeuSerValSerLeuValAsnGlnLysPhe 247  
 DB 431 TTCGCTGTGTGGAGAGACAGAGAGTGAAGCTCAAGCTCTCTGTGTAACACAGAAATTC 490  
 QY 248 LysAlaGlnLeuAlaAspSerGlnSerProTyrTyrGlnGlnLeuAlaGlyLysSerGln 267  
 DB 491 AAGCAGAGCTCGCTGACTCCCACTCCCAATTHCCAGAGCTACGAGAAAGTCCAA 550  
 QY 268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287  
 DB 551 CTTCAAGATGCAAAAGATTTTAAGAACTTCAGAGATTCAGAAAAATCAAGTGTAGGA 610  
 QY 288 PheArgProLysLysGlnLysAspGlySerSerSerThrGlnMetGlnLeuThrAlaIle 307  
 DB 611 TTTAGACCAAGAAAGAAAGAAAGATGCTCAAGCTCCACAGAGATGCACTTAAGGCTTC 670  
 QY 308 PheLysArgHisSerAlaGlnAlaLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
 DB 671 TTTAAGAGACACATGACAGAGCAAAAGCCCTCAAGTACCTCTCTCTTTGATTC 730  
 QY 328 AsnLysIleGlnSerGlnGlnValTyrHisGlyThrMetGlnGlnAspLysGlnProGln 347  
 DB 731 AACCAAAATTTGAAGTGAAGAGTCAATCATAGAACCAATGAGAGACCAACCAAGAA 790  
 QY 348 IleTyrLeuThrAlaTyrAspLeuLysArgLeuIleSerLysAlaLeuGlnGlnGln 367  
 DB 791 ATCTATCTCACAGCTACGACCTCAAAAGCTGATGCAAGCACTAGAGAGAAAGAA 850  
 QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
 DB 851 TCTTTGATGTGGGAGCAATTCATTCATCTGATGAATGTGTGATCACTGCCAGCCTTT 910

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QY 388 GYProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407
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QY 408 LeuSerProGluLeuProProValGluProGluLeuThrValAspGlyValGluHis 427
DB 971 TTGAGTCCAGAACTTCTCTGTTGAACCCAGCTTGAGACAGTGAGACGAGACAGCAT 1030
QY 428 GYLeuProAspThrSerThrSerProProAlaMetAlaSerThrSerLeuSerGlu 447
DB 1031 GGTCTACCGACACTTCTTGCTCCACCTGCTATGAGCTCTTACCTCCCTGCAAGCT 1090
QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467
DB 1091 CCACCTTTCTTATGGCATCAAGCATCTTCTCTGACGATCAAGGACCCACATATCA 1150
QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487
DB 1151 ATGGCCACTGACACAGCATGCTAGTACAGAGGCTCACCATCCACACAGTATTATCT 1210
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArg 507
DB 1211 GCAATCAGCAACTGGCTCTGGAAATTTCATCCACCTGACATCTTCAGATGACAGCGCA 1270
QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
DB 1271 TCAAGTGCAGGTGGGGAAGATATGGTCAGACACCTAGATGAATGATGTGCTGACACT 1330
QY 528 ProAlaProSerGluValProGluLeuSerGlyTyrValSerValProAspHisPheLeu 547
DB 1331 CTGGCCCCATCGAGGTACACAGGCTCAGCGCAATGCTTCTGCTCCAGATCATTTCTTG 1390
QY 548 GluAspThrThrProValSerAlaLeuGlnIleThrIleThrSerSerMetThrIleAla 567
DB 1391 GAGGATACCACTCTGCTCAGCTTACAGTATATCACACATGTTCTATGACCATGGCC 1450
QY 568 ProGlyGlyArgGluLeuValAlaPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
DB 1451 CCCAAGGGCGAGAGCTGGTACTGTTCTTCACTGCGGTGCTCAACATGGCCCTTCTCC 1510
QY 588 AsnAspLeuPheAsnLysSerSerLeuGlyTyrArgAlaLeuGlnGlnInPheThrGln 607
DB 1511 AACGACCTGTTCAACAAGAGCTCTCGAGTACCGGAGCTCGAGACAAATTCACACAG 1570
QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheValGluLeuGluLeuLeu 627
DB 1571 CTGGGTTCATATCTACGATCAATCTTACAGATTTAAACCACTTGAATACTTAC 1630
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647
DB 1631 TTCAGAAACGGAGTGTGATTTGTGAATACCAAAATGAAGTTTCTTAAGCTGTGCCGAT 1690
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667
DB 1691 AACCTCACCAAGGCTGTGACACGGGCTTGGAGAGATTTTCGTTGCTGCTCAACCCAAACA 1750
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlnProAlaAspGlnAlaAspPro 687
DB 1751 CTTCATCTGAAATATACAGCTACTCTTCAACATTGAACCAAGCTGATTAACCAAGATCCC 1810
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluThrGlnGlu 707
DB 1811 TGCAGATTCTGGCCCTGGCCGCAATTTGCCCAATGTGTAACCAACGACCTGAGAA 1870
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
DB 1871 GCGGAGTGTGCTGCAAAACAGGATATGACAGCAGGAGGAGCTGGAACGCTGGAACA 1930
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGlyValLeuGlnGlyLysGlyValProCys 747
DB 1931 GGCCTCTGTGG-CTTGGAACAAAGGATCGAGGTCTTCAGAGAAAGGAACTCCATC 1989
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysPheGlnAsn 767

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DB 1990 G--GTTCAGATCTCTGAAATCAAGACATACAAACTACTGTTAA-AAGTTCAAAT 2046
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
DB 2047 CAACAATAATACAGATATCATTAAGAATTTCTGATTAATACCGTGAATATGAA 2106
QY 788 GluPheAsnHisGlnAspTyrGluGlyAsn 797
DB 2107 GAATTTAACATCAAGATTGGAAAGAAAT 2136

RESULT 9
AAA46329
ID AAA46329 standard; DNA; 2244 BP.
XX
AC AAA46329;
XX
DT 04-SEP-2000 (first entry)
XX
DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.
XX
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
XX chromosome 6q13-q15; ocular disease; retinal detachment;
XX choroidretinal degeneration; retinal degeneration; cone degeneration;
XX age related macular degeneration; photoreceptor degeneration;
XX retinal pigment epithelium degeneration; mucopolysaccharidosis;
XX rod-cone dystrophy; cone-rod dystrophy; se.
XX
OS Homo sapiens.
XX
PN WO20026367-A2.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025440.
XX
PR 29-OCT-1998; 98US-00183972.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Hageman GS, Kuehn MH;
XX
DR WPI; 2000-365616/31.
XX
PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
PT preventing, diagnosing and treating ocular disorders such as retinal
PT detachment and choroidretinal degeneration.
XX
XX
XX Claim 3; Fig 19; 1833p; English.
XX
XX The present sequence represents a splice variant of an interphotoreceptor
XX matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an
XX additional intron after exon 5. The protein is an IPM component (IPMC).
XX Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
XX is located on chromosome 6q13-q15, between markers CHDC, GAT11P10 and
XX D6S284. The IPM proteins may be used to supplement a patient's own
XX production of the protein or to rectify alterations in their nucleic
XX acids that result in expression of an inactive protein. The IPM nucleic
XX acids may be used in this way to treat ocular diseases such as retinal
XX detachment, choroidretinal degeneration, retinal degeneration, age related
XX macular degeneration, photoreceptor degeneration, RP (retinal pigment
XX epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
XX cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
XX also be used to assay for other modulators of IPM proteoglycan expression
XX and activity that may be used to treat ocular diseases. The nucleic acids
XX and proteins may also be used as diagnostic reagents to detect the
XX presence of IPM nucleic acids and their products in samples from patients
XX according to standard methodologies
XX
SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
XX

Alignment Scores: 2,966-259 Length: 2244
Pred. No.:

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Score: 3323.00 Matches: 667  
 Percent Similarity: 95.564 Conservative: 0  
 Best Local Similarity: 95.564 Mismatches: 10  
 Query Match: 80.718 Indels: 23  
 DB: 3 Gaps: 1

US-10-007-270-2 (1-797) x AAA46329 (1-2244)

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 DB 151 ATGTATTTGGAAACTGAAAGAGCTATTTGTTTTTGGATTTTCTCCAAAGTTCAAGAA 210  
 QY 21 ThrTyrAspIleSerIleAsnIleTyrHisSerGluThrTyrAspIleAspAsnPro 40  
 DB 211 ACCAAAGATATCTCCATTACATATACCTTCGAAACTTAAGACATTAACAATGCCCA 270  
 QY 41 ArgAsnGluThrThrGluSerThrGluTyrMetTyrTyrMetSerThrMetArgArgIle 60  
 DB 271 AGAAATGAAACCAACTGAAAGTACTGAAAAAATGTACAAATGTCACACTATGAGACGAATA 330  
 QY 61 PheAspLeuAlaTyrHisArgThrTyrAspSerAlaPhePheProThrGlyValTyrVal 80  
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 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 391 TGTCCACAGGAATCCATGAAACAGATTTTAGACAGCTTCACAGCTTATTAATGATTGAGA 450  
 QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 451 GTGTGCAGGAAGACAGCATGGGAGCAATCCGATCTTTCTGGATCGCATCCCTGACACA 510  
 QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 511 GGGGAATACAGACATCGGGTCAGCATCTGCCAGCAGACACCTTCCTCTTGGACATT 570  
 QY 141 GlyTyrAsnPheSerAsnSerGlnGlnIleLeuAspLeuLeuGlnArgIleLysGln 160  
 DB 571 GGAATAAACTTCAGCAATTCCTCCAGAGCATCGGATCTTCTCCAGCAGAAATTAAGACG 630  
 QY 161 ArgSerPheProAspArgTyrAspGluIleSerAlaGluTyrThrLeuGlyLupProGly 180  
 DB 631 AGAAGTTTCCCTGACGAAAGATGAATATCTGCAGAGACACATTTGGAGAGGCTGGT 690  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 691 GAAACCATTTGTCAATTCACAC-AGCAATCTACATTTCAAAAGCTGGGCGCATTTCTAAGA 749  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 750 AAACCTCAGAAAGACAAATTCAAGATGTGGCCACGTCCTCACTTGGGCTTTCCTCTC 809  
 QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
 DB 810 ACTCCGATGAGACACCTCTCTCAATGGAATTCCTGATTAATACCTCAACACACCAAGATG 869  
 QY 220 ProThrThrGlnArgGluThrGluPheAlaValLeuGluGlnGlnArgValLupLeuSer 239  
 DB 870 CCTACAAACGAAAGGAAACAAATTCCTGTTGGAGAGACAGAGGGGTGAGCTCAGC 929  
 QY 240 ValSerLeuValIleAsnGlnTyrPheTyrValIleGluAlaAspSerGlnSerProTyrTyr 259  
 DB 930 GTCTCTCTGGTAAACCAAGAGTTCAAGGAGAGCTGCTGACTCCACAGTCCCAATATATAC 989  
 QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnTyrIlePheTyrValSerProGly 279  
 DB 990 CAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTTTAAGAAATTTCCAGCA 1049  
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 DB 1050 TTCAAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGAAAGATGCTCAAGCTCC 1109  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheTyrValTyrHisSerAlaGluAlaLysSerProAla 319

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 DB 1170 AGTGACCTCTCTGCTTTTGAATCCAAACAAATTTGAAGTGAAGAGTATATCATGGAAAC 1229  
 QY 340 MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle 359  
 DB 1230 ATGAGAGAGACAAACCAACAAATCTATCTCACAGCTTACAGACTCAAAAGGCTGATC 1289  
 QY 360 SerLysAlaLeuGluGluGluGlnSerLeuAspValGlyTyrIleGlnPheThrAspGlu 379  
 DB 1290 AGCAAGACATAGAGAGAAACAAATCTTTGATGTGGGACAAATTCAGTTCCTGATGAA 1349  
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 DB 1350 ATTGCTGGATCATCTCCAGCCTTTGGTCTGTGACACCAATCAGAGCTGCCCACATCTTT 1409  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
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 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrSerProProAlaMet 439  
 DB 1470 GAGACAGTGCAGAGAGACAGATGTCTACTGACATTTCTTGGATCTCCACCTGATG 1529  
 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
 DB 1530 GCCCT-ACCTCCCTGTCAAGAGCTCACCTTTCTTATAGGATCAAGATCTTCTCTG 1588  
 QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
 DB 1589 ACTGATCAAGGACCAAGATACAAATGCGCACTGACACAGACAAATCTGATACAGAGGCTC 1648  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
 DB 1649 ACCATCCCAACAGATTAATTTCTGCATACGCCAATCGGCTCTGGAAATTCACATCCA 1708  
 QY 500 ProAlaSerSerAspAspSerAspSerSerAlaGlyGlyGluAspMetValArgHisLeu 519  
 DB 1709 CCTGCATCTTCAGATGACAGCGCATCAAGTGAGGTGGCGAAGCATAGAGACAGACCTA 1768  
 QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerLupTyr 539  
 DB 1769 GATGAAATGATCTGCTGACACATCTCCCATCTGAGGTACCAAGAGCTCGCAATAT 1828  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
 DB 1829 GTTCTGTCCAGATCAATTTCTTGAGGATACCACTCTGCTCAAGCTTTACAGTATATC 1888  
 QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValIlePhePheSerLeu 579  
 DB 1889 ACCACTAATTTCTATACCATTTGCCCAAGGCGAGAGCTGTGATGTCTTCAAGTCTG 1948  
 QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
 DB 1949 CGTGTGCTTAACATGCTCTCCCAACGACCTGTTCACAAAGAGCTAATTTGGAGTACCGA 2008  
 QY 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuAspSerAsnLeuThrGly 619  
 DB 2009 GCTCTGAGCAACAAATTAACAAGCTGTGTGATTCATATCTACAGATCTTAACAGAA 2068  
 QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValIleAsnSerLysMet 639  
 DB 2069 TTTTAAGCAACTTGAATAATCTTAATCTTCAAGAAACGAGATGTGATTTGAATGCAAAATG 2128  
 QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValIleHisGlyValLeuGluAsp 659  
 DB 2129 AAGTTTGTAAAGTCAAGTCCGATATACCTTCAACAAAGGCTGTGACAGGGGCTTGTGAGAT 2188  
 QY 660 PheArgSerAlaAlaIleGlnGlnLeuHisLeuGluIleAspSerTyrSerLeu 677



Db 1110 ACAGAGATGCAACTTACGGCCATCTTTAAGACACAGTCAGAAAGCAAAAAGCCCTGCA 1169  
 QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValIleThrIleGlyThr 339  
 Db 1170 AGTGAACCTCTGCTTTTATGATTCACAAATTTGAAGAGAGAGTCTATCATGAGAAC 1229  
 QY 340 MetGluGluAspLysGlnProGluIleTyrluLeuThrAlaThrAspLeuLysArgLeuIle 359  
 Db 1230 ATGAGAGAGACACAGACACAGAAATCTATCTCACAGCTACAGACTTCAAAAGGCTGATC 1289  
 QY 360 SerLysAlaLeuGluGluGlnIleSerLeuAspValIleThrIleGlnPheThrAspGlu 379  
 Db 1299 ACCAAAGCACTAGAGAGAAACAATCTTGGATGTGGGACAATCAGTTCATGATGAA 1349  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
 Db 1350 ATTGCTGATCACTGCCACCTTGGTCTCTGACACCCAACTCAGAGCTGCCCATCTTTT 1409  
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 Db 1410 GCTGTTATACAGAGATGCTACTTGTAGTCCAGAACTTCTCTGTGAAACCCAGCTT 1469  
 QY 420 GluThrValAspGlyAlaGluIleGlyLeuProAspThrSerTrpSerProAlaMet 439  
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 Db 1589 ACTGATCAAGGACCAACATGCAATGCGCTGACCAACAATGCTACTACAGGGCTC 1648  
 QY 480 ThrIleProThrSerAspTyrlSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
 Db 1649 ACCATCCCAACAGATGATTAATCTGCAATCAGCCAACTGGCTCTGGAAATTCACATCCA 1708  
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 Db 1709 CCTGCATCTTCAGATGACAGCCGATCAAGTGCAGAGTGCAGAGATGACAGACCTTA 1768  
 QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlyTr 539  
 Db 1769 GATGAAATGATCTGTCTGACACTCTGCTCCATCTGAGTACCAAGAGCTCAGCAATAT 1828  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnIle 559  
 Db 1829 GTTTCGTCCAGATCAATTTCTTGAGATACCACTCTGCTCAGCTTACAGTATATC 1888  
 QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValPhePheSerLeu 579  
 Db 1889 ACCACTAGTTCATGACCATTCGCCCCAGAGGCCGAGAGCTGTGATGTTCTTCAGTCTG 1948  
 QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerLeuGluTyrlArg 599  
 Db 1949 CGTGTGCTCAATGCGCTTCTCCACAGCTGTTCACAAACAGATTTTGAAGTACCCA 2008  
 QY 600 AlaLeuGluGlnGluPheThrGlnLeuLeuValProTyrlLeuArgSerAsnLeuThrGly 619  
 Db 2009 GCTCTGAGACAAACATTCACACAGCTGCTGCTTCATCTACATCAGATCTTACAGGA 2068  
 QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
 Db 2069 TTTAAGCAACTTGAATATCTTAACCTTCAAGAACGGAGTGTATGTAATGCAAAATG 2128  
 QY 640 LysPheAlaLysSerValProTyrlAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659  
 Db 2129 AGTTTGTCAATGCTGCTGCTGATACCTCAGCAAGGCTGTCAAGGGCTCTTGTGAGAT 2188  
 QY 660 PheArgSerAlaAlaAlaGlnIleuHisLeuGluIleAspSerTyrlSerLeu 677  
 Db 2189 TTTGCTTCTGCTGACGCCCAACATCTCCTGGAATGACAGCTACTCTCTC 2242

RESULT 11  
 ADAL4844  
 ID ADAL4844 standard; cDNA; 2244 BP.  
 XX  
 AC ADAL4844;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Human Interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.  
 KW ss; gene; human; IPMC 150 isoform C; gene therapy;  
 KW Interphotoreceptor matrix component; IPMC; ocular disorder;  
 KW macular degeneration; photoreceptor death; retinal detachment.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 151..747  
 FT /\*tag= b  
 FT /product= "IPMC 150 isoform C"  
 FT sig\_peptide 151..200  
 FT /\*tag= a  
 FT /note= "Signal sequence"  
 FT mat\_peptide 201..744  
 FT /\*tag= c  
 FT /note= "Mature IPMC 150 isoform C"  
 FT 265..267  
 FT /\*tag= d  
 FT /note= "Encodes Pro"  
 FT 346..348  
 FT /\*tag= e  
 FT /note= "Encodes His"  
 PN US2002160954-A1.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 08-NOV-2001; 2001US-00007270.  
 XX  
 PR 29-OCT-1998; 98US-00183972.  
 PR 29-OCT-1999; 99US-00430195.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Hageman GS, Kuehn MH;  
 XX  
 DR MPI, 2003-238235/23.  
 DR P-PSDB; ADAL4845.  
 XX  
 PT New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.  
 XX  
 PS Claim 3; Page 36-37; 76pp; English.  
 XX  
 CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform C.  
 XX  
 SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;  
 Alignment Scores: 2,96e-259 Length: 2244  
 Pred. No.: 3323.00 Matches: 667  
 Score:

Percent Similarity: 95.56%      Conservative: 0  
 Best Local Similarity: 95.56%      Mismatches: 10  
 Query Match: 80.71%      Indels: 23  
 DB: 10      Gaps: 1

US-10-007-270-2 (1-797) x ADA14844 (1-2244)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValIlePheThrIlePheLeuGluValGluGly 20  
 DB 151 ARGTAATTGGAAACAGAGAGCTAATTTTGTGTTTGGATTTTCTCCAAATTCAGAGA 210  
 QY 21 ThrTyrAspIleSerIleAsnIleTyrHisSerGluThrTyrAspIleAspAsnProPro 40  
 DB 211 ACCAAAGATATCTCCCTTAACATATACATTCGAAACTAAAGACATAGACAAATCCCA 270  
 QY 41 ArgAsnGluThrThiGluSerThrGluTyrMetTyrLeuMetSerThrMetProArgIle 60  
 DB 271 AGAAATGAAACAACTGAAAGTACTGAAAAATGTACAAAATGTCAAAATGTAGAGCGAATA 330  
 QY 61 PheAspLeuAlaTyrHisArgThrTyrAspSerAlaPhePheProThrGlyValIleVal 80  
 DB 331 TTGGATTTGGCAAGATGAGAACAAAGATCCGCAATTTTCCCAACGGGGTTAAAGTC 390  
 QY 81 CysProGluGluSerMetTyrGluIleLeuAspSerLeuGluAlaTyrTyrArgLeuArg 100  
 DB 391 TGTCCACAGGAATCCATGAAACAGATTTAGACAGCTTCAAGCTTATATAGATTGAGA 450  
 QY 101 ValCysGluGluValAlaIleProGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 451 GGTGTTCAGAGAAAGCAGCATGGAGAGCATTCGGATCTTCTGATCGCATCCCTGACACA 510  
 QY 121 GlyGluTyrGluAspTyrValSerIleCysGluGluGluThrPheCysLeuPheAspIle 140  
 DB 511 GGGGATATCAGAGACGGGTGAGCATCTCCAGCAGAGACCTTCCTGCTTTCACAT 570  
 QY 141 GlyTyrAsnPheseAsnSerGluGluHisLeuAspLeuLeuGluGluArgIleTyrGlu 160  
 DB 571 GGAATAAACTTCGCAATTCACAGAGACCTGGATCTTCTCCAGAGAGAAATTAACAG 630  
 QY 161 ArgSerPheProAspArgIleAspArgIleSerAlaGluTyrThrLeuGluValGluProGly 180  
 DB 631 AGAAGTTTCCCTGACGAAAGATGAAATATCTGCAGAGAACATTTGGAGAGCTGTGT 690  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 691 GAAACCATTTCTATTCAAC-AGCATCTACATTTCAAAGACTGGGCACTATTCTAAGA 749  
 QY 188 -----AapValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 750 AAACCTCAGAAAGAGCAAAATTCAAGATGTGGCAAGCTCACTTGGGCTTTCCTCTC 809  
 QY 200 ThrProAspAspThrIleLeuAsnGluIleLeuAspAsnThrIleAsnAspThrIleMet 219  
 DB 810 ACTCCGTGATGACACCTCTCTCAATGGAATCTCGATTAATACACTCAACACCAAGAG 869  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValIleGluGluGluArgValGluLeuSer 239  
 DB 870 CCTACAAACGAAAGAGAAACGAATTCGCTGTGTGAGAGAGCAGGGGTGAGCTCAAC 929  
 QY 240 ValSerLeuValAsnGluTyrPheValIleGluLeuAlaAspSerGluSerProTyrTyr 259  
 DB 930 GTCTCTCTGGTAAACAGAAAGTTCAAGGCGAGACTGCTGACTCCAGTCCCAATATAC 989  
 QY 260 GlnGluLeuAlaGlyTyrSerGluGluMetGluGluTyrIlePheTyrValLeuProGly 279  
 DB 990 CAGGAGCTGACAGAGAAAGTCCCAACTTCAGATCAAAAGATATTTAAGAAACTTCCAGA 1049  
 QY 280 PheTyrLeuIleHisValLeuGlyPheArgProTyrLeuGluTyrAspGlySerSerSer 299  
 DB 1050 TTCAAAAAAATCCATGTGTTAGATTAGCCAAAGAGAAAGAAATGCTCAACTCC 1109  
 QY 300 ThrGluMetGluLeuThrAlaIlePheTyrArgHisSerAlaGluAlaTyrSerProAla 319

DB 1110 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGCTGCAGAGCAAAAAAGCCCTGCA 1169  
 QY 320 SerAspLeuLeuSerPheAspSerAsnTyrIleGluSerGluGluValTyrHisGlyThr 339  
 DB 1170 AGTGACCTCTGTCTTTGATTGATTCCAACAAATTTGAAATGTAGAGAGTCTATCATAAGAAC 1229  
 QY 340 MetGluGluAspTyrGluGluProGluIleTyrLeuThrAlaThrAspLeuTyrArgLeuIle 359  
 DB 1230 ATGGAGAGAGACCAAGCAACCAAGAAATCTATCTCACAGCTACAGACTCAAAAAGGCTGATC 1289  
 QY 360 SerTyrAlaLeuGluGluGluGluSerIleAsnAspValGlyThrIleGlnPheThrAspGlu 379  
 DB 1290 AGCAAGACACTAGAGAGAAACAACTTTGATGATGGAGACAAATTCAGTTCACTGATATA 1349  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGluSerGluLeuProThrSerPhe 399  
 DB 1350 ATTGCTGATCAGCTGCCAGCTTGTGTCTGACACCAATCAGAGCTGCCACATCTTTT 1409  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGluLeu 419  
 DB 1410 GCTGTTATACAGAGAGATGCTACTTGAATCCAGAACTTCCTGTTGAACCCAGCTT 1469  
 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrPheProAlaMet 439  
 DB 1470 GAGACAGTGAACGGAGCAGAGCATGTCTACTGACATTTCTGTCTCCACCTGTCTATG 1529  
 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
 DB 1530 GCCCT-ACCTCCCTGTCAAGAGCTCCACCTTCTTTATGGATCAAGCATCTTCTCTG 1588  
 QY 460 ThrAspGluGlyThrThrAspThrMetAlaThrAspGluThrMetLeuValProGlyLeu 479  
 DB 1589 ACTGATCAAGGACACACAGATACATGACCTGACCTGACAGACATCTAGTACAGAGGCTC 1648  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGluLeuAlaLeuGlyTyrIleSerIlePro 499  
 DB 1649 ACCATCCCAACAGATGATTAATCTGCAATCAGCCAACTGGCTCTGGAAATTCACATCCA 1708  
 QY 500 ProAlaSerSerAspAspSerAspThrProAlaProSerGluValProGluLeuSerGly 519  
 DB 1709 CTTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCAAGATATGACAGACACTA 1768  
 QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlyTyr 539  
 DB 1769 GATGAATAGGATCTGTGACACTCTGCCCATCTGAGGTACCAAGACTCAGCAATAT 1828  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGluTyrIle 559  
 DB 1829 GTTTCGTCCAGATCATTTCTTGGAGAGATACCACTCTGTCTCAGCTTTACAGATATATC 1888  
 QY 560 ThrThrSerSerMetThrIleAlaProTyrGluArgIleValIlePhePheSerLeu 579  
 DB 1889 ACCACTAGTCTATACCAATTCGCCCCAAGGGCCAGAGCTGTGATGTCTTTCAGCTTG 1948  
 QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnTyrSerSerLeuGluTyrArg 599  
 DB 1949 CCGTGTCTGAACATGGCTCTTCCAAACGACCTGTTCACAAAGAGCATTTGAGATACGA 2008  
 QY 2009 GCTCTGGAGCAACAATTCAACAGCTGTGTGATCAATATCTCAAGATCTTTCACAGA 2068  
 DB 2069 PheTyrGluGluGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerIleMet 639  
 QY 640 IlyPheAlaTyrSerValProTyrAsnLeuThrTyrAlaValHisGlyValLeuGluAsp 659  
 DB 2129 AAGTTTGTAAATCAGTGCCTGATTAACCTCAACAAAGGCTGTCAGGGGCTTTGGAGAT 2188  
 QY 660 PheArgSerAlaAlaGlnGluLeuHisLeuGluIleAspSerTyrSerLeu 677  
 DB 2189 TTTGCTTGTGTCAGCCCAACACTCCATCTGAAATATAGACAGCTACTCTCTC 2242

RESULT 12  
ACCS7950  
ID ACCS7950 standard, cDNA, 3668 BP.  
XX  
XX  
AC ACCS7950;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Mouse interphotoreceptor matrix IPM 150, isoform A, cDNA.  
XX  
KM Mouse; interphotoreceptor matrix; IPM 150; chromosome 9; IPMC; receptor;  
XX ophthalmological; gene therapy; gene; ss.  
XX  
OS Mus sp.  
XX  
XX Key Location/Qualifiers  
FH 196.2592  
FT CDS /\*tag= a  
FT /product= "IPM 150"  
XX  
XX MO2003039346-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 08-NOV-2002; 2002MO-US036090.  
XX  
XX 08-NOV-2001; 2001US-00077270.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Hageman GS, Kuehn MH;  
XX  
XX WPI, 2003-441440/41.  
XX  
XX P-PSDB; ABR42345.  
XX  
XX New interphotoreceptor matrix proteins and polynucleotides, useful for  
XX treating or preventing photoreceptor death or retinal detachment, or for  
XX treating ocular disorders.  
XX  
XX Claim 1; Page 81-82; 105pp; English.  
XX  
XX The present sequence is that of cDNA encoding isoform A of novel mouse  
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
XX is located on chromosome 9. Members of the IPMC gene family have been  
XX identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and  
XX rat IPM. 2 Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or  
XX IPM2). The invention provides IPM 150 and IPM 200 polynucleotides and  
XX polypeptides, antibodies that specifically bind the polypeptides, and  
XX vectors comprising the polynucleotides. A claimed method of treating or  
XX preventing photoreceptor death or retinal detachment involves  
XX administering an IPMC polynucleotide, polypeptide or antibody. Also  
XX claimed is a method for identifying a compound capable of modulating IPMC  
XX gene expression  
XX  
SQ Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;  
XX  
Alignment Scores:  
Pred. No.: 3,576-196 Length: 3668  
Score: 2548.50 Matches: 528  
Percent Similarity: 75.12% Conservative: 79  
Best Local Similarity: 65.35% Mismatches: 180  
Query Match: 61.90% Indels: 21  
DB: 9 Gaps: 9  
US-10-007-270-2 (1-797) x ACCS7950 (1-3668)  
QY 1 Metcrlleugluthrargrghalalephevalphepillepheleuglnvalqngly 20  
DB 196 ATGAATTTTCAATGATCATCTTCTTTGGATTTTGGATTTTCTCCAGTTCAAGCA 255  
QY 21 Thrlysaaprlleaserlleasmlerlyrhissergluthrlysaaprlleaspsanpropro 40

DB 256 ATCAAGTACTCTATTAAATATTCAGTTCTGAAATTTAAACATAGACAAACCCCA 315  
QY 41 Argaengluthrthrghluserthrghluserlysmeserthrmeargrgrile 60  
DB 316 AGAATCGAAACAAATGAAAGTACTTCAACAGTGCACAAAGTGTCAACATGAAACGAAAT 375  
QY 61 Pheaprlleualalyghlarythrlyargrseralaphneprothrghlyvallyval 80  
DB 376 TTCGATTTGCCAAGCTTCGAACCAAGATCAGACTTTTCCCA---GCTGCTAACATC 432  
QY 81 Cysproglnglusermetlyeglnlleueuapserlleuglnalalyrlyrargueury 100  
DB 433 TGTCCACGAAATCTTGAAGACAGATTTTACAGATCTTCAAGATTTATTAGCTGAGA 492  
QY 101 Valcyeglnglualavaltrpqlualatyrargllepheleuasparglleproapthr 120  
DB 493 GTATGTCAAGAAAGTGTGTGGGAAGCATATCGTATCTTTGTGACCGAATTCCTGACCA 552  
QY 121 Glyglutryrglnaprtprvalserllecyeglnglngluthrphcyleuapheaprlle 140  
DB 553 GAGGAATATCAAGACTGGGTGACGCTTCGCCAAGAAAGAACTTGCCTTTTACACT 612  
QY 141 Glylysaenpheserarserserglnglulhlsleuaprlleuaglnglnarggilleysgln 160  
DB 613 GGGAAAACTTCAGACACTCCACGAGACACTAGATCTTCTTACACAGAAATTAACAG 672  
QY 161 Argserpheproasparglysaapglulleseralaglutrythrleuglygluprogly 180  
DB 673 AGAAGCTTCCCTGGGAGAAAGATGACAGACGCTTCATGAGAGACCTGGAAGCAGCTACT 732  
QY 181 Gluthrillevalleserthrapsvalalaenvalserleuglypropheproleuthr 200  
DB 733 GAAGCCCTGTGTGATACCCACAGATGTTTCCAGATGCTCCGTGGGCTTCCACTTCT 792  
QY 201 Proaspaapthrleuansnglulileuanspanthrleuansapthrlysmecpro 220  
DB 793 TCTGATGACACAGACTCAAGAGATTTCTCAGTGTCACTTCACAGCAATTCAAAAGCC 852  
QY 221 Thrthrlyarggluthr-----gluphealavalileuglngluln 234  
DB 853 ACAAGAAAGTAAAGAAAGAACTATTCACGATGTGTGAATTTCTCA-----TCAGAGAG 906  
QY 235 Argvalgluleuservalserleuvalaenglnlyphelybalaagluleualaapser 254  
DB 907 AAGGTGAATTCAGATCTCTCTGCAAAACCAAGTTCAAGGCGAGACTCAACACTCT 966  
QY 255 Glnserprotyrtyrglngluleualaglylysserglnleuglnmetglnlysllephe 274  
DB 967 GGGTACCATACTACAGAACTGGTGGACAGTCCCAACTGCACTTGCAAAAGATATTT 1026  
QY 275 Lyslysaueuproglyphelylysllethlvalleuglypheargprolyelyslylys 294  
DB 1027 AAGAACTTCCAGAGATTCGAGAAATCCGTATATTAGATTAGCCAAAGAAAGAAAGA 1086  
QY 295 Aepglyserserserthrghlmeeglnleuthralalepheleuaprhghlsseralaglu 314  
DB 1087 GATGTTCAACCTCACAGAAATACAGCTTATGCGCATCTTAAAGAGGACCATCACAGA 1146  
QY 315 Alalysserproalaseraspleuuserpheaspsarlanlyslleuglserglnglu 334  
DB 1147 GCAAAAGCCCTGATAGCATCTACTGTCTTGTATTCACAAATTAAGAAAGTAAAGA 1206  
QY 335 Valtyrhlsaglythrmecgluluaaplysglnproglulietryleuthralathzap 354  
DB 1207 ATCCATCATGAGTCAT---GAAGACAAACACACAGAAACCTTACAGCTACAGAC 1263  
QY 355 Leulysargleulleserlysalaleuglnglulnglinsersleuapvalglythrile 374  
DB 1264 CTCAAAACCAATCATACACTACTGATGAGACCTGTCTTGTGAGAAAGGAAATTT 1323  
QY 375 Glnphethrapsrglulileaglyserleuaproalaphneglyproaspthrghlserglu 394

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Db      1324 CCAATTGGGTGATGAAGTTACTGGGACACTC-----TTCAAGACTGTCACTGAACCAAT 1377
Qy      395  LeupProthrSerPheAlaValIlePheRguIuaAplAaThrLeuSerProGluLeuProPro 414
Db      1378 CTGGCCAAAGCCCTTGTGATGTCAACAGAGATGCGACTTGTGAATGTCAGAACTCTCTTTC 1437
Qy      415  ValGluProGluLeuGluIuThrValAapGlyAlaGluHISGlyLeuPro----- 430
Db      1438 GTTGAAGCCTAGGCTTGAAGCAGTGAACAGAGAAGATCGAGCTCCCTGGATATGCTCC 1497
Qy      431  ---AapThrSerTyrSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449
Db      1498 AAGAGACAGTTCTTGGTCTCCACCTGTATCAAGCCTCAATTTCCCGATCAAGAAATCTACCT 1557
Qy      450 PhePheMetAlaSerSerIlePheSerLeuThrAapGluIuThrThraAapThrMetAla 469
Db      1558 TCGTTT---ACACCTAGACATCTTCTCTAGATGCTCAAGGCCCTCCCTTGTATGACC 1614
Qy      470 ThrAapGluIuThrMetLeuValProGlyLeuThrIleProThrSerAapTyrSerAlaIle 489
Db      1615 ACTGGCCCAACAGCACTATATCCCAAGCCCACTCTCCCACTATGATTTATCTACCATC 1674
Qy      490 SerGluLeuAlaLeuGlyIleSerHISProProAlaSerSerAapAapSerAapSerSer 509
Db      1675 CGCCAAATGCTCTGGAATCGTCACATGGCTGCTGATCTCCAGATGACAGAGAGCTGATC 1734
Qy      510 AlaGlyGlyIuAapMetValArgHISLeuAapGluMetAapLeuSerAapThrProAla 529
Db      1735 ACAAGCAGCCATGACATCCAGAACCTAGATGAGCATGATGATGTCGACACGCCACCC 1794
Qy      530 ProSerGluValIleProGlyLeuSerGluTyrValIleSerValProAapHISPheLeuGluAap 549
Db      1795 TTGTGCAAAATATCAAGACTGATGATTCGATTCCTGCTCGGTCAGTCTTGAAGATG 1854
Qy      550 ThrThrProValISerAlaLeuGluIuTyrIleThrThrSerSerMetThrIleAapProIys 569
Db      1855 ACCACACCCATCCCAACAGATAGCTTCAATCACACAGCTCCGAAACCATTCACCAAG 1914
Qy      570 GlyAapGluLeuValIlePhePheSerLeuArgValAlaAapMetAlaPheSerAap 589
Db      1915 GGCCAGAGACTATGATTTCTTCAAGCTGCGCTGTGCTCAACATCCGTTCTCTATGAC 1974
Qy      590 LeuPheAapIysSerSerLeuGluTyrArgAlaLeuGluGluIuPheThrGluLeu 609
Db      1975 CTGTTCAACAAAGATTCTCTGAGATATCAAGCCCTGGAACAACGATTCACAACTGCTG 2034
Qy      610 ValProTyrLeuArgSerAapLeuThrGlyPheIysGluLeuGluIleLeuAapPheArg 629
Db      2035 GTTCCCTATCTACGATCGAATCTTACGGGATTTAAGCACTGGAATATCTCAGCTTCAGA 2094
Qy      630 AangIysSerValIleValAapSerIysMetIysPheAlaIysSerValProTyrAapLeu 649
Db      2095 AACGGAAAGTATCTGATGACAGCAAGGCGGTTTGCAAGCGGTATCCCTACAACTC 2154
Qy      650 ThrIysAlaValHISGlyValLeuGluAapPheArgSerAlaAlaIaGluIuLeuHIS 669
Db      2155 ACCCAAGCCGCTGCGCGGCTTTCGAGATCTTCGCTCAACCGAGCTCAAGGCTCAAT 2214
Qy      670 LeuGluIleAapSerTyrSerLeuAapIleGluProAlaAapGluAlaAapProCybIys 689
Db      2215 CTGGAAATCGAAAGCTACTCCCTCGCATTTGAACCGATGATCAAGCGGATCCCTGCAAA 2274
Qy      690 PheIysAlaCybGlyGluPheAlaGluIuCybValIysAapGluArgThrGluIuGluAla 709
Db      2275 CTCTTAGACTGTGGCAAAATTTGCCCGGTGTGAAGAAATGAATGAGCAAGAGAACAGAG 2334
Qy      710 CybArgCybLeuProGlyTyrAapSerGluIysSerLeuAapGlyLeuGluProGlyLeu 729
Db      2335 TGTCTGTGACAGAGGACATGAGACCGGAGACCTGATCAACAGACCTGAACTTC 2394
Qy      730 CybGlyProGlyThrIysGluIuCybGluValIleGluIuGlyIysGlyValAProCybArgLeu 749
Db      2395 TGTCCCTCTGA---AAGACTGTGTGTGGCGCGGAGCAAGCAACTCTCATGCAAGGCCA 2451

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Qy      750  ProAapHISSerGluAapGluAlaTyrIysSerValIysIysPheGluAapGluIu 769
Db      2452 CCAAGTTCCTTACAAACCAAGCTCAGAACCTGCTGTAAAGCTA-----GTCAG 2505
Qy      770  AapAapIysValIleSerIysArgAapSerGluLeuLeuThrValIuTyrGluIuPhe 789
Db      2506 CAATATAGGTATCAAGAAAGAAATTTCTTAAGTATCAGCTATAGATTTGAGAAATTT 2565
Qy      790  AapHISGluAapTyrGluIuGlyAapN 797
Db      2566 GAAAGCAGAGCTGAGAGGAAAT 2589

RESULT 13
ID      ADA14847 standard; cDNA; 3668 BP.
AC      ADA14847;
DT      06-NOV-2003 (first entry)
XX      Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
DS      es; gene; mouse; IPMC 150 isoform A; gene therapy;
KM      interphotoreceptor matrix component; IPMC; ocular disorder;
KW      macular degeneration; photoreceptor death; retinal detachment.
OS      Mus sp.
FH      Key Location/Qualifiers
FT      CDS 196..2592
FT      /tag=a
FT      /product="IPMC 150 isoform A"

XX      US2002160954-A1.
XX      31-OCT-2002.
XX      08-NOV-2001; 2001US-00007270.
XX      29-OCT-1998; 98US-00183972.
XX      29-OCT-1999; 99US-00430195.
XX      (IOWA ) UNIV IOWA RES FOUND.
XX      Hageman GS, Kuehn MH;
XX      WPI; 2003-238235/23.
XX      P-PsDB; ADA14848.
XX      New isolated or recombinant interphotoreceptor matrix component
XX      polynucleotide and polypeptide, useful for diagnosing, preventing,
XX      treating or prognosticating ocular disorders, e.g. macular degeneration
XX      or retinal detachment.
XX      Claim 3; Page 39-41; 76pp; English.
XX      The invention relates to an isolated or recombinant interphotoreceptor
XX      matrix component (IPMC) polynucleotide. Also disclosed is a vector
XX      comprising a promoter of an interphotoreceptor matrix component (IPMC)
XX      gene operatively linked to the IPMC polynucleotide. The IPMC
XX      polynucleotides, polypeptides and antibodies are useful for diagnosing,
XX      preventing, treating or prognosticating ocular disorders, e.g. macular
XX      degeneration, photoreceptor death or retinal detachment. They are also
XX      useful for identifying a compound capable of modulating IPMC gene
XX      expression in a cell. The present sequence represents cDNA encoding mouse
XX      interphotoreceptor matrix component, IPMC, 150 isoform A.
XX      Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;

Alignment Scores: 3.57e-196 Length: 3668
Pred. No.: 2548.50 Matches: 528
Score:

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Percent Similarity:	75.12%	Conservative:	79
Best Local Similarity:	65.35%	Mismatches:	180
Query Match:	61.90%	Indels:	21
DB:	10	Gaps:	9

US-10-007-270-2 (1-797) X ADA14847 (1-3668)

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	196	ATGAATTTTCAATTAACATGCTACTTTGTTTTGGGATTTTTCTCCAGTTCAGGA	255
QY	21	ThrLybAerPIIleSerIleasnIleTyriHisSerGluThrLybAerPIIleasnPro	40
Db	256	ATCAAGATACCTCTATTAAATAATATTCAGTTCTGAATTAATAAACAATAGCAAAACCCCA	315
QY	41	ArgAenGluThrThrGluSerThrGluGlyMetTyriVmeSerThrMetArgGlyIle	60
Db	316	AGAAATCGAAACAATTGAAGTACCTTCACACAGGCAACAAAGTGCACCACTGAACAAATA	375
QY	61	PheAspLeuValAlaYrHisIaArgThrLybAerSerAlaPhePheProThrGlyValIysVal	80
Db	376	TTTCGATTTGCCAAAGCTTCGAACCAAAAGATCAGACCTTTTCCCA---GCTGTAAACATC	432
QY	81	CysProGlnGluSerMetLeuGlnIleLeuAerSerLeuGlnAlaTyriTyriArgLeuArg	100
Db	433	TGTCACACGGAATCCTTTAGACAGATTTTACAGAGCTTCGAAGATATTATAGACTGAGA	492
QY	101	ValCysGlnGlnAlaValITrpGluAlaTyriArgIlePheLeuAspArgIleProAspThr	120
Db	493	GTAATGTCAAGAAAGTGTGTGGAGACATATGCTATCTTTCTGGACCGAAATCCTTGACACA	552
QY	121	GlyGluTyriGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle	140
Db	553	GAGCAATATCAAGACTGGGCTCAGCTCTGCACGAAAGAAACCTTCGCTCTTGGACATT	612
QY	141	GlyLybAerPheSerAsnSerGlnGlnIleLeuAerPheLeuGlnArgIleIleYrGln	160
Db	613	GGGAAAACTTCAGCAACTCCACGAGGACCTCAAGATCTTCTTCAGCAGGAATTAACACG	672
QY	161	ArgSerPheProAspArgLybAspGluIleSerAlaGluLybThrLeuGluYrGluProGly	180
Db	673	AGAAGCTTCCCTGGGAGGAAGATGAGACAGCTCCATGAGACACTGGAGACACTTA	732
QY	181	GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr	200
Db	733	GAACCCCCCTGGGTGATCCACAGATTTTCCAGAGTCCCTCGGGCCCTTCCCACTTCC	792
QY	201	ProAspAspThrIleLeuAsnGluIleLeuAerAsnThrIleuAsnAspThrIleMetPro	220
Db	793	TCTGTATGACACAGACTCTCAGAGAGATTTCTCAGTGTCAACCTTCAAGAGCACTTAAAGCCC	852
QY	221	ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln	234
Db	853	ACAACAGAAATGAACAGAACTATTACGCTGCTCAATTTCTCA-----TCAGGAGG	906
QY	235	ArgValGluLeuSerValSerIleuValaengIlybPheLybAlaGluLeuAlaAspSer	254
Db	907	AAGGTGGAAATTCAGATCTCTCTGCAAAACCAAGTTCAGAGCAAGCTCAACCACTT	966
QY	255	GlnSerProTyriTyriGlnIleuValaGlyLybSerGlnLeuGlnMetGlnIlybIlePhe	274
Db	967	GGGTCAACATCTACAGAACTGCTGGGACAGCTCCCACTCAGATTCGAAAAAGATATT	1022
QY	275	LybLybLeuProGlyPheLybAlaYrHisIleValIleuGlyPheArgProLybLybGluYb	294
Db	1027	AAGAAACTTCAGAGATTGCAAGAAATCCGTGTATTAGATTAGACCAAAAGAAAGAGAA	1082
QY	295	AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLybArgHisSerAlaGlu	314
Db	1087	GATGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAAGGGAACATGACAGA	1144
QY	315	AlaLybSerProAlaSerAlaPheLeuLeuSerPheAspSerAsnLybIleGluSerGluGln	334

Db	1147	GCAGAAAGCCCTGATGACATCTGATCTCTTGTATTCGAAACAAATTTGAAGGGAAGA	1268
Qy	335	ValYrYHlVgLYThMeSGlUaBrLySGlNProGluLiEYUleUthPAlaThrAer	354
Db	1207	ATCCATGATGAGTCAATG---GAAGACAAACACACGAAACCTGCTCACAGCTACAGAC	1263
Qy	355	LeuYUaRgLeuLiSeSerLYaLaLeuGluGluGluInSerLeuAerValGlyThrTle	374
Db	1264	CTCAAAAACCTCATTCATCAACATGATGAGGAGACCTGCTCTTGTAAGAGGAAATTT	1323
Qy	375	GlnPheThrAerGluLiLeaAGLYSerLeuProAlaPheGlyProAerThrInSerGlu	394
Db	1324	CCATTCGGGTATGAAAGTATCTGGGACACTC-----TTCAAGCCTGTGACTGAACAGAT	1377
Qy	395	LeuProThrSerPheAlaValLleThrGluAerAlaThrLeuSerProGluLeuProPro	414
Db	1378	CTGGCCCAAGCCCTTGTGCTGATGTGCACAGAGGATGSCACTTGTAGTCCAGAACTTCCTTC	1437
Qy	415	ValGluProGluLeuGluThrValAerGlyAlaGluHlVgLYLeuPro-----	430
Db	1438	GTTTAGGCTTGAAGCTTGTGAGGACGTGGACAGAAAGATCTGAGCTGCTGGATGTCTCC	1497
Qy	431	---AerThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro	449
Db	1498	AAAGACAGTCTTGTGTGTCCACCTGTATCAAGCTCAATTTCCCGATGAAGAAATCTAAT	1557
Qy	450	PhePheMetAlaSerSerLlePheSerLeuThrAerGlnGlyThrThrAerThrMetAla	469
Db	1558	TGCGTT---ACACTGACATCTTCTCTGTAGTGTCAAAAGCCCTCCCTGATGAC	1614
Qy	470	ThrAerGlnThrMetLeuValProGlyLeuThrTleProThrSerAerTYrSerAlaLle	489
Db	1615	ACTGGCCCAACAGACATCATGCCCAAGCCCACTCCCTCCCATGATTTGTTATTCATCATG	1674
Qy	490	SerGlnLeuAlaLeuGlyLleSerLleProProAlaSerSerLleAerAerAerSerSer	509
Db	1675	CGCCATATGCTCTCGAATGTGCATATGCTGCATGCTCCGATCTCCAGTGCACAGAGCTGATC	1734
Qy	510	AlaGlyGlyGluAerMetValAerGluValLeuAerProLueAerLeuSerAerThrProAla	529
Db	1735	ACAAGCAGCGCATGACACATGCCAGACCTGATGATGCGATGTGTGTGACACGCCAGCC	1794
Qy	530	ProSerGluValProGluLeuSerGlyTYrValSerValProAerPheLeuGluAer	549
Db	1795	TTCGCAAAATATTCAGAACTGAGTGCATGATTCGCTCCGCGGTGAGTCTTGAGATG	1854
Qy	550	ThrThrProValSerAlaLeuGlnTYrLleThrThrSerSerMetThrLleAlaProLy	569
Db	1855	ACCAACACCCATCCCAACAGTACGGTTCATGACCAACCGCTCCAGACCATTTGCCACCAAG	1914
Qy	570	GlyAerGlyLeuAerValPhePheSerLeuAerValAlaAerMetAlaPheSerAerAer	589
Db	1915	GGCCAGAGCTAGTGTATCTTCAGCTGCGGTGCTGATGCTCAATGCCGTTCTCTGATGAC	1974
Qy	590	LeuPheAerLySerSerLeuGluTYrAerAlaLeuGluGlnGlnPheThrGlnLeuLeu	609
Db	1975	CTGTTCACAAAGAGTCTCTGGAGTATCAAGCCCTGGAAACAAGATTCAACAGACCTGCTG	2034
Qy	610	ValProTYrLeuAerSerAerLeuThrGlyPheLYrGlnLeuGluLleLeuAerPheAer	629
Db	2035	GTTCCTCCATCTACAGATCGAATCTTACGGGATTTTAAGCACTGGAATAATCACTGCTCAGA	2094
Qy	630	AerGlySerValLleValAerSerLyMetLeuPheAlaLySerValProTYrAerLeu	649
Db	2095	AAAGGAAAGTGTATCGGAAACAGCAAAAGTCCGGTTGGCAAAAGCGCGTCAACCTCAACCTC	2154
Qy	650	ThrLYaLlValHlVgLYLleuGluAerPheAerSerAlaAlaLlAGlnGlnLleHlH	669
Db	2155	ACCCAGGCGCTGGCGGGGCTCTTGAGAGANTCTTGCCACCGCAGCTCAAGGGCTCAAT	2214
Qy	670	LeuGluLleAerSerTYrSerLeuAerHlVgLYrProAlaAerGlnAlaAerProCYrLy	689
Db	2215	CTGGAATTCGAAAGCTACTCCCTCGCATTTGAACACAGCTGATCAAGGCGAGTCCCTCGAAA	2274

Oy		690	PheLeuAlaCyGsglygluPhealaglncysVallysaengluwgrThrlugluAlaActu	709
Db		2275	CTCCTAGACTGTGGCAATTGTGCCCGACGTGTAAAGAATGATGTGAACAAGAAAGCAAG	2334
Oy		710	CysArgCylvSPProglYTYrAspsergInglySerLeuAapglYLuegluPrOgLYeu	729
Db		2335	TGTCGCTGCACAACAGAGGACATGAGAGCCACGGGACCCTTGACATCACCAACCTTAACCTT	2394
Oy		730	CysglYProglYTHrLVLySgluCysgluValleugInglyLySglYAlaProCYsaRrgLeu	749
Db		2395	TGTCGCCCTGTGA---AAGACTTTGTGTGGCCGGCCGAGAAACAAGCAACTCATGCAAGCCA	2451
Oy		750	ProAsphISsergluaenGlAlaIryTrysThrseVallylVlvSpPhelnaenglnIn	769
Db		2452	CCAGATCACTCTACAAACCAAGCTCAGAACCTGTGTATAAANAACCTA-----CGTCAG	2505
Oy		770	AbsAnlyValIlleSerLyArGaBnserrgluleutHrVaIGluTyrgluInpHe	789
Db		2506	CAAATTAAGTAGTCAAGAAAAGAATTCTTAACATATACGATATAGGATTTGAAGAAITTT	2565
Oy		790	AsnHlsGlnAsPTTPglUGlyAsn	797
Db		2566	GAAAGCCAGACTGGAGGAGGAAT	2589
<b>RESULT 14</b>				
ID	AAAA6309	standard, cDNA, 3206 BP.		
XX	AAAA6309;			
DT	04-SEP-2000	(first entry)		
XX		cDNA encoding an Interphotoreceptor matrix proteoglycan (IPM150).		
DE		Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;		
KW		chromosome 6q3-q15; ocular disease; retinal detachment;		
KW		chorioretinal degeneration; retinal degeneration; cone degeneration;		
KW		age related macular degeneration; photoreceptor degeneration;		
KW		retinal pigment epithelium degeneration; mucopolysaccharidosis;		
KW		rod- cone dystrophy; cone-rod dystrophy; ss.		
XX				
OS	Mus sp.			
XX				
FH	Key	Location/Qualifiers		
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FT	/transl_except=	(pos: 55..57, aa: Ala)		
FT	/transl_except=	(pos: 58..60, aa: Tyr)		
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FT	/note=	"Xaa is an unspecified amino acid"		
PN	WO200026367-A2.			
PD	11-MAY-2000.			
PF	29-OCT-1999;	99WO-US025440.		
PR	29-OCT-1998;	98US-00183972.		
PA	(IOWA ) UNIV IOWA RES FOUNd.			
PI	Hageman GS, Kuehn MH;			
WI	WPI, 2000-365616/31.			
DR	P-PSDB; AAY93338.			

**Claim 2, Fig 6A, 183bp; English.**

The present sequence encodes an interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome 6q13-q15, between markers CHC.GTAIIIF10 and D6S284. The IPM proteins may be used to supplement a patient's own production of the protein or to rectify alterations in their nucleic acids that result in expression of an inactive protein. The IPM nucleic acids may be used in this way to treat ocular diseases such as retinal detachment, choroidretinal degeneration, retinal degeneration, age related macular degeneration, photoreceptor degeneration, RPS (retinal pigment epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also be used to assay for other modulators of IPM proteoglycan expression and activity that may be used to treat ocular diseases. The nucleic acids and proteins may also be used as diagnostic reagents to detect the presence of IPM nucleic acids and their products in samples from patients according to standard methodologies

US-10-007-270-2 (1-797) x AAA6309 (1-3206)

Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
Sequence 3206 BP; 937 A; 778 C; 686 G; 793 T; 0 U; 12 Other;	2,366-167	2192.00	74.08%	64.37%	53.24%	3
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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99 LeuArgValCyGlnGluAlaValIrrGluAlaTYrArgIllePheLeuAspArgIlePro 118  
::: :  
25 ATCAAGATATGTCAAGAAAGTCGTGGAGGAAGATGATCGTATCTTTCTGGANNAGAATTCC 84  
  
119 AspThrngYgluTyrglinspTrpValserIlleCyGlnGlnGlnuthrPheCyseuPpe 138  
:  
85 GACACAGAGGAATATCAAGGCTGGGTGCACCCTTGCCAAAGAAACTTGCCCTCTT 144  
  
139 AspIleGlyLysasnPheserasnserGlnIuhIsleAspLeuengIngnIarGile 158  
:  
145 GACATTGGGAAAACTCGAGCAACTCCCGAGGACACTTGATCTTTTCAGCAGAAATA 204  
  
159 LysGlnArsgSerPheProAsparglyAspargIuleseralGluIubyrThrIeuNgIygu 178  
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205 AAACAGAGAGACTTCCTCGGAGGAAAAGATGMACAGCTCCCATGAGACACTGGAACA 264  
  
179 ProGlygluthrIlleValIlleserThraapValAlasnaValserIeuNgIyProphePro 198  
:  
265 CCTACTGragccctCGTGTATCCACAGATGTTTCAGAGATGTCCTCGGGGCCMTTCCA 324  
  
199 LeuThrrProAspAspThrIleueuansnguIileueAspAsnthrIeusnasapThrIye 218  
:  
325 CTTCCTTGATGACAGAACCTCAAGAGATTCTCAGTGTCAccttCAAGAGACATTCAA 364  
  
219 MetProthnrThgluaRgsluthr-----GluphealavalLeuglu 232  
:  
365 AAGCCCAACAAGAAAGTAAAGTAAACGAACCTATTCATGTCGTAATTCTCA-----TCA 438  
  
233 GluGlnarValGluLeuSERVALserLeuvalAenGlnIbyPheylsalagIuleuAla 252  
:  
439 GAGGAGAAAGGTGGAATTTCAGCATCTCTCTGCCAAACCAAGAGTTCAAGGAGAGCTCAC 498  
  
253 AapsrserInserrProtyrTyrglngIuleualaglLyseGrlneuGImetGlnIye 272  
:  
499 AACCTGGGTACCAATACTACAGAGAACTGGTGGACAGTCCCAACTGCGATTGCAAAAG 558  
  
273 IllepelyValeuProGlyPheylsVylleHlaValleuGlyPhearGProlylsye 292



PT creating ocular disorders.

XX Claim 1: Page 82-83; 105bp; English.

XX The present sequence is that of cDNA encoding isoform D of novel mouse  
CC Interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
CC Interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 9. Members of the IPMC gene family have been  
CC identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and  
CC rat. IPM 2 subfamilies are designated IPM 150 (or IPMq1) and IPM 200 (or  
CC IPMq2). The invention provides IPM 150 and IPM 200 polynucleotides and  
CC polypeptides, antibodies that specifically bind the polypeptides, and  
CC vectors comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression

XX Sequence 1726 BP; 541 A; 383 C; 388 G; 414 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7,38e-99 Length: 1726  
Score: 1342.50 Matches: 310  
Percent Similarity: 44.96% Conservative: 51  
Best Local Similarity: 38.61% Mismatches: 99  
Query Match: 32.61% Indels: 343  
DB: 9 Gaps: 9

US-10-007-270-2 (1-797) x ACCS7951 (1-1726)

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QY 21 ThrIlyAspIleSerIleAsnIleTyrHisSerGluThrIlyAspIleAspAsnProPro 40  
DB 199 ----- 199  
QY 41 ArgAsnGluThrThrGluSerThrGluIlyMetTyrIlyMetSerThrMetArgArgIle 60  
DB 199 ----- 199  
QY 61 PheAspLeuAlaIlyHisArgThrIlyArgSerAlaPhePheProThrGlyValIlyVal 80  
DB 199 ----- 199  
QY 81 CysProGlnGluSerMetIlyGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
DB 200 -----ATCAA 205  
QY 101 ValIlyGlnGluAlaValIleProGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
DB 206 GATATGCAAGAGCTGCTGGAGAGCATATCGTATCTTCTGACCGAATTCCTACACA 265  
QY 121 GlyIlyTyrGlnIlyAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
DB 266 GAGGAATATCAAGACTCGGCTCAGCTCTGCCAGAAAGAACTTCTGCTTTGACATT 325  
QY 141 GlyIlyAsnPheSerAsnSerGlnGluIlyLeuAspLeuLeuGlnGlnArgIleIlyGln 160  
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QY 161 ArgSerPheProAspArgIlyAspArgIlyIleSerAlaGluIlyThrLeuGlnIlyGluProGly 180  
DB 386 AAGAGCTTCCCTGGAGGAAAGATGAGACAGCTTCATGAGACACTGAGAACACCTTCT 445  
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
DB 446 GAAAGCCCTGTGTGATCCCAAGATGTTTCCAGAGATGCTCCCTGGGCGCATTTCCACTTCT 505  
QY 201 ProAspAspThrLeuLeuAsnGluIlyIleLeuAspAsnThrLeuAsnAspThrIlyMetPro 220  
DB 506 TCTGATGACACAGACCTCAAGGAGATTCTCAGTGTCAACCTCAAGAGCATTCATAAAGGCC 565

QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln 234  
DB 566 ACAAAGAAAGTATACAGAAACCTATTCACTGTCTGATTTCTCA-----TCAGAGGAG 619  
QY 235 ArgValGluLeuSerValSerLeuValAsnGlnIlyPheIlyAspGluLeuAlaAspSer 254  
DB 620 AAGGTGAGGTTCAAGATCTCTCTCCAAACCAAGAGGTTCAAGGAGAGCTCAACCACTCT 679  
QY 255 GlnSerProIlyTyrGlnGlnIlyLeuAlaGlyIlySerGlnIlyLeuGlnMetGlnIlyIlePhe 274  
DB 680 GGGTCACCATCTACAGAACTGCTGGAGACAGTCCCAACTGACGAGTTGCAAAAGATATT 739  
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QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGlnLeuProPro 414  
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QY 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474  
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DB 1177 ----- 1177  
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DB 1177 ----- 1177  
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Db 1177 ----- 1177
QY 615 SerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIle 634
Db 1178 -----AGAAAGATCTGAGCTG 1195
QY 635 ValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHis 654
Db 1195 ----- 1195
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QY 735 LysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGlu 754
Db 1355 AAGACTGTGTGCGCGCGCGAGAACAGCACTCCATGCGAGCGCAACAGATCATCTACA 1414
QY 755 AsnGlnAlaTyrLysThrSerValLysLysPheGlnAsnGlnAsnAsnLysValIle 774
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Copyright (c) 1993 - 2006 CompuGen Ltd.

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Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents NA:\*

- 1: /cgcn2\_6/prodata/1/ina/1 COMB.seq:\*
- 2: /cgcn2\_6/prodata/1/ina/5 COMB.seq:\*
- 3: /cgcn2\_6/prodata/1/ina/6A COMB.seq:\*
- 4: /cgcn2\_6/prodata/1/ina/6B COMB.seq:\*
- 5: /cgcn2\_6/prodata/1/ina/H COMB.seq:\*
- 6: /cgcn2\_6/prodata/1/ina/PCTUS COMB.seq:\*
- 7: /cgcn2\_6/prodata/1/ina/PP COMB.seq:\*
- 8: /cgcn2\_6/prodata/1/ina/RE COMB.seq:\*
- 9: /cgcn2\_6/prodata/1/ina/backfile01.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	188.5	4.6	1721	3	US-10-029-517-3
2	183.5	4.5	1804	3	US-10-029-517-17
3	162	3.9	4935	3	US-09-949-016-1019
4	162	3.9	4935	3	US-09-949-016-5054
5	158	3.8	13815	3	US-10-149-736-2
6	157	3.8	19307	3	US-08-836-022A-10
7	157	3.8	19307	3	US-09-427-048A-10
8	146	3.5	8982	3	US-08-976-255-5
9	145.5	3.5	6192	2	US-08-479-537A-1

10	145.5	3.5	6192	3	US-09-083-116-1	Sequence 1, Appl1
11	145.5	3.5	6192	3	US-09-134-916A-1	Sequence 1, Appl1
12	145	3.5	8224	9	5180808-1	Patent No. 5180808
13	144.5	3.5	2472	3	US-09-248-796A-2596	Sequence 2596, Ap
14	144.5	3.5	3104	3	US-09-418-780A-2	Sequence 2, Appl1
15	144.5	3.5	3106	3	US-09-392-714-4	Sequence 4, Appl1
16	142.5	3.5	2610	3	US-09-949-016-1892	Sequence 1832, Ap
17	141.5	3.4	6407	2	US-08-616-844-7	Sequence 7, Appl1
18	141.5	3.4	6407	2	US-08-599-654-7	Sequence 7, Appl1
19	141.5	3.4	6407	3	US-08-944-868A-7	Sequence 7, Appl1
20	141.5	3.4	6407	3	US-08-944-423A-7	Sequence 7, Appl1
21	141.5	3.4	6407	3	US-08-944-496-7	Sequence 7, Appl1
22	141	3.4	1230230	3	US-09-438-165A-1	Sequence 1, Appl1
23	139.5	3.4	6852	3	US-10-172-502-3	Sequence 1, Appl1
24	138	3.4	580073	3	US-08-545-528D-1	Sequence 1, Appl1
25	137.5	3.3	2156	2	US-08-178-477B-31	Sequence 31, Appl1
26	137.5	3.3	2156	3	US-09-304-121-1	Sequence 1, Appl1
27	137.5	3.3	2156	3	US-09-023-655-1111	Sequence 1111, Ap
28	137.5	3.3	2230	3	US-09-949-016-2043	Sequence 2043, Ap
29	137.5	3.3	2458	3	US-09-513-783A-175	Sequence 175, App
30	137.5	3.3	2458	3	US-10-100-957A-175	Sequence 175, App
31	135.5	3.3	2835	3	US-09-134-001C-1515	Sequence 1515, Ap
32	135.5	3.3	3561	3	US-09-134-001C-1685	Sequence 1685, Ap
33	135.5	3.3	4828	3	US-09-620-312D-329	Sequence 329, App
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35	135.5	3.3	12057	3	US-10-149-736-47	Sequence 47, Appl1
36	135.5	3.3	13957	3	US-10-149-736-1	Sequence 1, Appl1
37	135.5	3.3	13957	3	US-09-782-378A-22	Sequence 22, Appl1
38	135.5	3.3	13977	3	US-09-484-970B-60	Sequence 60, Appl1
39	135.5	3.3	32392	3	US-09-662-254B-27	Sequence 27, Appl1
40	135.5	3.3	50000	3	US-09-662-254B-23	Sequence 23, Appl1
41	134.5	3.3	7888	3	US-09-919-497-48	Sequence 48, Appl1
42	134.5	3.3	8312	3	US-09-620-312D-1048	Sequence 1048, Ap
43	134.5	3.3	11443	3	US-10-149-736-44	Sequence 44, Appl1
44	134	3.3	13473	3	US-09-993-777-1	Sequence 1, Appl1
45	134	3.3	13473	6	PCT-US96-03916-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-10-029-517-3  
; Sequence 3, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 3  
; LENGTH: 1721  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (58)...(1605)  
US-10-029-517-3

## Alignment Scores:

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Score:	188.50	Matches:	84
Percent Similarity:	40.06%	Conservative:	59
Best Local Similarity:	23.53%	Mismatches:	147
Query Match:	4.58%	Indels:	67
DB:	3	Gaps:	15

US-10-007-270-2 (1-797) x US-10-029-517-3 (1-1721)

QY 367 GlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAla 386  
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Qy      387 PheGlyProAspThrLeuInserGluLeuProThrSerPheAlaValIle----- 402
Db      337 TGGGACAGAGATGTCACTGTG---GTCCAGGTCAACAGGCCAGCCCTGGGCTCCACCAACC 393
Qy      403 -----ThrGluAspAlaThrLeuSerProGluLeuProPro-----ValGlu 416
Db      394 CCGGACAGCCACAGATGTCACTGACCCCGGACCAACAAGCCAGCCCGGGCTCCACCGCC 453
Qy      417 ProGluLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr----- 432
Db      454 CCCCCAGCCACCGGTGTCACTGTGCCC-----CCGACACACAGCGCGCCCGCC 501
Qy      433 ---SerTyrSerProAlaMetAlaSerThrSerLeuSerGluAla-----ProPro 449
Db      502 GGGTTCACGCGCCCCCGGACGCCAGGTGTCACTGCGCCCGGACCAACAGCGCGCCCGCC 561
Qy      450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
Db      562 GGGTTCACGCGCGCCCGGACGCCAGCCAGGTGTCACTG-----TGC 597
Qy      470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSer-----AspTyr 486
Db      598 GCCCGGACACACAGCGCGCGCGGCTCCACCGCCCGCCAGCCATGATGTCACTGCG 657
Qy      487 SerAlaIleSerIleLeuAlaLeuGlyIleSerHisProPro-----AlaSerSer 503
Db      658 GCCCGGACACAGCGCGCGGCTGTGGGTGTCAACGCCCTTCAGATCCACAATGTCACTGCG 717
Qy      504 AspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAsp 523
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Db      1168 -----ACCATCATATGTCACGACGTGAGACACAGTTCAATCATATAAAGGAAGCA 1221
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RESULT 2  
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 ; Sequence 17, Application US/10029517

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; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO: 17
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(1500)
US-10-029-517-17

Alignment Scores:
Pred. No.: 4,8e-09 Length: 1804
Score: 183.50 Matches: 78
Percent Similarity: 38.82% Conservative: 54
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Query Match: 4,46% Indels: 73
DB: 3 Gaps: 12

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Qy      387 PheGlyProAspThrLeuInserGluLeuProThrSerPheAlaValIleThrGluAspAla 406
Db      352 TGGGACAGAGATGTCACTGTG----- 372
Qy      407 ThrLeuSerProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlu 426
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Qy      427 HisGlyLeuProAspThrSerTyrSerProAlaMetAlaSerThrSerLeuSerGlu 446
Db      418 CACGATGTCACTCAGCCCGGACCAACAAGCCCGCGGCTCCAC----- 465
Qy      447 AlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAsp 466
Db      466 GCCCCCCCA-----GCCACGATGTCACTGAGCCCGGAC----- 501
Qy      467 ThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSer----- 484
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Qy      485 ---AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro----- 500
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Qy      521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540
Db      664 TCTGCCAGGCTAACCAACCCCGGACCAAGACATCCCA-----TTC 708
Qy      541 SerValProAspHisPheLeuGluAspThrThrProVal----- 553
Db      709 TCATATCCAGCACACACTGTATCTCTACACCTTGCCAGCATAGACCAAGACT 768
Qy      554 -----SerAlaLeuGlnTyrIleThrThrSerSerMetThrIle 566
Db      769 GATGCCAGTAGCACTCAACCATAGCAACGTAACCTCTCACTCTCCATATCAACGACT 828
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RESULT 3
US-09-949-016-1019
; Sequence 1019, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1019
; LENGTH: 4935
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1019

Alignment Scores:
Pred. No.: 6.16e-06 Length: 4935
Score: 162.00 Matches: 155
Percent Similarity: 32.90% Conservative: 101
Best Local Similarity: 19.92% Mismatches: 304
Query Match: 3.93% Indels: 218
DB: 3 Gaps: 32

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      655 AATTTACAAACACCTCAACACCCCATGCTGCTTCCAGCCAAATTCACAGATTGATGAG 714
      79 LySvalCyapProGluInginSerMetLySginlleuAapSerLeugluAlaTyraG 98
      715 GAAATAGACCAAGACGTTTCATTAATAAGATATCGAATAAGACAGACGAGCTAATGAG 774
      99 LeuAgsValCyapGluInginAlaValTPrguAlaTyraGluPheLeuAapAgtIlePro 118
      775 CAGCGCTGGAAGCTAAGCT-----CGA 798
      119 AapThGlyTyraGluInginAapTPraLySerlleCyapGluInginThryPheCyapLeuPhe 138
      799 GAAGCTGCAGAACTTGAAGA-----GTTCACTGAGTGCAGACAGATGATTCAT 852

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      853 CCGAAGGAGTGGCTCTCTGCTGCTCTGCTCTTCAAGACGCTGAGACAGACCA 912
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      913 CTGAGACTCAGACGACATTGCCACGAAGAAGCTCTCAATTTCTGAGAGAAAGGTGAC 972
      170 lleserAlaGluLyS-----ThryLeuglyGluProGlyGluThrylleVallleSerThraP 188
      973 TCTGATGATGAGAAACCAAGAAAGAAAGACATCATTCAGGTTCAGACAGCAAG 1032
      189 ValAlaAenValSerLeuglyProPheProLeu-----ThryPro 201
      1033 GCAGCTAACTGTCTGAGGGCAGCCAACTGTGAGAGAAAGAGATCAAGAAACCT 1092
      202 AapAapThryLeuAaenGluLeuAapAenThryLeuAapThrySmetProThr 221
      1093 TCCAGAAACCTA-----AGGTCAGACGATGAAATTTGAAACG 1134
      222 ThryGluAgsGluThryGluPheAlaValleugluGluInginAgsValSer 241
      1135 GAGAGGAAGAAAGAGAGAGAGAGAGAGAAAGATGATGAAGAGAGAGAGTAT 1194
      242 LeuValAaenGluLySPhaLyAlaGluLeuAlaAapSerGlnSerProTyraGluIngin 261
      1195 GATGAGGACAAAAATCTAG-----GAGGCACCAATCTGAAAGAG 1236
      262 LeuAlaGlyLySserGluInginMetGluLySlePheLyLyLeuProGlyPheLy 281
      1237 TTTAAGAAAGAGGGA-----GAGTACTTGAATTA 1272
      282 LySlelleValleuglyPheAgsProLyLyS-----Glu 293
      1273 CCAAGAGATATGATGATAGAGACCCAAACAAGATCCACAGACAGAGCTTTAGAG 1332
      294 LyAapGly-----SerSerThryGluMetGluInleuThryAlallePheLyAgsH 311
      1333 ACAGAGGAGATTTAAACAAGATCCCGAAGAGGTAGAAAGATCATGTGCCACAGACAG 1392
      312 SerAlaGluAlaLySserProAlaSerAapLeuLeuSerPheAapSerAenlylleGlu 331
      1393 CAGCAGAGAGAAATGAAACAACATCTCCCTTACAGAGAGAAAGAAATTA 1452
      332 SerGluGluValTyraHileGlyThryMetGluGluAapLySginProGluTyraGluThry 351
      1453 TCTTCACAA-----GGCTTAAAGAAATAAGATCTCTTCCCTCTGACAG 1503
      352 AlathraPheLeuLyAgsGluLeuLeuSerLyAlaLeugluGluInginSerLeuAapVal 371
      1504 ACTGAAGATCGAAAGAG----- 1521
      372 GlyThrylleGluPheThryAapGluLeuAlaGlySerLeuProAlaPheGlyProAapThry 391
      1522 -----GCTCACTTGAAGCTGCTCCAGACCAACT 1551
      392 GlnSerGluLeuProThrySerPheAlaVallleThryGluAapAlathraLeuSerProGlu 411
      1552 GCCAGCAGAGAGAGACTCTCCACCTTATCTCAACAAAGAGACT----- 1599
      412 LeuProProValAluProGluInginGluThryValAapGlyAlaGluHileGlyLeuProAap 431
      1600 TCTCCACCACTCATCAACAGCTCATACGAAGAAATAGAG-----CCCATG 1650
      432 ThrySerThryProProAlaMetAlaSerThrySerLeuSerGluAlaProProPhePhe 451
      1651 GAAGGCCAGCCCTCTGCTCTCATTCATTCAT-----CTCTCT----- 1692
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      1693 -----AATACAGATGCTGACACCAAGGAGCTATTATCTCAG 1731

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DB 1732 CATACGTGC-----CAG 1743
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DB 1744 TTGGTAGAGGCGCTGTCT---CCTTGTCAAGTCTCTTCAGACCAAGCAAGCAATCTCCA 1800
QY 512 GlyGlu-----Asp 514
DB 1801 GCAGAGAAAGTCCAGAGAGAGTGTCTGCTCTGTTCAAAAAAGCACTGCTGAC 1860
QY 515 MetValArgHisLeuAsp-----GluMetAspLeuSerAspThrProAlaProSer 531
DB 1861 TACTCAGCCCAAGAAAGATCTTGAACCTGAGTCAGACAGATCTGCTCAGCCCTCCTCTGA 1920
QY 532 GluValProGluLeu----- 536
DB 1921 AAAAATTGAGAAATTAGCACTGCGCAAGGAATCACTGAAGAAATGTTGAAACAGCATCT 1980
QY 537 -----SerGluTyrValSerValProAspHisPheLeuGlu 548
DB 1981 TTGGACAGAGAAAGAGCAAGAAAGCTTCTCAATCCCTTCTCCAAACCAAGATTGAA 2040
QY 549 AspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaPro 568
DB 2041 CAGTCAGCTGATTCATCTCTAGCCGCTCCTCCTCATCTTCTCTCCAGTTCTAGATCA 2100
QY 569 LysGlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsn 588
DB 2101 AATCTCTGC-----TCTCT 2115
QY 589 AspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThrGlnLeu 608
DB 2116 GAC-----AGTTCAGATTCTCGGTCTCTCAACCGCTAGATCCAAAGAGAGATGTA 2169
QY 609 LeuValProTyrLeuArgSerAsnLeuThrGlyPheGlyLeuGlnIleLeuAsnPhe 628
DB 2170 GCCCAGGACGTAATCATGCAACCAACCTCGTGTAGACCAAG-----ATGGGCTCC 2220
QY 629 ArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsn 648
DB 2221 AATCAACAATCAGAGTCAGATCCAGATCAAGTCAAGTTCAGTTCCTGTCAGATCAAGCAAC 2280
QY 649 LeuThrIleValIleHis---GlyValLeuGluAspPheArgSerAlaIleAlaGlnGln 667
DB 2281 AGCAGAAAATCTCTGAGCCCTGAGTCTCCAGGACAGACAC----- 2325
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAla-----AspGln 684
DB 2326 -----AGCTAATAGTAAACCAAGATCCCTCTGTCAGAGAGTT 2367
QY 685 AlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValIleAsnGlnArg 704
DB 2368 GCAACTCCA-----CCAGTGCACAACCTGACAGTCTGTAGCCAAAGAGAGAG 2415
QY 705 ThrGlu-----GluAlaGluCysArgCysLysProGlyTyrAspSer 718
DB 2416 ACTTCACACTCTCTCATCTCTGTCAGAGAGCGCTGATGATCAAGCTTAATCACTGAA 2475
QY 719 GlnGlySerLeuAspGlyLeuGluProGlyLeuGlyGlyProGlyThrLysGluCysGlu 738
DB 2476 AAGCATGTGACCAAGAGTTACAGCTGAGCGGGAGGCCA-----AAGAAAGTGTGA 2529
QY 739 ValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGln 756
DB 2530 GCTGAAGAGCAGAGCCACAGCTGCACACAGCCCAAACTCAGAGACTGAG 2583

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RESULT 4  
 US-09-949-016-5054  
 / Sequence 5054, Application US/09949016  
 / Patent No. 6812339  
 / GENERAL INFORMATION:

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/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USRS THEROF
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5054
/ LENGTH: 4935
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-5054

Alignment Scores:
Pred. No.: 6.16e-06 Length: 4935
Score: 162.00 Matches: 155
Percent Similarity: 32.90% Conservative: 101
Best Local Similarity: 19.92% Mismatches: 304
Query Match: 3.93% Indels: 218
DB: 3 Gaps: 32

US-10-007-270-2 (1-797) x US-09-949-016-5054 (1-4935)
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DB 656 AATTAGAGAAACCTCAACACCCCATGCTGATTCAGCCAAATTCACAGATTGCTGAG 715
QY 79 LysValCysProGlnGlnSerMetLysGlnIleLeuAspSerLeuAlaIleTyrTyrArg 98
DB 716 GAAATGACCAGAACAGTTTCAATAAACGATATCGAAAAAGCAGACAGACTACTTAGG 775
QY 99 LeuArgValCysGlnGluAlaValIleProIleAlaTyrArgIlePheLeuAspArgIlePro 118
DB 776 CAGCCTCTGAACCGTAAGCT-----CGA 799
QY 119 AspThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPhe 138
DB 800 GAGCTGCAAACTTGAAGAA-----GCTTCAGCTGAGTGGAGAGAGATGATTCAT 853
QY 139 AspIleGly-----LysAsnPheSerAsnSerGlnIleHisLeuAsp 152
DB 854 CTTGAGGAGAGTGGCTTCCCTGCTGCTCTGCTTCAAGACGCTGGAAGACCAAG 913
QY 153 LeuLeuGlnGlnArg-----IleLysGlnArgSerPheProAspArgLysAspGlu 169
DB 914 CTGAGAGCTCAGACATATTCGCCCAAGAAAGCTCTCAATTTCTGAAGAGAAAGTGAAC 973
QY 170 IleSerAlaGluLys---ThrLeuGlyGluProGlyGluThrIleValIleSerThrAsp 188
DB 974 TCTGATGATGAAACCAAGAAAGAGAAAGACATCATCTAGAGTCAAGACAGCAAGA 1033
QY 189 ValAlaAsnValSerLeuGlyProPheProLeu-----ThrPro 201
DB 1034 GCAGCTTAACGTCTGAGAGGAGCCCAACCTCTGAGAGAGAGAGATCAAGAAACACT 1093
QY 202 AspAspThrIleLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetProThr 221
DB 1094 TCCAGAAACCTA-----AGGTCAGAGCAGATCGAAATTTGAAACCA 1135
QY 222 ThrGluArgGluThrGluPheAlaValLeuGlnGlnGlnArgValGluLeuSerValSer 241
DB 1136 GAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1195
QY 242 LeuValaGlnGlyPheLysLeuAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGlu 261
DB 1196 GATGAGGAGCAAAATCTAGG-----GAGGCACCAATCTCTGAAAGAG 1237

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QY 262 LeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLeuProGlyPheLys 281
Db 1238 TTTAAGAAAGAGGAAA-----GAGTAACTTAGATGTAATAA 1273
QY 282 LysIleHleValLeuGlnPheArgProLysLys-----Glu 293
Db 1274 CCAAGAGATATGATGATGATGAGACCCAAACAAAGATCCCAAGAACAGAGCTTAAAG 1333
QY 294 LysAspGly-----SerSerThrGlnMetGlnLeuThrAlaIlePheLysArgHis 311
Db 1334 AGAGAGGAGGATTTTACAGATCCCAAGAGAGCTAGAAAGATCATCTGGCCACAGAC 1393
QY 312 SerAlaGlnAlaLysSerProAlaSerAspLeuLeuSerPheAspSerLysIleGlu 331
Db 1394 CAGCAGAGAAAGAAATGAAACAAACATCTCCCTTGAGAGAGAAAGAAATGAA 1453
QY 332 SerGlnGluValTyrHisGlyThrMetGlnGluAspLysGlnProGluLysTyrLeuThr 351
Db 1454 TCTTCCAA-----GGCTTAAAGAAATGCAAGCTCTTCCCTCCTCGACTG 1504
QY 352 AlaThrAspLeuLysArgLeuLysSerLysAlaLeuGlnGlnGlnSerLeuAspVal 371
Db 1505 ACTGAAGATCGAAAGAG----- 1522
QY 372 GlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThr 391
Db 1523 -----GCCCTCACTTGAGCGCTGCAGAGCAAACT 1552
QY 392 GlnSerGluLeuProThrSerPheAlaValIleThrGlnAspAlaThrLeuSerProGlu 411
Db 1553 GCCAGGAGAGAGAGACTCTCTCCACTTACTAACAAAGAGCAATCT----- 1600
QY 412 LeuProProValGluProGlnLeuGlnThrValAspGlyAlaGluHisGlyLeuProAsp 431
Db 1601 TCTCCACCACTCATCCACAGAGCTCCATAGAGAAAGAAATAGAG-----CCCAAG 1651
QY 432 ThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGlnAlaProPhePhe 451
Db 1652 GAAGGCCCGCCCTCTCTCTCATTCAGTTATCT-----CCTCCT----- 1693
QY 452 MetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAsp 471
Db 1694 -----AATACAGATGCTGACACCAAGAGCTAATAGTATCTGAC 1732
QY 472 GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491
Db 1733 CATACTGTC-----CAG 1744
QY 492 LeuAlaLeuGlyIleSerHisProProAlaSerAspAspSerArgSerAlaGly 511
Db 1745 TTGGTAGAGAGCTCTGCT---CCTTGTCAGTCTTTCAGACCCAAAGACAGATCTCA 1801
QY 512 GlyGlu-----Asp 514
Db 1802 GCAGAGAAAGTCCACAGAGAGTGTCTGCTTGTTCAAGAAAGCACTGGCTGAC 1861
QY 515 MetValArgHisLeuAsp-----GluMetAspLeuSerAspThrProAlaProSer 531
Db 1862 TACTAGCCCAAGAGATCTTGAACCTGAGTCAAGACAGATCTGCTGCTCTCTCA 1921
QY 532 GluValProGluLeu----- 536
Db 1922 AAAATTTGAGAAATTAGCACTGGCCAAAGAAATCATGAAGAAATGTCGAAACAGCATCT 1981
QY 537 -----SerGluTyrValSerValProAspHisPheLeuGln 548
Db 1982 TTGGAAACAGAAAGAGCAAGAGCTTCTCAACCTTCTCCAAAGCCACAGATTGAAA 2041
QY 549 AspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaPro 568
Db 2042 CAGTCACTGATTCATCTCTAGCGGCTCTCTCATCTTCTCTCCAGTTCTTAGATCA 2101

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QY 569 LysGlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsn 588
Db 2102 AGATCTCGC-----TCTCCT 2116
QY 589 AspLeuPheAsnLysSerSerLeuGlnTyrArgAlaLeuGlnGlnPheThrGlnLeu 608
Db 2117 GAC-----AGTTCAAGTTCTCGGTCTCATCCAGCTCATGATCCAAAGACAGATGTA 2170
QY 609 LeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluLeuAsnPhe 628
Db 2171 GCCCAGGACAGTACTCATGCAACCCCTGCTGATAGCCCAAG-----ATGGCTCC 2221
QY 629 ArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsn 648
Db 2222 AGATCAACATCTAGAGCTCCAGATCAAGTCAAGTCAAGTCTCTGTCACATCAAGCAAC 2281
QY 649 LeuThrLysAlaValHis---GlyValLeuGluAspPheArgSerAlaIleAlaGlnGln 667
Db 2282 AGCAGAAATCTCTAGAGCTCCAGTCTCCAGGACAGCAGAC----- 2326
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAla-----AspGln 684
Db 2327 -----AGTATATCTGAACCAAGATCCCTCTTCTGTCAGGAGTT 2368
QY 685 AlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArg 704
Db 2369 GCMACTCCA-----CCAGTGCACAACTGCAAGTCTGTGAGCCAAAGAGAGAG 2416
QY 705 ThrGlu-----GluAlaGluCysArgCysLysProGlyTyrAspSer 718
Db 2417 ACTTCCACTCTCTCATCTCTGTCAGGACAGCGCTGAGTCAAGCTGAATCAGCTGAA 2476
QY 719 GlnGlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGlu 738
Db 2477 AAGCATGAGACCCAGAGGTATACGCTGAGCGGGAGGCCA-----AAGAAGTGTGA 2530
QY 739 ValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGln 756
Db 2531 GCTGAAGAGCAGAGCCACCAAGCTGCCAACAGCCCAAACTCAGAGACTGAG 2584

RESULT 5
US-10-149-736-2
; Sequence 2, Application US/10149736
; Patent No. 6869777
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
; FILE REFERENCE: US-06968
; CURRENT APPLICATION NUMBER: US/10/149, 736
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/31126
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,848
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 13815
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-149-736-2

Alignment Scores:
Pred. No.: 0.000107 Length: 13815
Score: 158.00 Matches: 174
Percent Similarity: 35.82% Conservative: 152
Beet Local Similarity: 19.12% Mismatches: 316
Query Match: 3.84% Indels: 268
DB: 3 Gaps: 45

US-10-007-270-2 (1-797) x US-10-149-736-2 (1-13815)

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QY 14 ILePheLeuGlnValGlnGlyThrLyAspIleSerIleAsnIleTyrHis---SerGlu 32  
 Db 6317 CTTTAAAGCAGAGAGAGTCTTAAAGATATATAAAGCAATTTCACAAATTCAGAGT 6376  
 QY 33 ThrLyAspIleAspAsnProArgGangluThrThrGluSerThrGluLysMetTyr 52  
 Db 6377 CGGATTGATATATTATTCACAAAGAAAGACAGACGCTTGCAAAAGCCACTCCATGGAA 6436  
 QY 53 LysMetSerThr-----MetArg 59  
 Db 6437 AAGCGTAAAGTACAGAAAGCCGTGGCAGACGATGATTCACAGGGGAAAACTTCATAGA 6496  
 QY 60 IlePheAspLeuAlaLysHisArgThrLyArgSerAla-----PhePhePro 75  
 Db 6497 ATGTACAAAGAAAGCAGCAAGGCGGATTCGACAGATCAGTTGAAAAATGGCGACACTTTCAT 6556  
 QY 76 ThrGlyValLysValCysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAla 95  
 Db 6557 TATGATATGAAAGTA-----TTTAATCAATGCGTGAATGAAAGTTTACAG 6601  
 QY 96 TyrTyrArgLeuArgValCysGlnGluAlaValTyrGlu-----AlaTyrArgIlePhe 113  
 Db 6602 TTTTTCAAA---AAGACACAAAAATCTGAAAACTGGAAACATGCTAAATACAAATGGTAT 6658  
 QY 114 LeuAspArgIleProAsp----- 119  
 Db 6659 CTTAAGAACTCCAGATGCGATCGGACGCGTCAAGCTGTTCAGAAACATGATGA 6718  
 QY 120 ThrGlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAsp 139  
 Db 6719 ACTGGGGAA-----GAAATATTTCAACAG----- 6742  
 QY 140 IleGlyLysAsnPheSerAsnSerGlnGluIleLeuAspLeuLeuGlnGlnArgIleLys 159  
 Db 6743 -----TCTTCAAAAACAGATGTCATATTTCTACAAAAAATTTAGCA 6784  
 QY 160 Gln-----ArgSerPheProAspArgLysAspGluIle 170  
 Db 6785 ACCTTGAGTCTGCGGTGCGACGACATCTGCAGAAAGCTGCGAGAAAGAGAAAGAGAT 6844  
 QY 171 SerAlaGluLysThrLeu-----GlyGluProGlyGluThrIleValIle 185  
 Db 6845 GAAGAACAAGAAATCTCTGTGAGATTTCAAGAGATTTAAAGAAATTTCTTTTGTGG 6904  
 QY 186 SerThrAspValAlaAsnValSerLeuGlyProPheProLeuThrProAspPheThrLeu 205  
 Db 6905 CTGGAAAGAGCAGATACATGCTATTAATCTCACTT-----GGAATAGACAGCAG 6955  
 QY 206 LeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGlu 225  
 Db 6956 CTAAAGAA-----CACTTGAACAAGTCAAGTTCAGGACAGAAAGATTGCC 7003  
 QY 226 ThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSerLeuValangln 245  
 Db 7004 CTGGCGCAGGAGATTTCTAAACAATTAATGAACAGACAGACGATCTTGAAGTCT 7063  
 QY 246 LysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLys 265  
 Db 7064 CCCATTAAGGCCAGAAAGCAGCAAGTAAA-----CTTGAAGAAAGCTCAACAG 7111  
 QY 266 SerGlnLeuGlnMetGlnLysIlePheLysLysLeuPro-----GlyPheLysLys 282  
 Db 7112 ACAAAATCTCAGTGAATTAAGGTCTCCAGAGCTTTCAGAGAAACAGAGAGCTTGAG 7171  
 QY 283 IleHisValLeuGlyPheArgProLysLysGlyLysAspGlySerSerSerThrGluMet 302  
 Db 7172 GTTCACTTAAAGATTTTAGGCGAGCTTGAAAGCAG-----CTGGATCAGCTGCTTCG 7225  
 QY 303 GlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeu 322  
 Db 7226 TGGCTCTCTCTATT-----AGAAACCAAGTTGAAATTTATATACCAACCAAGCAGCA 7279  
 QY 323 LeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGln 342

Db 7280 GGACCGCTTGACATTAAGAGAT-----GAAGTAAACAGTTCAAGG----- 7321  
 QY 343 AspLysGlnProGluIleTyrLeuThrAlaThrPheLeuLysArgLysIleSerLysAla 362  
 Db 7322 ---AAACAA-----GCGATGGAGAAAGCTTTGTTCAGAAAGCG 7357  
 QY 363 -----LeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
 Db 7358 CAGCATTTGTATAGAAAA----- 7378  
 QY 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
 Db 7379 -----CAAAGCAGCTAG----- 7390  
 QY 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu 420  
 Db 7391 -----CCAGTGAAGAGAGATTTAGAA 7411  
 QY 421 ThrVal-----AspGlyValaGluHisGlyLeu----- 429  
 Db 7412 GATCTGAGGTCTGAGTGGAGGCTGTAAACATTTACTTCGGAGCTGAGCAAAAGCAG 7471  
 QY 430 ProAspThrSerTyrSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
 Db 7472 CCGTACCGGTCC-----CTGAGCTGAGCACTACTGAGCCTT----- 7510  
 QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
 Db 7511 -----GCCAGTCAAGCTGTACTCTA-----GTGACCAATCTGTGGTT 7549  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle 489  
 Db 7550 ACTAAGGAACCT---GTCATCTCCAACTTAAGAAATGCCATCTTCT----- 7591  
 QY 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerAspAspSerArgSerSer 509  
 Db 7592 -----TTGCTGTGGAGGTA-----CCTGCAGCTGAGCACTCAACCGAGCTTGG 7636  
 QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
 Db 7637 ACAGAACTTACAGACTGCTGCTCTGCTTATGAGATTAAATCAAGAGAGTATG 7696  
 QY 530 ProSerGluValProGluLeuSerGluTyrVal-----SerValProAsp 544  
 Db 7697 GTGGGTATCTGGAAGACATCAATGAATGATCATCAACAGAAAGCAACTGCAAGAT 7756  
 QY 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564  
 Db 7757 -----TTGAAACAGAGACGCCCC-----CAATTGAAAGAACTCATTAAGTCCAG 7804  
 QY 555 ThrIleAlaProLys-----GlyArgGluLeuValAlaPhePheSerLeuArgValAla 582  
 Db 7805 AATTTGAAAAACAAGAACCAAGATCAAGAACTGAAGCTTAATCTGAATTTGAA 7864  
 QY 583 AsnMetAlaPheSer----- 587  
 Db 7865 AGAATTCAGATTCAGTGGATGAGTTCAAGAACGCTGCAGAACAGACAGCAAGTTG 7924  
 QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThrGln 607  
 Db 7925 AATGAAGATGTA---AAGATTTCAACAAATGCGTGAAGGTAAGAGAAAGCCAG 7981  
 QY 608 LeuLeu-----ValPro 611  
 Db 7982 GTCATAGACAGAGTCAAGAGCAAGCTTGATCAGAAAGAGGTCTCACAGATAT 8041  
 QY 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeu-----GluIleLeuAsnPheArg 630  
 Db 8042 GCAATCCAAAGAAAGATACAGAAACCAAGCAGTTGGCCAAAGACCTCGTCAACAGGAG 8101  
 QY 631 GlySerValIleVal-----AsnSerLysMetLysPheAlaLysSerValProTyrAsn 648

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Dd      8102 ATAAAGTGAACGCTGGCAAAATGATTGGCAGTCGAAACTCTTCGGGACTATTCTGCTGAT 8103
Oy      649 LeuThrIyValaValHisGlyValLeuGluAspPhe----- 660
Dd      8162 GATACCCAGAAAAGTACACATGATATACAGACAGATATACATCTCTTCGGGAGAAACATTGAT 8221
Oy      661 -----ArgSerAlaIalaIaIaGlnGlnLeuHISleuGlnIlaAspSerIyr 675
Dd      8222 AAAAGAGTAAATGACCAAGAGGCTGCTTTGGAGAAACTCATAGATTACTGCAGACAGTTTC 8281
Oy      676 SerLeuAsnIleGluProAlaAspGlnIlaAspProCybIysPheLeuAlaCybGlyGlu 695
Dd      8282 CCTCTGACCTGGAG-----AGTTCTTTCTCGATTAACG 8317
Oy      696 PheAlaGlnCybValIysAsn-----Glu 703
Dd      8318 GAAAGCAAAACAACTGCCAATGTCCTTAACAGACGCTTCCCGTAAGAGAAAGCTCCTAGAA 8377
Oy      704 ArgThrGluGluIaIaGluCybArgCybIysProGlyIyrAspSerGlnGlySerLeuAsp 723
Dd      8378 GACTCCAGCGGAGTCAAGAGCTGATGTAACCAATGCGCAAGATCTCCCAAGGAGAAATTGAA 8437
Oy      724 -----GlyLeuGluProGlyLeuCybGlyProGlyThrIysGluCybGluValLeu 740
Dd      8438 ACTCACACAGATATCTATCACATCTTATGAAATATGCCCCAAAATCTTGAGATTCCTTG 8497
Oy      741 GlnGlyIysGlyAlaProCybArgLeuProAspHisSerGluAsnGlnIaIaIyrIysThr 760
Dd      8498 GAAAGTTCCGATGAAGACACCCCTGTTTCAAAAGAGTTTGATTAATCAATTCAGATTCAGTCG 8557
Oy      761 Ser-----ValIysPheGlnAsnGlnIaAsnIysValIleSerIysArgAsn 778
Dd      8558 AGTAACTTCAGAAAAGTCTCTCAACATTAAGTCCCATTTGGAAGCAAGTTCTGACACAG 8617
Oy      779 SerGluLeuLeuThrValGluIyrGluGlu 788
Dd      8618 TGGAAAGCTTGACATCTTCTCTTCAGGAA 8647

RESULT 6
US-08-836-022A-10/c
: Sequence 10, Application US/08836022A
: Patent No. 6001557
: GENERAL INFORMATION:
:   APPLICANT: Trustees of the University of Pennsylvania
:   APPLICANT: Wilson, James M.
:   APPLICANT: Fisher, Krishna J.
:   APPLICANT: Chen, Shu-Jen
:   APPLICANT: Weltman, Matthew
:   TITLE OF INVENTION: Improved Adenovirus Virus and
:   NUMBER OF SEQUENCES: 10
:   CORRESPONDENCE ADDRESS:
:   ADDRESS: Howson and Howson
:   STREET: Spring House Corporate Cntr, P O Box 457
:   CITY: Spring House
:   STATE: Pennsylvania
:   COUNTRY: USA
:   ZIP: 19477
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/836, 022A
:   FILING DATE:
:   CLASSIFICATION: 435
:   PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 08/331,381
:   FILING DATE: 28-OCT-1994
:   ATTORNEY/AGENT INFORMATION:
:   NAME: Bak, Maty E.
:   REGISTRATION NUMBER: 31,215
:   REFERENCE/DOCKET NUMBER: GNPVN.008PCT

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TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 215-540-9200  
/ TELEFAX: 215-540-5818  
/ INFORMATION FOR SEQ ID NO: 10:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 19307 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: cDNA  
/ US-08-836-022A-10

Alignment Scores:  
Pred. No.: 0.000252 Length: 19307  
Score: 157.00 Matches: 173  
Percent Similarity: 35.60% Conservative: 151  
Best Local Similarity: 19.01% Mismatches: 318  
Query Match: 3.81% Indels: 268  
DB: Gaps: 44

US-10-007-270-2 (1-797) x US-08-836-022A-10 (1-19307)

QY 14 ILeheleungInValGInGlyThrLysAspIleSerIleAsnIleTyrHis---SerGlu 32  
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QY 33 ThrLysAspIleAspAsnProProArgAsnGluThrThrGluSerThrGluLysMetYr 52  
DB 8308 CGAGTTGATATATTATTACACAAAGAAAGACAGCACCCTTGCAAAAGTCCACCTCCATGAA 8243  
QY 53 LysMetSerThr-----MetArgArg 59  
DB 8248 AAGGTGAAGATACAGAAAGCCGTGCACAGATGATTTCCAGGGGGAAGAACTTCATACGA 8189  
QY 60 ILeheAspLeuAlaLysHisArgThrLysArgSerAla-----PhePhePro 75  
DB 8188 ATGTACAAAGAACAGCAAGAGCGCATTCGACAGATTCAGTGAAGAAATGCGCACACTTCAT 8129  
QY 76 ThrGlyValLysValCysProGInGluSerMetLysGlnIleLeuAspSerLeuGlnAla 95  
DB 8128 TATGATATGAAAGTA-----TTTAATCAATGGCTGAATGAAGATTGAACAG 8088  
QY 96 TyrTrpArgLeuArgValCysGInGlnAlaValTrpGlu-----AlaTyrArgIlePhe 113  
DB 8083 TTTTTCAAA---AAGACACAAATCTCGAATACTGGMAACATGCTAATATACAAATGCTAT 8027  
QY 114 LeuAspArgIleProAsp----- 119  
DB 8026 CTTAAGAAACCTCCAGATGGCATGGATGGCAGCGTCACACTGTTGTACAGAACCTGAATGCA 7967  
QY 120 ThrGlyGluTyrGlnAspTrpValSerIleCysGInGInGluThrPheCysLeuPheAsp 139  
DB 7966 ACTGGGGA-----GAAATATTCACACG----- 7943  
QY 140 ILeGlyLysAsnPheSerAsnSerGlnIleHisLeuAspLeuLeuGInGlnArgIleLys 159  
DB 7942 -----TCTTCAAAAACGATGTCATATTCATACAAAGAAAATTGACA 7901  
QY 160 Gln-----ArgSerPheProAspArgLysAspGluIle 170  
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QY 186 SerThrAspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeu 205  
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QY 206 LeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrTrhGluArgGlu 225  
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CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, P O Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/427,048A  
FILING DATE: 21-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,022  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: GNVFN.008PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-427-048A-10  
Alignment Scores:  
Pred. No.: 0.000252 Length: 19307  
Score: 157.00 Matches: 173  
Percent Similarity: 35.60% Conservative: 151  
Best Local Similarity: 19.01% Mismatches: 318  
Query Match: 3.81% Indels: 268  
Gaps: 44  
US-10-007-270-2 (1-797) x US-09-427-048A-10 (1-19307)  
QY 14 I l e p h e l e u g l i n v a l g l n g l y t h r l y s a s p i l e s e r l l e a n l l e t y r h i s --- s e r g l u 32  
Db 8368 C T T T T T A A G C A A G A G A G C T C T T A A G A T A T A A A G A C A A T T T G C A A C A A T T C A G G T 8309  
QY 33 T h r l y s a s p i l e a s p a n p r o f a r g a n g i u t h r t h g l u s e r t h r g l u y s m e t y r 52  
Db 8308 C G G A T T A T A T A T T A T T C A C A A G A A G A A G A C A G C C T T G C A A A G T G C C A C C T C C A T G G A 8249  
QY 53 L y s m e t s e r t h r --- m e c a r g l a r g 59  
Db 8248 A A G G T A A A G T A C A G A A C C C T G C A C A G A T G A T T T C C A G G G A A A A A C T T A T C A T 8189  
QY 60 I l e p h e a s p l e u a l a l y s i s a r t h r l y s a r g s e r a l a --- p h e p h e p r o 75  
Db 8188 A T G T A A G A A G A A C G A C A G G G G A T T C C A C A G A T C A G T T G A A A A A T G G C G A C A C T T T C A T 8129  
QY 76 T h r g l y v a l l y s v a l c y e p r o g l i n g l u s e r m e t l y s g i n l l e u a s p e r l e u g l i n a l a 95  
Db 8128 T A T G A T A T C A A G A G T A --- T T A A T C A A T G C T G A A T G A A G T T G A A C A G 8084  
QY 96 T y r t y r a r g l e u a r g v a l c y e g i n g l u a l a v a l t t p g l u --- a l a t y r a r g l i e p h e 113  
Db 8083 T T T T C A A A --- A A G A C A A A A A T C T G A A A C T G G A A C A T G C T A A A T A C A A A T G G T A T 8027  
QY 114 L e u a s p a r g l i e p r o a s p --- 119  
Db 8026 C T T A A G A A C T C A A G A T G C A T T G G G C A G C G T C A A G C T T G T T G C A G A A C A C T G A A T G C A 7967

QY 120 T h r g l y l u t y r g l i n a s p t r p v a l s e r l l e c y s e g i n g l i n g l u t h r p h e c y l e u p h e a s p 139  
Db 7966 A C T G G G A A --- G A A T A A T T C A A C G --- 7943  
QY 140 I l e g l y s a n p h e s e r a s n s e r c l i n i s l e u a s p l e u g l i n a r g l i l e y s 159  
Db 7942 --- T C T T C A A A A C A G A T G C A A T A T T C T A C A A A A A T T A G C A 7901  
QY 160 G l n --- A r g s e r p h e a s p a r g l y s a s p l u l l e 170  
Db 7900 A G C T T A G C T G C G G T G C A G A C A T C G C A A A G A G C T G C A A A A G A A G A A G A G A T T 7841  
QY 171 S e r a l a g l u t y r t h r l e u --- g l y l u p r o g l y g l u t h r l l e v a l l e 185  
Db 7840 G A A G A A C A A A A G A T T G T C T G C A A T T T C A A A G A G A T T A A A G A A T T G T T T G T G C 7781  
QY 186 S e r t h r a s p v a l a l a s n v a l s e r l e u g l y p r o p h e p r o l e u t h r p r o a s p a s p t h r l e u 205  
Db 7780 C T G A A G A A G C A G A T A C A T T G C T A T T A C T C A C T T --- G A A G A T A G C A G C A G 7730  
QY 206 L e u a n g l u l l e l e u a s p a n t h r l e u a n a s p t h r l y s m e t p r o t h r t h r g l u a r g l u 225  
Db 7729 C T T A A A G A A --- C A C T T A C A G A C A G T A C T G C A G A A G A G T T G C C 7682  
QY 226 T h r g l u p h e a l a v a l l e u g l u g l u g l i n a r g v a l g l u s e r v a l s e r l e u a l a n g l n 245  
Db 7681 C T G C C C A G G A A T T C T A A A C A A T T A A T G A A A C A G A G A G A G C A G T C T T G T A A G T C T 7622  
QY 246 L y s p h e l y s a l a g l u l e u a l a s p s e r c l i n s e r p r o t y r t y r g l i n g l u l e u a l a g l y s 265  
Db 7621 C C C A T A A G C C A A A G A A G C A A A G A T A A --- C T T G A A A A G A G C T C A A A C A G 7574  
QY 266 S e r g l i n e u g l i n m e g l i n l y s i l e p h e l y s l y s e u p r o --- G l y p h e l y s l y s 282  
Db 7573 A C A A A T C C C A G T G A T A A A G T C C A G A C T T A C C T G A A A A C A A G A A G A G C T T G A G 7514  
QY 283 I l e h i s v a l l e u g l y p h e a r g p r o l y s l y s g l u y s a s p l y s e r s e r t h r g l u m e t 302  
Db 7513 G T T C A C T T A A A A G A T T T T A G C A G C C T T G A A G A G C --- C T G A T C A C C T G 7466  
QY 303 G l i n e u t h r a l a l e p h e l y a r g h i s e r l a g l u a l a l y s e r p r o a l s e r a s p l e u 322  
Db 7465 C T T C T G G G G T C T C T A T T A G A A C C A G T T G A A A T T T A A C C A A C A A G T C A G C A 7406  
QY 323 L e u s e r p h e a s p e r a s n l y s i l e g l u s e r g l u g l u a l t y r h i a g l y t h r m e c g l u g l u 342  
Db 7405 G A C C G T T T G A C A T A A A G A A G A T T --- G A A G T A C A G T T C A C G T --- 7364  
QY 343 A s p l y s g i n p r o g l u i l e t y r l e u t h r a l a t h r a s p l e u l y s a r g l e u l l e s e r l y s a l a 362  
Db 7363 --- A A A C A A --- G C G A T G T G A A A G G C T T T T G C A A A G G G 7328  
QY 363 --- L e u g l u g l u g l i n s e r l e u a s p v a l g l y t h r l i e g l i n p h e t h r a s p l u l l e 380  
Db 7327 C A G C A T T T G T A A G A A A A --- 7307  
QY 381 A l a g l y s e r l e u p r o a l a p h e g l y p r o a p t h r g l i n s e r g l u l e u p r o t h r s e r p h e a l a 400  
Db 7306 --- C A A G A C T C A G --- 7295  
QY 401 V a l l i e t h r g l u a s p a l a t h r l e u s e r p r o g l u e u p r o p r o v a l g l u p r o g l i n l e u g l u 420  
Db 7294 --- C A G T G A A A G A A G A A G T T A G A A 7274  
QY 421 T h r v a l --- A s p c l y a l a g l u h i a g l y l e u --- 429  
Db 7273 G A T C G A G C T T G A T G G A G A G C T G T A A C A T T T A C T C G G A G C T G A G A C A A A G C A G 7214  
QY 430 P r o a s p t h r s e r t r p s e r p r o p r o a l a m e r a l a s e r t h r s e r l e u s e r g l u a l a p r o p r o 449  
Db 7213 C T G A C C G T G C --- C T G A C T G A G A C A C T A C T G A G C T C T --- 7175

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Qy 450 PhepMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
Db 7174 -----GCCAGTCAGACTGTACTCTA-----GGACACCATCTGTGTT 7136
Qy 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle 489
Db 7135 ACTAAGGAACCT--GTCATCTCCAAACTAGAAATGTCATCTCTCT-- 7094
Qy 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerAspAspSerArgSerSer 509
Db 7093 -----TTGCTGTGGAGTA-----CTGCACCTGGCAGACTTACCGAGCTGG 7049
Qy 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
Db 7048 ACAGACTTACAGACTGCTGTCTGTCTGTAGTAAATCAACAGAGTAGTG 6989
Qy 530 ProSerGluValProGluLeuSerGluTyrVal-----SerValProAsp 544
Db 6988 GTGGGTGATCTGAGAACATCAATGAATGATCATCAACAGAAAGCAACCTGCAAGAT 6929
Qy 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564
Db 6928 -----TTGGAACAGAGACGCCCC-----CAATTGAGAAGACTTACTGTGCTGCCAG 6881
Qy 565 ThrIleAlaProLys-----GlyArgGluLeuValValPhePheSerLeuArgValAla 582
Db 6880 AATTGAAACAAACAAACAGCAATCAAGAACTAGAACATCATTAATGCAATGCAATGAA 6821
Qy 583 AsnMetAlaPheSer----- 587
Db 6820 AGAATTTCAGATTTCAGTGGATGAGTTCACAGAACAGCTGCAGAACAGACAGATGG 6761
Qy 588 AsnAspLeuPheAsnLeuSerSerLeuGlnTyrArgAlaLeuGlnGlnGlnPheThrGln 607
Db 6760 AATGAAATGTTA--AAGGATTCACACAAATGGCTGGAGCTAAGAGAAAGCCGAAAG 6704
Qy 608 LeuLeu-----ValPro 611
Db 6703 GTCATAGACAGAGTCAGAGGCAAGCTTGACTGAAAGAAAGCTCTCACACAGTAGAT 6644
Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeu--GluIleLeuAsnPheArgAsn 630
Db 6643 GCATTCCTCAAAAGAAAGATCAGAAACCAAGCAGTTGGCCAAAGCTTCGCAACGCGAG 6584
Qy 631 GlySerValIleVal-----AsnSerIleMetLysPheAlaLysSerValProTyrAsn 648
Db 6583 ATTAAGTGTAGACGTGGCAATGATTTGGCACTGAAACTTCTTGGGACTATTCTGCTGAT 6524
Qy 649 LeuThrIlyAlaValHisGlyValLeuGluAspPhe----- 660
Db 6523 GATACCAAGAAAGTACATGATTAACAGAAATATCATACTCTTGGGGAACATTCAT 6464
Qy 661 -----ArgSerAlaAlaAlaGlnLeuHisLeuGlnIleAspSerTyr 675
Db 6463 AAAAGAGTAACTGAGCAAGAGCTGCTTTGGAGAAACTCATAGATTCTGCACAGCTTC 6404
Qy 676 SerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlu 695
Db 6403 CCTCTGGACCTGGAG--AAGTTCTTCTTCTGGAATTACG 6368
Qy 696 PheAlaGlnCysValIlyAsn-----Glu 703
Db 6367 GAAGCAGAAACAACTGCCAATGTCTACAGACGCTTCCGTAAGAGAAACTCTTAGAA 6308
Qy 704 ArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAsp 723
Db 6307 GACTCCAGGAGAGTCAGAGCTGATGAACCATGCAAGATCTCCAGAGAGAAATTTGAA 6248
Qy 724 -----GlyLeuGluProGlyLysGlyProGlyThrIlyGluCysGluValLeu 740
Db 6247 ACTCACACAGATATCTATCATCAATCTTATGATGAAATGGCAAAATATCTTGAAGATCCTTG 6188
Qy 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrIlyThr 760

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Db 6187 GAAGTTCCGATGAGACCCCTTTACAAAGCGTTTGGATTAACATGAATTTCAAGTGG 6128
Qy 761 Ser-----ValIlyLysPheGlnAsnGlnAsnAsnLysValIleSerLysArgAsn 778
Db 6127 AGTAACTTCAGAAAGAGTCTCTCCACATTAAGGCCATTTGGAAAGCAAGTTTGACGAG 6068
Qy 779 SerGluLeuLeuThrValGluTyrGluGlu 788
Db 6067 TGAAGCGTTTGATCTTCTCTTCAGGAA 6038

RESULT 8
US-08-976-255-5
; Sequence 5, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plozman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-976-255-5

Alignment Scores:
Pred. No.: 0.000966 Length: 8982
Score: 146.00 Matches: 175
Percent Similarity: 32.72% Conservative: 109
Best local Similarity: 20.16% Mismatches: 302
Query Match: 3.55% Indels: 283
DB: Gaps: 38

US-10-007-270-2 (1-797) x US-08-976-255-5 (1-8982)
Qy 40 ProArgAsnGlnThrThrGluSerThrGluLysMetLysMetSerThrMetArgArg 59
Db 2203 CCTTCAACATATATTTAATGATGTGACAAATCGAAGATTTGGCCAGTCACCAAAA 2262
Qy 60 IlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLys 79

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Db      2263 ATATTCGACTTAATGAATTAAACGAGTTCAACGCACTTAAACCTGCACCTTAAAGT 2322
Qy      80 ValCys-----ProGlnGluSerMetLeuGlnIleLeuAspSerLeuGlnIleIleTyr 96
Db      2323 TCCAGTTTGGATTAACCCCAAGAGTCACTC----- 2352
Qy      97 TyrArgLeuArgValCysGlnGlnIleValIleProGlnIleValIlePheLeuAspArg 116
Db      2352 ----- 2352
Qy      117 IleProAspThrGlyGluTyrGlnAspTyrVal-----SerIleCysGlnGlnIleTyr 134
Db      2353 -----ATAACAGGCCACTTTGAGAAAGAAAGCCCGTAAGATTTTGAACAGTGAAGCT 2406
Qy      135 PheCysLeuPheAsp----- 139
Db      2407 CTCCTGCCTATCAATTAATCTTATGACACAGATTAATTGATTCATTGAATGTTCAAGAA 2466
Qy      140 IleGlyLeuAspPhe-----SerAsnSer 147
Db      2467 TTCTCGAAGAAACTTTTATTTCTTCAAGAGAAAACTTACTTAAGGCTCATTTGTCAGC 2526
Qy      148 GlnGlnIleLeuAspLeuLeuGlnGlnIleArgIleLeuGlnIleArgSerPheProAspArgIle 167
Db      2527 AAAGAACACATTAATATGATCTTCAGACAGAACTTAAGAAATGCTGTTTACTGAAGCTATG 2586
Qy      168 AspGlnIleSerIleGluIleTyrIle-----GlyIlePro 179
Db      2587 TTAGAAGCTCACTGATGAAACTCTTATGATCTAGCTTCAGTTGCTCGAATAATAGCA 2646
Qy      180 GlyIleThrIleValIleSerThrAspValIleAsnValSerLeuGlyProPheProLeu 199
Db      2647 GGC-----TTGCTCTTTGTCAGAGAAAGCTAAGC-----ACA 2679
Qy      200 ThrProAspAspThr-----LeuLeuAsnGlnIleLeuAspAsnThrLeuAsn--- 215
Db      2680 AAGGTGACGATACATGATGATCATGCTCACAGGTGACACTTTGAGCACTCATTTGCACTGCT 2739
Qy      216 -----AspThrIleMetProThrThrGlnIleArgIleThrGlnIlePheIleValIleGlnIle 233
Db      2740 TCCCCCGAAGTGCAGTACTCTCTCACTCTTCGAAACAGAAAGAAAGCCCGCTCGGAGTA 2799
Qy      234 GlnArgValIleLeuSerValSerLeuValAsnGlnIlePheIleValIleGlnIleAsp 253
Db      2800 CCCCAGACTCACTCCCAACACAGGAGAAACCCAGCCCACTGTTAAGATGTTATGTC 2859
Qy      254 SerGlnSerProTyrTyrGlnIleValIleGlyLeuSerGlnIleGlnIleMetGlnIleVal 273
Db      2860 CCGAGAGACTGTCCTCCACAGGACATCATGCTGACCTGCTCCCGGTGAATTT 2919
Qy      274 PheIleValLeuProGlyPheIleValIleIleValIleGlyPheIleArgProIleValIle 293
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Qy      294 LysAspGlySerSerSerThrGlnMetGlnIleThrAlaIlePheIleValIleIleSerAla 313
Db      2968 TCTCTCGGAGAGTGAAGAGACCTGCACTCAC-----GAAAGTGACTCTGTT 3018
Qy      314 GlnIleAlaLeuSerProIleAspLeuLeuSerPheAspSerAsnIleGlnIle---Ser 332
Db      3019 CTTCGTCGATGACATCTCTGCGACAGGTGAAGTGAAGGATGCTCCCGGAACCTGGA 3078
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Qy      353 ThrAspLeuLysArgLeuIleSerIleValIleGlnIleGlnIleSerIleAspValGly 372
Db      3124 -----CGCGGCTAGAGAAAACTTAGAGGCTGTGAGACTTAAATACGCTC 3171
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Db      3172 AATTCAAAAGACGACAAAGAAAGAGGCTTGCTGCTCTCTCCCTCGACTCA--- 3228

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Qy      393 SerGlnLeuProThrSerPheAlaValIleThrGlnAspAlaThrIleuSerProGlnLeu 412
Db      3229 -----ACCACTAGAGACAGACTCTCTGAGAGAC---AGCTTTCAGACACCTTCC 3273
Qy      413 ProProValIleProGlnIleGlnIleThrValIleAspGlyValIleGlu--- 426
Db      3274 CCAAGCTCTGAGCCGCTCTGAGAAACCCGAGACTCTCTGAGTCAAGTGAATGCCAGAA 3333
Qy      426 ----- 426
Db      3334 GCGCTACTGAGACTTTAGATCTCAGACTCCCAAGAACTAGTCCCGCATTAAGCCG 3393
Qy      427 -----HisGlyLeuProAspThrSerTyrSer---ProProAla 438
Db      3394 GAGACAGTGCCTACGAAACAGAGAACTTGAAGTCTCCGAGTGAACCTTGATCCCGCT 3453
Qy      439 MetAlaSerThrSerLeuSerGlnIleAlaProPhePheMetAlaSerSerIlePheSe 458
Db      3454 CCGAGAGGACCCGACAGCTCAAGAACAGCCACACGAGGATGACGAGCCACAGCGGTCTG 3513
Qy      458 rLeuThrAspGlnIleTyr----- 464
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Qy      465 -----ThrAspThrMetAlaThrAspGln 472
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Qy      472 nThrMet---LeuValIleProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491
Db      3634 GACATGACTCTGAGCCCGAGAAAGGTCGTGAGAGGTCCTCGGGA-ACCTCCCACTCCGC 3692
Qy      491 nLeuAlaLeuGlyIleSerIlePro-----ProAla 501
Db      3693 CTTCGATGTTGTGAACAGAGACAGCCCTCAACGAGCCAGTCTCCCGAGCAAAAGTCTCCG 3752
Qy      501 aSerSerAsp-----AspSerArgSerSerAlaGlyIleGlnIleAspMetValIleArgIle 518
Db      3753 TCCCGAGATTAAGCTGCTCGTGAAGCCAGAAAGAGCCAGCCAGATGAAGTGTCTCTCCG 3812
Qy      518 nLeu-----AspGlnMetAspLeuSerAspThrProAlaProSerGln-----Val 533
Db      3813 TTTCGACAACTTCAGTGAACCTGAATTAAGACCCACGCGAGCCAGCACAGACTGCTGT 3872
Qy      533 lProGlu-----LeuSerGln 538
Db      3873 TCCCGAGAGGTGATCCACAGGAAGAGAGCCAGCACTCCCTGAGTGTGCTGAATCC 3932
Qy      538 uTyrValSerValIleProAspIlePhe---LeuGlnAspThrThrProValSer----- 554
Db      3933 AGAATTAACAGCGGAGTGAAGTTCAGACACAGAGACGATTCGCCCTTGACACCTCGCTTC 3992
Qy      555 -----AlaLeuGlnIleTyrIleThr 561
Db      3993 CACGGGAGCAACAGAAAGAACTCTGCTCAACCAATTTGCGCTGAGACAGTCCCT 4052
Qy      562 -SerSerMetThrIleAlaProIleGlyArgGlnIleValIle-----PhePhe 577
Db      4053 GTCCAGACCACTCCGAGGCGCCGAACTTGAAGAGCCGAGACATCAAGAAAGGAATACCTGG 4112
Qy      577 eSerLeuArgValIleAlaMetAla---PheSerAsnAsp----- 589
Db      4113 GAAACTCGGAGGTGTCAGGATGCTGACCTTCAGAGACGAGATGATGATGACAGAGGA 4172
Qy      590 -----LeuPheAsnLysSerSerLeuGln 597
Db      4173 GAGCAAAACAGCGACGACTGCGAGAGACCTGCGGCTTCAACCTGCAATGACCTCAG 4232
Qy      597 uTyrArgIleLeuGlnIleGlnIlePheThrGlnIleLeuValIleProTyrIleArgSerAsnIle 617
Db      4233 CTCGAGTTCGAGAGAGAG---ACCGAGACCCCGTGCCTCATCTCCAGCAACA 4286

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Oy      617  uThnglyhelysGlnleuGluIleLeuansPhenrgansnlgyservalIleValaense 637
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Db      4318  -----CCNACAGCGGCCCATGCCCCGACCCACTGCC----- 4350
Oy      657  uGluasPhe---ArgseralalaIglnglnleuHtseuGluIleasPertyse 676
Db      4351  -GAGAGCTCGAAGAAAGAAAAGAAAGCGAGTCACGTTTTTCATGATGCACAGTCACTACT 4409
Oy      676  rleuansnlgIu---ProAlaapGlnAlaIasProcyelysPheleuAlaCyglYgl 695
Db      4410  GTTGACACAGAGACCCCAACCAAGAGCTGGAGCCCTGTGGAGAGAGAGCGTGGGCCC 4465
Oy      695  u-----PhealagInCyseVallyas 702
Db      4470  GGACCTGAGCGGCGCCACGCCCTCAGGCTCTCCCTACCTGAGCAGAGTGCATCACTC 4528
Oy      702  ngluArgThrgIuAlaIglu 709
Db      4530  CGAAGCTCACACCGACGAAGAA 4551

RESULT 9
/ Sequence 1, Application US/08479537A
/ Patent No. 5861381
/ GENERAL INFORMATION:
/ APPLICANT: CHAMON, Pierre
/ APPLICANT: KIENY, Marie-Paule
/ APPLICANT: LATHE, Richard
/ APPLICANT: HARBOVENT, Maira
/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
/ TITL OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22133-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/479,537A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 90/13101
/ FILING DATE: 23-OCT-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/FR91/00835
/ FILING DATE: 23-OCT-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/039,320
/ FILING DATE: 04-APR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/403,576
/ FILING DATE: 14-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Teeklin, Robin L.
/ REGISTRATION NUMBER: 35,030
/ REFERENCE/DOCKET NUMBER: 017753-025
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:

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1 LENGTH: 6192 base pairs
2 TYPE: nucleic acid
3 STRANDEDNESS: single
4 TOPOLOGY: linear
5 MOLECULES TYPE: DNA (genomic)
6 FEATURE:
7 NAME/KEY: s1g_peptide
8 LOCATION: 58..120
9 FEATURE:
10 NAME/KEY: repeat_region
11 LOCATION: 439..5239
12 OTHER INFORMATION: /note= "The nucleotides spanning
13 OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
14 OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
15 OTHER INFORMATION: The number of such repeats varies from 1 to 80."
16 FEATURE:
17 NAME/KEY: mat_peptide
18 LOCATION: 121..6166
19 FEATURE:
20 NAME/KEY: repeat_region
21 LOCATION: 457
22 OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
23 OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
24 OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
25 FEATURE:
26 NAME/KEY: repeat_region
27 LOCATION: 487
28 OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
29 OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
30 OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
31 FEATURE:
32 NAME/KEY: repeat_region
33 LOCATION: 496
34 OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
35 OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
36 OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
37 US-08-479-537A-1
38
39 Alignment Scores:
40 Pred. No.: 0.000558 Length: 6192
41 Score: 145.50 Matches: 74
42 Percent Similarity: 38.11% Conservative: 51
43 Best Local Similarity: 22.56% Mismatches: 144
44 Query Match: 3.53% Indels: 59
45 DB: 2 Gaps: 13
46
47 US-10-007-270-2 (1-797) x US-08-479-537A-1 (1-6192)
48
49 Oy 389 ProAepThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeu 408
50 Db 4921 CCGGACGNNAGG---CCGNNCCGGGCTCCACCGCCCCGNNNGCCACGGTGTACCTCG 4977
51 Oy 409 SerProGluLeuProPro-----ValGlnProGlnLeuGluThrValAspGly 424
52 Db 4978 GCCCGGACGNNAGGCGCGNNCCGGGCTCCACCGCCCCGNNNGCCACGGTGTACCTCG 5037
53 Oy 425 AlaGluIleGlyLeuProAepThr---SerTyrSerProAlaMetAlaSerThrSer 443
54 Db 5038 GCCCGGACGNNAGGCGCGNNCCGGGCTCCACCGCCCCGNNNGCCACGGTGTACCTCG 5097
55 Oy 444 LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGly 463
56 Db 5098 GCCCGGACGNNAGGCGCG-----NNNCCGGGC 5124
57 Oy 464 ThrThrAspThrMetAlaThrAspGlnThrMetLeu-----ValProGly 478
58 Db 5125 TCACCGCGCCCGNNNGCCACAGGTGTACCTCGGCCCGGACGNNAGGCGCGNNCCGGGC 5184
59 Oy 479 LeuThrIleProThrSer-----AspTyrSerAlaIleSerGlnLeuAlaLeuGly 495
60 Db 5185 TCACCGCGCCCGNNNGCCACAGGTGTACCTCGGCCCGGACGNNAGGCGCGNNNTTGGC 5244
61 Oy 496 IleSerIleProPro-----AlaSerSerAspAspSerArgSerSerAlaGlyGly 512

```

Db 5245 TCACACGGCCCTTCATCCACATATGCACCTCGGCTCAGGCTCTGCATCAGGCTCAGCT 5304  
Qy 513 GluAepMetValArgHisLeuAepGluMetAepLeuSerAepThrProAlaProSerGlu 532  
Db 5305 TCTACTCTGTGTGACCAACGACCTCTGCACGGGTACACCAACCCACGACAGAGC 5364  
Qy 533 ValProGluLeuSerGluThrValSerValProAepHisPheLeuGluAepThrThrPro 552  
Db 5365 ACTCCACCC-----ACATCTCCAGGACCACTCATCTCTCTTACTCTCTTACCCACC 5409  
Qy 553 Val-----SerAlaLeuGluThr 558  
Db 5410 CTTCGACAGCATGACCAAGCATGATGCCAGTACATCACCATGACAGGATCCTCCT 5469  
Qy 559 ILeuThrSerSerMetThrIleAlaProGlyArgGluLeuValPhePhe--- 577  
Db 5470 CTCACCTCTCCCATACAGCACTTCTCCCAAGTGTCTACTGGGGTCTCTTTCTTTTTC 5529  
Qy 578 ---SerLeuArgValAlaMetAlaPheSerAepAepLeuPheAepLeuSerSerLeu 596  
Db 5530 CTGCTCTTTTCACTTTCAAACTCCAGTTTAATTCCTCTGTGAMAGATCCACGACCGAC 5589  
Qy 597 GluThrArgAlaLeuGluGluGlnPheThrGlnLeuLeuValProThrLeuArgSerAep 616  
Db 5590 TACTACCAAGAGCTGCAGAGACATTTCTGAAATGTTTTCGAAATTAATAACAGAGG 5649  
Qy 617 LeuThrGlyPheGlyGlnLeuGluIleLeuAepPheArgAepGlySerValIleValAep 636  
Db 5650 -----GTTTTCTGGGCTCTCCCATTAATTAAGTTTCAAGCCAGCACTGTGGTGTACAA 5703  
Qy 637 SerLeuMetLeuPheAlaLeuSerValProThrAepLeuThrIleValHisGlyVal 656  
Db 5704 TTGACTCTGGCCCTTCGAGAAGGT-----ACCATCATGTCTCCACGACGCG 5748  
Qy 657 -----LeuGluAepPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAep 673  
Db 5749 GAGACACAGTTCAATCATGATTAACGAGAGAGCTCTGTGATTAATTAACGATCTCA 5808  
Qy 674 SerThrSerLeuAepGluPro 681  
Db 5809 GACGTACGCGTGTGATGTGCA 5832  
RESULT 10  
US-09-083-116-1  
/ Sequence 1, Application US/09083116  
/ Patent No. 6203795  
/ GENERAL INFORMATION:  
/ APPLICANT: CHAMBERON, Pierre  
/ APPLICANT: KIENEY, Marie-Paule  
/ APPLICANT: LATHIE, Richard  
/ APPLICANT: HAREUVENI, Mara  
/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE  
/ TITILE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR  
/ NUMBER OF SEQUENCES: 5  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
/ STREET: P.O. Box 1404  
/ CITY: Alexandria  
/ STATE: Virginia  
/ COUNTRY: United States  
/ ZIP: 22313-1404  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/083,116  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/479,537

Qy 389 ProAepThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAepAlaThrLeu 408  
Db 4921 CCGAGACNNAGG---CCGNNCCGGGCTCCACCGCCCCNNNGCCACAGGTGTCACTCG 4977  
Qy 409 SerProGluLeuProPro-----ValGluProGlnLeuGluThrValAepGly 424  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/FR91/00835  
FILING DATE: 23-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,320  
FILING DATE: 04-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/403,576  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 017753-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6192 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 58..120  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 439..5239  
OTHER INFORMATION: /note= "The nucleotides spanning 439-5239 constitute a repeated region wherein the repeat is 6 nucleotides and encodes 20 amino acids, 17 of which are fixed  
OTHER INFORMATION: The number of such repeats varies from 1 to 80."  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 121..6166  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 457  
OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN  
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA  
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 487  
OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN  
OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA  
OTHER INFORMATION: or ACG; and Asn = AAT or AAC."  
FEATURE:  
NAME/KEY: repeat\_region  
LOCATION: 496  
OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN  
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA  
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."  
US-09-083-116-1  
Alignment Scores:  
Pred. No.: 0.000558  
Score: 145.50  
Percent Similarity: 38.11%  
Best Local Similarity: 22.56%  
Query Match: 3.53%  
DB: 3  
Length: 6192  
Matches: 74  
Conservative: 51  
Mismatches: 144  
Indels: 59  
Gaps: 13  
US-10-007-270-2 (1-797) x US-09-083-116-1 (1-6192)

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Db      4978  GCCCGGAGCANNAGCCGNNCCGGGCTCCACCGCCGCCNNNNCCCAAGCTGTCACCTCG 5037
Qy      425  AAGAGTGGTLeuProAspThr---SerTserProProAlaMetAlaSerThrSer 443
Db      5038  GCCCGGAGCANNAGGCGGNNCCGGGCTCCACCGCCGCCNNNNCCCAAGCTGTCACCTCG 5097
Qy      444  LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGly 463
Db      5098  GCCCGGAGCANNAGGCGG-----NNNCCGGGCG 5124
Qy      464  ThrThrAspThrMetAlaThrAspGlnThrMetLeu-----ValProGly 478
Db      5125  TCCACCGCGCCCGCANNNGCCCAAGCTGTCACCTCGCGCCCGGACNNNAGCCGNNCCGGGCG 5184
Qy      479  LeuThrIleProThrSer-----AspTyrSerAlaIleSerGlnLeuAlaLeuGly 495
Db      5185  TCCACCGCGCCCGCANNNGCCCAAGCTGTCACCTCGCGCCCGGACNNNAGCCGNNNTTGGGCG 5244
Qy      496  IleSerHisProPro-----AlaSerSerAspAspSerAspSerAspIleGlyGly 512
Db      5245  TCCACCGCGCCCTCCAGTCCAGATGTCACCTCGCGCTCAGGCTCGATCAGCTCAGCTCAGCT 5304
Qy      513  GluAspMetValArgHisLeuAspGlnMetCAspLeuSerAspThrProAlaProSerGlu 532
Db      5305  TCTACTCTGTGTCCACACGCGACCTCTGCCAGGCGCTACCACCAACCCCAAGCAGCAAGAGC 5364
Qy      533  ValProGluLeuSerSerGluTyrValSerValProAspHisPheLeuGluAspThrPro 552
Db      5365  ACTCCACCC-----ACATTTCCAGCCACACCTCTGATTCCTCTTACCCACC 5409
Qy      553  Val-----SerAlaLeuGlnTyr 558
Db      5410  CTGGCAGCCATAGCACAAGACTGATGCCAGTAGAGACTCACCATTAGACGCGTACTCTCT 5469
Qy      559  IleThrThrSerSerMetThrIleAlaProGlyGlyArgGlnLeuValAlaPhePhe--- 577
Db      5470  CTCACCTCTCTCCATTCACACGACCTCTCCCGCAGTGTCTACTGGGCTCTCTTCTTTTTC 5529
Qy      578  ---SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeu 596
Db      5530  CTGTCTTTTCACTTCAATTCACAACTCCAGTTAATTCCTCTCTGAAAGATCCCGACCGAC 5589
Qy      597  GluTyrArgAlaLeuGlnGlnIlePheThrGlnLeuLeuValProTyrLeuArgSerAsn 616
Db      5590  TACTACCAAGAGCTGAGAGAGACATTTCTGAATGTTTTCAGATTAATAACAAGG 5649
Qy      617  LeuThrGlyPheLeuGlnLeuGlnIleLeuAsnPheArgAsnGlySerValIleValAsn 636
Db      5650  ---GGTTTCTGGGCTCTCCCAATATTAAATTCAAGCCAGAACTCTGTGGTGGTACAA 5703
Qy      637  SerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyVal 656
Db      5704  TTGACTCTGGCTTCGAGAGAGGT-----ACCATCAATTCACACGACG 5748
Qy      657  -----LeuGluAspPheArgSerAlaAlaAlaGlnGlnLeuHisLeuGlnIleAsp 673
Db      5749  GAGACACAGTTCATGATGATATAAAGCAAGACGCTCTCATATTAACCTGACGATCTCA 5808
Qy      674  SerTyrSerLeuAsnIleGluPro 681
Db      5809  GACGTCAAGCTGATGATGTGCCA 5832

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; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 2213-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,916A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURES:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURES:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; NAME/KEY: repeat_region
; LOCATION: 496

```

OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN  
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA  
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."  
US-09-134-916A-1

## Alignment Scores:

Pred. No.:	0.00058	Length:	6192
Score:	145.50	Matches:	74
Percent Similarity:	38.11%	Conservative:	51
Best Local Similarity:	22.56%	Mismatches:	144
Query Match:	3.53%	Indels:	59
DB:	3	Gaps:	13

US-10-007-270-2 (1-797) x US-09-134-916A-1 (1-6192)

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QY 389 ProAapThrglnSerGluLeuProThrSerPheAlaValIleThrglnApeAlaThrLeu 408
DB 4921 CCGGACNNNAGG---CCGNNCCGGGCTCCACCGCCCCNNNGCCACAGGTGTCACTCG 4977
QY 409 SerProGluLeuProPro-----ValGluProGlnLeuGluThrValAapGly 424
DB 4978 GCCCGGACNNNAGGCGGNNCCGGGCTCCACCGCCCCNNNGCCACAGGTGTCACTCG 5037
QY 425 AlaGluHisGlyLeuProAapThr---SerTrpSerProAlaMetAlaSerThrSer 443
DB 5038 GCCCGGACNNNAGGCGGNNCCGGGCTCCACCGCCCCNNNGCCACAGGTGTCACTCG 5097
QY 444 LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAapGlnGly 463
DB 5098 GCCCGGACNNNAGGCGG-----NNNCCGGGCG 5124
QY 464 ThrThrAapThrMetAlaThrAapGlnThrMetLeu-----ValProGly 478
DB 5125 TCCACCGCCCCNNNGCCACAGGTGTCACTCGCCCGGACNNNAGGCGGNNCCGGGCG 5184
QY 479 LeuThrIleProThrSer-----AapTrpSerIleAlaSerGlnLeuAlaGly 495
DB 5185 TCCACCGCCCCNNNGCCACAGGTGTCACTCGCCCGGACNNNAGGCGGNNNTTGGCG 5244
QY 496 IleSerHisProPro-----AlaSerSerAapAapSerAapSerAapGly 512
DB 5245 TCCACCGCCCTCCAGTCCACATGTCACCTCGGCGCTCAAGGCTGTCATCAAGCTAGCT 5304
QY 513 GluAapMetValArgHisLeuAapGluMetAapLeuSerAapThrProAlaProSerGlu 532
DB 5305 TCTACTCTGTGTACACACGACCTCTCCAGGGCTACCAACACCCAGCAGCAAGAC 5364
QY 533 ValProGluLeuSerGluThrValSerValProAapHisPheLeuGlnAapThrPro 552
DB 5365 ACTCCACCC-----AGCATTCCTCAGCCACCTGTGATCTCTCTACACCC 5409
QY 553 Val-----SerIleLeuGlnThr 558
DB 5410 CTTCGACAGCCATAGCAACAAGTGTGCGAGTAGACATCACCATGACACGCTACTCT 5469
QY 559 IleThrTrpSerSerMetThrIleAlaProGlyArgGluLeuValIlePhePhe--- 577
DB 5470 CTCACCTCTCTCAATACACGACCTCTCCCACTGTCTACTAGGGGTCTCTTCTTTTC 5529
QY 578 ---SerLeuArgValAlaAapMetAlaPheSerAapAapLeuPheAapLeuSerSerLeu 596
DB 5530 CTGTCTTTTCAATTTCAAACTCCAGTTTAATCTCTCTGTGAAATCTCCAGCAGCAG 5589
QY 597 GluTrpArgAlaLeuGlnGlnIlePheThrGlnLeuLeuValProTrpLeuArgSerAap 616
DB 5590 TACTACCAAGAGCTGCAGAGAGACATTTCTGAATGTTTTTGAGAAATTATAACAAGG 5649
QY 617 LeuThrGlyPheLeuGlnLeuGluIleLeuAapPheArgAapGlySerValIleValAap 636
DB 5650 -----GGTTTCTGGGCTCTCCATATTATTAAGTTCAGGACCAATCTGTGGGTACAA 5703
QY 637 SerTrpMetLeuPheAlaLeuSerValProTrpAapLeuThrValAlaHisGlyVal 656

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DB 5704 TTGACTGTGGCCTTCCGAAAGT-----ACCATCAATGTCCACGACGNG 5748
QY 657 -----LeuGluAapPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAap 673
DB 5749 GAGACACAGTTCAATCATCATATATAACGGAAGCAGCTCTCGATATTAACCTGACATCTCA 5808
QY 674 SerTrpSerLeuAapHisGluPro 681
DB 5809 GACGTACAGGTGATCATGTGTGCCA 5832
RESULT 12
5180808-1
; Patent No. 5180808
; APPLICANT: RUOSLAHTI, ERKKI I.
; TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
; SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
; ANTIBODIES, AND METHODS OF DETECTING THE SAME
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/441,179
; FILING DATE: 27-NOV-1989
; SEQ ID NO:1:
; LENGTH: 8224
5180808-1
Alignment Scores:
Pred. No.: 0.00106 Length: 8224
Score: 145.00 Matches: 185
Percent Similarity: 31.30% Conservative: 128
Best Local Similarity: 18.50% Mismatches: 342
Query Match: 3.52% Indels: 346
DB: 9 Gaps: 43
US-10-007-270-2 (1-797) x 5180808-1 (1-8224)
QY 40 ProArgAangluThrThrglnSerThrglnSerThrglnSerThrglnSerThrglnSer 59
DB 4377 CCTCAAAATCAGACTGTCAAGTGGGACAGAGAAATC---CAGACTGATGACCAACAACC 4433
QY 60 IlePheAapLeuAlaValHisArgThrIleArgSerAlaPhePheProThrGlyValIle 79
DB 4434 ATTAATGAAACAAGACTTACAGAAATCTTCAACAGCAGAAAT----- 4478
QY 80 ValCyProGlnGluSerMetLeuGlnIleLeuAapSerLeuAlaTrpTrpArgLeu 99
DB 4479 -----ACGAAACAACAACATCTACTGATTTTCTGCTAGACCTTATGGTTT 4529
QY 100 ArgValCyGlnGluAlaValIleTrpGluAlaTrpArgIlePheLeuAapArgIleProAap 119
DB 4530 GAAATGGCCAAAGAAATTTGTTACATCAGACCAACAACATCTGACTTGATTAAGAACT 4589
QY 120 ThrGluGluTrpGlnAapTrpValSerIleCyGlnGlnIleThrPheCyLeuPheAap 139
DB 4590 TCTGAGAAAGATCTCGAAGAGTG-----GAT 4616
QY 140 IleGlyLeuAapPheSerAapSerGlnGluHisLeuAapLeuGlnGlnArgIleLeu 159
DB 4617 ATGTGTAATTCATT-----CACATCTGCAACTACTGAGCAACACGCAACGAC 4661
QY 160 GlnAapSerPheProAapArgIleAapGluIleSerAlaGluLeuThrLeuGluGluPro 179
DB 4662 CAAGAAGCAGACACACATTTGTTTCTGATGGCTCCGGAAGAAACATCTGAGGTGCCA 4721
QY 180 GlyGluThrIleValIleSerThrAapValAlaAapValSerLeuGlyProPheProLeu 199
DB 4722 AGCGTAAAGCTTACTGCTATGATGATTTCCACAGATTTCAAGT---ATGCTGCTCTT 4778
QY 200 -----ThrProAapAapThrLeuLeuAap----- 207
DB 4779 CATTCAGACAGACAAAGAACTCCCTGATCCAACTAGACACATCTCAATTAACAGTGTCA 4838
QY 208 -----GluIleLeuAapAapThr 213

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Db 4839 TATGAGAGTCCACAGACGGTAGTTCCAGACCGCTTTCAGGGAATTCAGAGATTCACACC 4898  
 Qy LeuAenAepThrLyMetProThrThrglu----- 223  
 Db 4899 TTTAAACCTTAACAGAAAAAACCCTGAAAATATTATTCATAGACCTGGACAAAGAGAC 4958  
 Qy 224 ArgGluThrgluPheAlaValIleuGluGluArgValGluLeuSerValSerLeuVal 243  
 Db 4959 AAGGATTTAATATTGACAACTTACAGAGATACCATCTTGAATTCCTAGCTGACGA 5018  
 Qy 244 AenGluYpHeuValIleGluLeuAlaAepSerGlnSerProTyrTyrGlnGluLeuAla 263  
 Db 5019 TCGGATTAATAATATCATATAGATATTGATCATCTAAACCTGTGTATGAAGACATTTCTT 5078  
 Qy 264 GlyYpSerGlnLeuGlnMetGlnIlePheYpLeuPheYpLeuProGlyPheYpLeuIle 283  
 Db 5079 GGA-----ATGCAAAACAGATTTAGATACAGAGTACCACTCA----- 5114  
 Qy 284 HisValIleuGlyPheArgProYpLeuYpGluYpAepGlySerSerSerThrGluMetGln 303  
 Db 5115 -----GAACCATAGACAGATATGATGAAGATGATGACAGACACTCA 5159  
 Qy 304 LeuThrAlaIlePheYpAepGlnHisSerAlaGluAlaYpSerProAlaSerAepLeu 323  
 Db 5160 GTTCAAGAGATCTATGAG-----GCAGCTGTCAACCTT 5192  
 Qy 324 SerPheAepSerAenIleIleGluSerGluGluValTyrHisGlyThrMetGlnGluAsp 343  
 Db 5193 TCTTTh-----ACTAGGAAACATTTGAGGCTCT----- 5222  
 Qy 344 LysGlnProGluIleTyrIleuThrAlaThrAepLeuYpArgLeuIleSerYpAlaLeu 363  
 Db 5223 -----GCGATGTTCTGGCTAGCTACACTCAGCAACACATGATGATCAATGACTTAT 5276  
 Qy 364 GluGluGluGlnIleuSerLeuAepValGlyThrIleGlnPheThrAepGluIleAlaGlySer 383  
 Db 5277 GAAAGATGAAGCAATCATGATCATGAGCTTTCACCTTCACTCAACT-----GAG 5324  
 Qy 384 LeuProAlaPheGlyProAepThrGlnSerGluLeu-----ProThr 397  
 Db 5325 ATCCCTGCT-----CTTAGCACAAACAGAAATTTAGACGTTTACTCCACGGCAACA 5378  
 Qy 398 SerPheAlaValIleThrGluAspAlaThrIleuSerProGluLeuProProValGluPro 417  
 Db 5379 TCCCTGCAATTCCTCGTAAGTGTGCGACAGTTATTCCAGAGATTGAAGAAATAAGCT 5438  
 Qy 418 GlnLeuGluThrValAsp----- 423  
 Db 5439 GAAAGCAAAAGCCCTGATGACATGTTGAATCAAGCACTTGTCTGATGTCAGCTATT 5498  
 Qy 423 ----- 423  
 Db 5499 GCAGACAAAGTGAATTAATACCAACATTTGGCCATTTGAAAAGACTCAGAGAGATAT 5558  
 Qy 424 -----GlyAlaGluHis 427  
 Db 5559 GAAAGCAAAAAACATGCTGCTCTTTTTCAGCCAGAAATCTCTTCAGAGACTGAGAG 5618  
 Qy 428 GlyLeu-----ProAepThrSerTyrPserProProAlaMetAlaSerThrSer 443  
 Db 5619 GCATATAGTACCACTACTCCCTATCATAGTATTGCTATACCTACCCATTTGATGATCAGAT 5678  
 Qy 444 LeuSerGluAla-----ProProPhePhe----- 451  
 Db 5679 GTTAACAGAGTCCCTGATGTGATGGAAGATCCAAATCCCATATTTACCTGATTCACACA 5738  
 Qy 452 MetAlaSerSerIlePheSerLeuThrAepGlnGlyThrThrAepThrMetAlaThr--- 470  
 Db 5739 TTAGAGATTTCAAATTTCGAAAGTTGCTCTTCAGACACACATCATCTCCCTCACTATC 5798  
 Qy 471 -----AepGlnThrMetLeuValProGly 478  
 Db 5799 TACTGAGGAGTGAAGCCTCTGAGACACAGAGATCCCCAGCCAGTGTCTGTCCAGAGA 5858

Qy 479 LeuThrIleProThrSer----- 484  
 Db 5859 ATAGACGTGGCTCATCTGTATGTCCCCACAGGATTTCTTTAAGAAATTCATGTAAT 5918  
 Qy 485 -----AepTyrSerAlaIleSerGlnLeuAlaGluGlyIleSerHisProProAla 501  
 Db 5919 ATTGAAGCACTTCAACACATCAAGTGAAGATATCTTACATTAAGTGAACCTCCCTCT 5978  
 Qy 502 SerSerAepAepSerAepSerSerAlaGlyGlyGluAsp---MetValArgHisLeuAsp 520  
 Db 5979 TTATCTCTGACACAAATTTGAACCTTCAGAGATGATGTGTAACCTGAGTTATTAGAA 6038  
 Qy 521 GluMetAepLeuSerAepThrProAla----- 529  
 Db 6039 GAAATGAGAGCTTCTCCACAGAACTTATGCTGTGGAAGGAACCTGAGATTTCTCAAGAT 6098  
 Qy 530 -----ProSer--- 531  
 Db 6099 TTCCAAAACAAACCGATGTCAAGTTTCTGAGAGACATCAAGATGTTTCCACCAATT 6158  
 Qy 532 GluValProGluLeuSerGluTyrValSerValProAepHisAep---LeuGluAspThr 550  
 Db 6159 AAAACACCTGAGGCTGGAACCTTATTACAACCTGCCATGAATTAAGTAAGGTGCT 6218  
 Qy 551 Thr----- 551  
 Db 6219 ACAAGTGGCCACACTCTTCTGCTTCCACCTATGGGGTGGAGGAGGTGTGTTG 6278  
 Qy 552 -----ProValSerAlaGluGlnTyrIleThrThrSerSerMetThrIleAla 567  
 Db 6279 CTTGGCTAAGTCCACAGACTTGTGAGAGGCCACGCTTCTTCTTCCAGAAATTAAC 6338  
 Qy 568 Pro-----LysGlyArgGluLeuValIlePhePheSerLeuArg 580  
 Db 6339 CTTGAACCTCAAGCACTTATATCAAGAGGAGGATTCACAGATTCAGCACTCAAGAACG 6398  
 Qy 581 -----ValAlaAenMetAlaPheSerAenAepLeuPheAenIleYpSerSerLeuGluTyr 598  
 Db 6399 CAAGTGGAGGAGGAATTTCTGATTTCCATGATATCAGCAACAGTAACCCGTGGAATTT 6458  
 Qy 599 ArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAenLeuThr 618  
 Db 6459 AAT-----ACTGAGGTTGCAACACCACTATTTCCCTTCTGAGACT 6500  
 Qy 619 Gly-PheYpGlnLeuGluIleLeuAenPheArgAenIleValIleAenSerIle 638  
 Db 6501 TCTAATGAACAGATTCCTGATTG-----GCATTAATGAAGAGTCA 6542  
 Qy 638 AMetYpPheAlaYpSerValProTyrAenLeu-----ThrYpAlaIle 653  
 Db 6543 GTGAAAGCAGCGCAATTTATTTACAGAGACTGATTCCTGCCAAATGAACCCGTGCTT 6602  
 Qy 653 HisGlyValIleuGluAepPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAs 673  
 Db 6603 A-----ACGAGAGCACTGTATTCTCTGAAACTTCC 6635  
 Qy 673 PserTyrSerLeuAenIleGlu-----ProAlaAepGlnAla-----AepThr 687  
 Db 6636 TACGTATACACC-TGTGAGCAGATACAGCGGAGACAGTGTGAACCTGATTTTGAAGA 6694  
 Qy 687 OcyYpAepHeuAlaCySGlyGluPheAlaGlnCyValIleYpAenGluArgThrGluGlu 707  
 Db 6655 ATGTCACTCTAATCCCTCTCTGATAGAGCCACTGTGTGATGTTTAAACACA----- 6749  
 Qy 707 ValaGluCyAepArgCyYpLeuProGlyTyrAepSerGlnYpSerLeuAepGlyLeuGluP 727  
 Db 6750 -TTCAAGGTGCTGTGCTTCCAAAGTTATGTTGCT----- 6782  
 Qy 727 OcyYpLeuYpGlyProGlyThrThrGluCyGluVal-----LeuGlnGly 743  
 Db 6783 -GCACCTTGTGAGCAAGATACCGAGACATGTGACTATGCTGGACAAATTCCTCAAGGCA 6841

QY 743 a-----GlyAlaProCysArgLeuProAspHisSerGluAsnGln----- 756  
Db 6842 GGGCTAACAATCTTGGCCATCGACGACATGGAGTGCAGTGAAGGGAATGCCGTCT 6901  
QY 757 -----AlaTyrIleSerValIleYsPheGlnAsnGlnGln----- 769  
Db 6902 GCAAGGTGCCATCTCACAGACATCTCTCTCAGCAAGAACAAATGTTTATTATCTGTCT 6961  
QY 770 -----AsnAsnIleValIleSerIleYs-----ArgAs 778  
Db 6962 GGGCCATGATTTATCATGTGATAGCCCTCAATGACAAAGATGTTTGACATGATCTCCGTTC 7021  
QY 778 nSerGluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797  
Db 7022 GACTATGCGACACACATGCAATACGAG-----AATTGAGACCCAAAC 7064  
RESULT 13  
US-09-248-796A-2596  
; Sequence 2596, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 2596  
; LENGTH: 2472  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-2596  
Alignment Scores:  
Pct. No.: 0.000136 Length: 2472  
Score: 144.50 Matches: 116  
Percent Similarity: 34.51% Conservatve: 70  
Best Local Similarity: 21.52% Mismatches: 211  
Query Match: 3.51% Indels: 142  
Gaps: 22  
US-10-007-270-2 (1-797) x US-09-248-796A-2596 (1-2472)  
QY 144 ProAspArgIleYsAspGluIleSerAlaGluIleYsThrLeuGluIleProGluGluThrIle 183  
Db 184 CCAGAAAGCACTGATGATGCTG-----ATCATCAAGAAACACACAACTTACT 231  
QY 184 ValIleSerThr-----AspValAlaAsnValSerLeuGlu 195  
Db 232 GTGACTTACCAACAGATTGTTGTCAGAAATCATTTGCCACTACTGAAACGTTAACTTACAGGG 291  
QY 196 ProPheProLeuThrProAspAspThrIleLeuAsnGluIleLeuAspAsnThrIleAsn 215  
Db 292 -----CCACTTGGGACCTGATGATGCTTATATACATGATCCATTGGAGAACTGCTTCT 345  
QY 216 AspThrIleYsMetProThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArg 235  
Db 346 AGTACTGCTATTGAGTCAAGTATCTATATATTTCAGCTCAGCTCAAGAT----- 396  
QY 236 ValGluLeuSerValSerIleValAsnGluIleYsPheIleValGluLeuAlaSerGln 255  
Db 397 -----TCATCCAGCTTGGTGAACGATCATTTACTTCT-----GCTACGAGACT 441  
QY 256 SerProTyrTyrGluGluLeuAlaGluIleYsSerGlnLeuGlnMetGlnIlePheIleYs 275  
Db 442 TCAAGTATATAGTT---GAATTGTCAATCAAGCTCAGACATTCATCAAGCTCAATT----- 492  
QY 276 IysLeuProGluIlePheIleValIleHisValLeuGluIlePheArgProIleYsGluIleYsAsp 295

Db 492 ----- 492  
QY 296 GlySerSerThrGluMetGlnLeuThrAlaIlePheIleYsArgHisSerAlaGluAla 315  
Db 493 GGGTTAACAATCTAGAGATCGCTTCTCTCAATGATATATAGTACTTCCAACTACT 552  
QY 316 -----LysSerProAlaSerAspLeuLeuSerPheAspSerAsnIleGluSerGlu 333  
Db 553 AGCGAATCATCTATTGCTTCAAGTATATAGTACTTCTGTCAGATGATGATGATGATGCTCT 612  
QY 334 GluValIleThrHisGluIleThrMetGluGluIleYsPheGlnProGluIleIleThrIleThrAlaThr 353  
Db 613 ACATTA-----TTAGTTCGATATATATCTGTCAGATGATCTGTATACCA 660  
QY 354 AspLeuIleYsArgLeuIleSerIleValLeuGluGlu-----GluGlnSer 368  
Db 661 AGCTTTTGGAGTTCCTTCAAGTTCGATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 720  
QY 369 LeuAspValGluThrIleGlnPheThrAspGluIleAlaGluSerLeuProAlaPheGly 388  
Db 721 ATCGATGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768  
QY 389 ProAspThrGlnSerGluLeuProThrSerPhe----- 399  
Db 769 ---AGCACAGTCAAGATTTATCATCAAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 825  
QY 400 ---AlaValIleThrGluAspAlaThr-----LeuSerProGluLeuProProValGlu 416  
Db 826 GATGCTTTAGTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 885  
QY 417 ProGluLeuGluThrVal-----AspGluAlaGluIleGluIleYsProAspThrSerThr 434  
Db 886 CCATCTAGACACATCTGCGCAGTGCAGATTTTCCACACATATATGTCGGAGACAGAT 945  
QY 435 SerProProAlaMetAlaSerThrSerLeuSerGlu----- 446  
Db 946 AGCCAATCAATCTCATTTATATCAATCTGTTGATGATTTTCAAGTATCGGTCTCTT 1005  
QY 447 -----AlaProProPhePheMetAlaSerSerIlePheSer----- 458  
Db 1006 ACAAGTACCCAGACAGAGATTTTATCATCTTATGATTTTATGATTTTATGATTTTATGATTTTATGAT 1065  
QY 459 -----LeuThrAspGluIleThrThrAspThrMetAlaThrAspGluIleMetLeuVal 476  
Db 1066 CTGCCATCCAGTACCAAGATGATTTTGAATCTCATGATTTTTCATGATTTTTCATGATTTTTCATGATTTTTC 1125  
QY 477 ProGluLeuThrIleProThrSerAsp----- 485  
Db 1126 CCATCTTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1185  
QY 486 -----TyrSerAlaIleSerGlnLeuAlaLeuGluIleSerHisProProAlaSer 502  
Db 1186 TCAACAATCATTCATGATCGGAATCCGAAGCTCATCTGCGCTTCCACCAATGCGCA 1245  
QY 503 SerAsp----- 509  
Db 1246 AGTAGGACGATATGATGACACATATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1305  
QY 510 AlaGluIleGluAspMetValArgHisIleYsAspGluMetAspLeuSerAsp----- 526  
Db 1306 ATTTGACACAGATTTCTTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365  
QY 527 -----ThrProAlaProSerGluValIleProGluLeuSerGluTyrValSerValPro 543  
Db 1366 GTAACAGGAT 1425  
QY 544 AspHisPheLeuGluAspThrThrProValSerAlaLeuGluIleThr----- 560  
Db 1426 TCTAGCTTTGTTGCTTCAGACACCCCACTCAGAGAAAGTGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485  
QY 561 -----ThrSerSerMetThrIleAlaIleProIleYsGluIleValIlePhePheSer 578

Db 1486 AATATGACTACGTGCAAAACAGTCTAGTCTTCACTAAATATATGATTGTTGTCGA 1545  
Qy 579 LeuArgValAlaAsp-----MetAlaPheSerAspAspLeu 591  
Db 1546 GATACAGTGAATTAATTCATTATTCGAAACGTCAACCTTATCATCTGAT----- 1599  
Qy 592 AsnLysSerSer-LeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeu 609  
Db 1600 ---GACACTACTCTCTCGGATACCGACATTAGCTCAACAACTCATGATCTG 1651

RESULT 14  
US-09-418-780A-2  
Sequence 2, Application US/09418780A  
Patent No. 6504009  
GENERAL INFORMATION:  
APPLICANT: Jones, Michael H  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR  
FILE REFERENCE: 06501-043001  
CURRENT APPLICATION NUMBER: US/09/418,780A  
CURRENT FILING DATE: 1999-10-15  
PRIORITY APPLICATION NUMBER: PCT/JP98/01762  
PRIORITY FILING DATE: 1998-04-17  
PRIOR APPLICATION NUMBER: JAPAN 9/116402  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 3104  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (106)...(2346)  
US-09-418-780A-2

Alignment Scores:  
Pred. No.: 0.000205 Length: 3104  
Score: 144.50 Matches: 150  
Percent Similarity: 34.23% Conservative: 116  
Best Local Similarity: 19.31% Mismatches: 321  
Query Match: 3.51% Indels: 191  
Gaps: 32

US-10-007-270-2 (1-797) x US-09-418-780A-2 (1-3104)

Qy 16 LeuGlnValGlnGlyThrLysAspLysSerLysLeuIleTyrHisSerGluThrLysAsp 35  
Db 764 CTGCACTTCAGCAGCTTAAAGCAAGTAGTGAATTTCTCCAACTTCACAGAA-AAATCA 822  
Qy 36 Ile-----AspAsnProProArgAsn----- 42  
Db 823 GTGGACACGCCACCTATAAAGAAATATGCCAAAGATGTTTGGCAGATTTCTCAGCA 882  
Qy 43 -----GluThrThrGlnSerThrGluLysMetTyrLysMetSerThrMet 57  
Db 883 CAATATATGTTGTGAGACTGTCTTAAAGTAATGTAACATTAAGCAGCTGTAGTGAAT 942  
Qy 58 ArgArgLysPheAspLeuAlaLysHisArgThrLysArgSerAlaPhePhe---ProThr 76  
Db 943 CTTAAAGAAATGCTTGAAGAAACATTTTTCATATGATGAGCCCTTTTATATCTGTT 1002  
Qy 77 GlyValLysValCysProGlnGlnLysMetLysGlnLysLeuAspSerLeuGlnAlaTyr 96  
Db 1003 GACGTTATGCTTGG-----GAGCTCCATACACTCTATGAGCTTGTCAAAATCCG 1053  
Qy 97 TyrArgLysArgValCysGlnGlnLysAlaValTyrGlnAlaTyrArgLysPheLeuAspArg 116  
Db 1054 ATGATCTTGAACATTAATAGAGAAATG----- 1083  
Qy 117 IleProAspThrGlnGlyTyrGlnAspThrValSerLysCysGlnGlnGluThrPheCys 136  
Db 1084 -----GATTAACCAAGAAATATTAAGATGATCATCTATTGGCGCA----- 1122

Qy 137 LeuPheAspLysGluLysAsnPheSerAsnSerGlnGlnIleLeuAspLeuLeuGln 156  
Db 1123 -----GATGTAGATTATATGCTATGATTCCTACAAATGTC----- 1158  
Qy 157 ArgLysGlnArgSerPheProAspArgLysAspGlnLysSerAlaGluLysThrLeu 176  
Db 1159 -----AATCTCCAGATCAGCAAGGTGTGACAAATGCAAGAAATGCTT 1200  
Qy 177 GlyLysProGlnGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyPro 196  
Db 1201 CAGAT-----GTTTTCGAAACGCAATTTTTCAAAGATCCGATTCGAACCT 1245  
Qy 197 PheProLeuThrProAspAspThrLeuLeuAsnGlnLysLeuAspAsnThrLeuAsp 216  
Db 1246 GTTAGAGTAGTCCCTTATATGTTACATCAAAACAGATATCACAGAAACCTGTTAGAG 1305  
Qy 217 ThrLysMetProThrThrGlnArgGluThrGluPheAlaValLeuGluGlnAlaArgVal 236  
Db 1306 AACACTAATGAAGCTCTGGAAGGAACTCTTGATGATTCGAAGATGAGCGAGT 1365  
Qy 237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerLys 256  
Db 1366 -----AAGCGTCTGCAAGCTTCAGAGCAGCAGCTTAAA 1398  
Qy 257 ProTyrTyrGlnGlnLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLys 276  
Db 1399 GCTGATCATCAACGCTCCAGCTTGTGTCGCAAGTACTTCCGTAAGCTTAATTAAG 1458  
Qy 277 LeuProGlyPheLysLysIleValLeuGlyPheArgProLysGluLysAspGly 296  
Db 1459 AAGAGAAAGCTTAAGG-----GAAAGAAAGAAAGAAAGGTTAAT 1500  
Qy 297 SerSerSer-----ThrGluMetGlnLeuThrAlaIlePheLys 309  
Db 1501 AACAGCAATGAATAATCCAGAAATAATGTGAGCAAAATGAGCTTAAGCAAAAGTCCAA 1560  
Qy 310 ArgHisSerAlaGlnAlaLysSerProAlaSerAspLeuLysSerPheAspSerAsnLys 329  
Db 1561 AGAAAT-----CAGCCAAAGAAAGAAACACAGTTCAATGGT----- 1599  
Qy 330 IleGluSerGlnGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyr 349  
Db 1600 CTTAAATCTGAAGAT-----GAAATATATGCTAAACCTATGAACATAT 1641  
Qy 350 LeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeuGluGlnGlnSerLeu 369  
Db 1642 -----GATGAGAAAGGACGTTAAGTGAATATGAACAACTCCCTGAGAT 1689  
Qy 370 AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro 389  
Db 1690 AAAGTGGCGAGTA-----GTTCACTAATATCAATCAAGAGACCTTCTGAGCAAT 1743  
Qy 390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409  
Db 1744 TCCATCTCGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1800  
Qy 410 ProGluLeuProProValGluProGlnLeuGlnThrValAspGlyAlaGlnHisGlyLeu 429  
Db 1801 -----GAATTAAGAAATAATGTTTGGCA-----TGCTTA 1830  
Qy 430 ProAspThrSerTyrSerProProAla-----MetAlaSerThrSerLeuSer 445  
Db 1831 AGAAGAGACCATTAATACTCTGCTTAAGAAATAATGATGATCCAAAGAAAGAACTTAC 1890  
Qy 446 GluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThr 465  
Db 1891 TCACAGAAAAAACAAGATGGAAGAGCGTTACTGATGATTAATTAATCAATTAATCT 1950  
Qy 466 AspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro---ThrSer 484  
Db 1951 AGAAGACGTCAAACAAATCTGATTAACCGAACCATTCAAAGCGTTGAAATGTTTCC 2010  
Qy 485 AspTyrSerAlaIleSerGlnLeuAlaLeuGlyLysSerHisProProAlaSerSerAsp 504



OY	277	LeuPProGluPheIleValIeHisValIeuGIyPheaArgProIyeIysGluIyeAspGly	296
Db	1461	AAAGGAAGACTTAAAAAG-----	GAAAAGAAAAAAGAAAGGTTAAT 1502
OY	297	SerSerSer-----	-ThrImetGlnLeuThrAlaIlePheIlys 309
Db	1503	AACACCAATGAATAATCCAAAGAAAAATGCTGTAGCAAATGAGCCTTAAGAAGAAAGTCCAAG	1563
OY	310	ArgHiseSerAlaGluAlaIleIysSerProAlaSerAspLeuLeuSerPheAspSerXnIlys	329
Db	1563	AGAAAT-----CACGCCAAAGAAAAAGAAACAACAGTTCAATTGGT-----	1601
OY	330	IIEgluSerGluGluValTyrtIseGlyThrMetGluGluAspIyGlnProGluIleTyR	349
Db	1602	CTAAAATCTGAAGAT-----	-GAAAGTAAAGCTAACCTATGAACAT 1643
OY	350	LeuThrAlaThrAspLeuLysArgPheIleSerLySalaIleuGluGluGlnSerIeu	369
Db	1644	-----GATGAGAAAAGCGCATTAATCTGAATATATAACAAACTCCCTGGAGAT	1691
OY	370	AspValIGlyThrIIegInPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro	389
Db	1692	AAACTGGCGCAGTA-----GTCCACATTAATACATCAAGAGAGCCTTCTGTGAGCAT	1745
OY	390	AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrIeusEr	409
Db	1746	TCCAATCCTGATGATAGATAGATAGACCTTGAAACACTG--AAAGCATCAACACTTAAGA	1802
OY	410	ProGluLeuProProValGluProGlnIleuGluThrValAspGlyAlaGlnHieGlyIeu	429
Db	1803	-----GAATTAGAAAATATGTTCCGCA-----TGCTTA	1833
OY	430	ProAspThrSerTrpSerProProAla-----MetAlaSerThrSerIeusEr	445
Db	1833	AGAAAGAGACCATTAATAACCTCTGCTAGAAATATGATATGTCCAAAGAAAGAACTTCAAC	1892
OY	446	GluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThr	465
Db	1893	TCACAGAAAAAACAAGAAATTTGAAAAACGGTTACTGATGTAAATACACTTAATATCT	1952
OY	466	AspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro---ThsEr	484
Db	1953	AGAAAAAGTCNAACAAATCTGATATAAACGCACACCTCCAAAGCTGTGAATAATGTTTCC	2012
OY	485	AspTrySerAlaIleSerGlnLeuAlaIeuGlyIleSerHieProProAlaSerSerAsp	504
Db	2013	GCACGTAGTAGAAGCAGCAGCAGCAGCAGCAGCAGCTCATGACATCGTAAGTAGCAGCAGCT	2072
OY	505	Asp-----SerArgSerSerAlaGlyGlyIuAspMetValArgHileuAspGlu	521
Db	2073	GACTTAAGCTCTTCAGACAGCAGTATCTGATCAGATACTTCCCTTAAGTTTACADAA	2133
OY	522	MetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyTylalser	541
Db	2133	GTAAAACCNAATGATTTCTCTTAAAGCATGTAAAAGAAATAGANAAGATGATCAT	2192
OY	542	ValProAsp-----HiePheLeuGluAspThrThrPro	552
Db	2193	CTGCCTGAAGAAAGAAACAGCGCTCACACAGATAGATATGCTGTGCAAGACCAACCTCT	2255
OY	553	Val---SerAlaIeuGlnTyrlleThrThrSerBerMetThrIleAlaProIyGlyArg	571
Db	2253	GCCAATACTACCTTGTTGATCAGACACCACTTCACATGATAGCCCAATATACAGC	2312
OY	572	GluLeuValValPhePheSerIeuArgValAlaIasMetAlaPheSerAsnAspIeuPhe	591
Db	2313	CAAATTAGCA-----TTT	2322
OY	592	AsnLysSerSerIeuGluTyRArgAlaIeuGlnGlnIlePheThr-----GlnIeuIeu	609
Db	2325	ATTATTCAGATTAAGACATTTACAGACTGTGAAAAACATTTTCACTTACAAATTTCTG	2388
OY	610	ValPro-----TyrlieuArgSerAsnLeuThrGlyPhe-----	620

Db 2385 CCTCCCTCAGGTGATTCTGAAACAGCTCTCAAAATGGCATTACTGTGATGCATCCATCTGGT 2444A  
 QY 621 -----||| ||| ||| ::| ::| |||-----LysGlnLeuGlu 624  
 Db 2445 GATAGTGACACAACGATGTTAGAATCTGAATGTCACAGCTCCTGTACAGAAAGATATAAAG 2504A  
 QY 625 ILeIeuAenPheAaIgaenGlySerValIleValAAsenSerIysmEtySphenAlaIysSer 644  
 Db 2505 ATTAAGAAAT-----GCAGATTCATGAGAAAAGTTTAGGCCAACCA 2543A  
 QY 645 Val---ProTyraenLeuThrIysAlaIeValIleGlyValLeuGluAAsPheArgSerIa 663  
 Db 2544 GTGAAGAACCATCAGGGGTAAATGAAATCCCTCAGATGAGCTCTTCAACCAATTTTAGAAAAGCA 2603A  
 QY 664 Ala-----AlaGlnGlnLeu-----HisLeuGluIle 672  
 Db 2604 GCCATTAGAAAAAGAAAGTAAAGAGCTCGGACACAGAGAACTCATACGGAAGCAATTTGGAAACA 2663A  
 QY 673 AAsPserTySerLeuAenIleGluProAlaAspGlnAlaAsPProCysIysPheIeuAla 692  
 Db 2664 AATAAAGAAAGAACTTAAAGACATCTCCAGAAAATATCAGAGAGATCTTTGGAAATGATGACT 2723A  
 QY 693 CysGlyGluPheAlaGlnCysValIysAenGluIArgThrGluGluAlaGlu 709  
 Db 2724 GTAGATCTCTTTTCAAATTAATATCAAAACAGAGCTCTGTGAAGAAAGACAG 2774A

Search completed: January 15, 2006, 04:15:47  
Job time : 524 secs

QY 610 ValPro-----TyrLeuArgSerAsnLeuThrGlyPhe----- 620

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 14, 2006, 21:46:50 ; Search time 10253 Seconds  
(without alignments)

4418.632 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117  
Sequence: 1 MYLERRAIFWIFLQVQ.....NSELTVEEERHODWEGN 797

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_p2n.model -DEV=xlh  
-Q=/cgn2.1/USPTO.spool/US10007270/runat.11012006.110803.10621/app.query.fasta\_1.967  
-DB=GenEmbl -QFMT=fastaop -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdt -LIST=45  
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10007270@cgn2.1.6870 @runat.11012006.110803.10621 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_ph:\*  
9: gb\_ph:\*  
10: gb\_ph:\*  
11: gb\_ph:\*  
12: gb\_ph:\*  
13: gb\_ph:\*  
14: gb\_ph:\*  
15: gb\_ph:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4117	100.0	3268	8 AF047492	Homo sapi
2	3370	81.9	2009	6 CO725539	Sequence
3	2759	67.0	3552	4 AB047844	Bos tauru

Result No.	Score	Query Match	Length	DB ID	Description
4	2548.5	61.9	3668	9 AP266478	
5	2546.5	61.9	2824	9 BC022970	
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9	933	22.7	3989	5 AF157624	
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2	3370	81.9	2009	6 CO725539	Sequence
3	2759	67.0	3552	4 AB047844	Bos tauru

AUTHORS Kuehn, M.H. and Hageman, G.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-OCT-1999) Ophthalmology and Visual Sciences,  
 University of Iowa, 200 Hawkins Drive, 1190E PFP, Iowa City, IA  
 52240, USA

REMARK Sequence update by submitter  
 On Oct 26, 1999 this sequence version replaced gi:2906231.

COMMENT location/Qualifiers

FEATURES

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 SOURCE  
 ORGANISM  
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 Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE  
 1 (sites)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Isolation and characterization of mucinlike glycoprotein associated  
 with photoreceptor cells  
 Invest. Ophthalmol. Vis. Sci. 41 (9), 2759-2765 (2000)  
 JOURNAL  
 PUBMED  
 10937595  
 REFERENCE  
 2 (bases 1 to 3552)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Direct Submission  
 Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University  
 Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,  
 Kagoshima 890-8520, Japan  
 (E-mail: f.uehara@meds.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,  
 Fax:81-99-265-4894).  
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## ORIGIN

## Alignment Scores:

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Percent Similarity:	80.624	Conservative:	80
Best Local Similarity:	70.744	Mismatches:	132
Query Match:	67.014	Indels:	27
DB:	4	Gaps:	5

US-10-007-270-2 (1-797) x AB047844 (1-3552)

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DB	215	ATCAAAAGATCTCTCCATTAATAATATACGGTTCGAAATTAAGACATAGATATGCCCCA	274
QY	41	ArgAsnGluThrThrGluSerThrGluYrMetYrLYMeSerThrMetArgArgIle	60
DB	275	AAACCTGAAGCAACCAAAATAATACCGCAAAACGTACAAAGTGTCAACCTGAGACCAATA	334
QY	61	PheAspLeuAlaIleHisIleArgThrLYAsArgSerAlaPhePheProthrgIyValLYsVal	80
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QY	101	ValCYeGlnGlnValAlaTYrPGLuAlaTYrArgIlePheLeuAspArgIleProAspThr	120
DB	455	GTGTCCAGAGAGCGGTGTGGAGAGCTTACCGGATCTTCTGATCTGCTCCCTGAGCGCG	514
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DB	515	GGGGATACCAAGACCTGGGTCAAGCTCTCCAGCAGAGAGACCTTCTGCTCTTTGACATC	574
QY	141	GlyLYAsnPheSerzAsnSerGlnGlnIuIleAspLeuLeuGlnGlnArgIleLYsGln	160
DB	575	GGGAAATAATTTTCAGCACTCCAGAGAGCACTGGATCTTCTTCAAGAGAGATGAACAG	634
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DB	695	CAAAACCCCTGGCTTCAACAGCTTGGCAAGTGTCTCACCCGGGCGCTTGCCTCTCCCT	753
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LOCUS      Mus musculus IPM 150 proteoglycan mRNA, complete cds.
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ACCESSION  AF266478
VERSION    AF266478.1 GI:9844921
KEYWORDS
SOURCE
ORGANISM   Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sciurognathi; Murididae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 3668)
  Kuehn,M.H., Wietzecki,D.T. and Hageman,G.S.
  Molecular characterization of the murine orthologue of the human
  retinal proteoglycan IPM 150
  Mol. Vis. 6 (2000) In press
JOURNAL
  2 (bases 1 to 3668)
  Kuehn,M.H., Wietzecki,D.T. and Hageman,G.S.
  Direct Sublimation
  Submitted (10-MAY-2000) Ophtalmology, University of Iowa, 2501
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 1 (bases 1 to 2924)  
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 Stachlekon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S.,  
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Abrahamson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Meyer, R.M.,  
Butcherfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,  
Schnerker, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Strausberg, R.  
Direct Submission  
Submitted (04-FEB-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulèsed, H.,  
Kovats, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILN, at: <http://image.lln.gov>  
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This clone was selected for full length sequencing because it  
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gene

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Query Match: 61.85% Indels: 21  
DB: Gaps: 9

US-10-007-270-2 (1-797) x BC022970 (1-2924)

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 SOURCE  
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 REFERENCES  
 1 (sites)  
 Uehara, F., Ohba, N. and Ozawa, M.,  
 Core Protein of rat Mucinlike Glycoprotein Associated with  
 Photoreceptor Cells  
 Published Only in Database (2000)  
 2 (bases 1 to 2850)  
 Uehara, F., Ohba, N. and Ozawa, M.,  
 Direct Submission  
 Submitted (28-AUG-2000) FumiYuki Uehara, Kagoshima University  
 Faculty of Medicine, Ophthalmology, 8-35-1 Sakuragaoka, Kagoshima,  
 Kagoshima 890-8520, Japan  
 (E-mail: f.uehara@meds.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,  
 Fax:81-99-265-4894)  
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US-10-007-270-2 (1-797) x AB047643 (1-2850)

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 LOCUS DEFINITION Mus musculus sialoprotein associated with cones and rods SPACK  
 mRNA, complete cds.  
 AF229929  
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 VERSION  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
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 Sciurionathi; Murioidea; Muridae; Murinae; Mus.  
 REFERENCES  
 1 (bases 1 to 3675)  
 Lee,J.W., Chen,Q., Rayborn,M.S., Shadach,K.G., Crabbs,J.W.,  
 Rodriguez,J.R. and Hollyfield,J.G.  
 SPACK in the photoreceptor matrix of the mouse retina:  
 molecular and biochemical characterization  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 3675)

AUTHORS Rodriguez,J.R., Lee,J.W. and Hollyfield,J.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JUN-2000) LRCMB, NEI-NIH, 6 Center Drive MSC2740  
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 ACCESSION AB070714  
 VERSION AB070714.1 GI:21623676  
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 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Qy ----- 400
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VERSION AF157624.1 GI:6467402
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Hominoidea; Homo.
1 (bases 1 to 3989)
Acharya,S., Fioletta,V.C., Lee,J.W., Rayborn,M.E., Rodriguez,I.R.,
Young,W.S., Ili and Hollyfield,J.G.
SPACRCAN, a novel human interphotoreceptor matrix
hyaluronan-binding proteoglycan synthesized by photoreceptors and
pinealocytes
JOURNAL
J. Biol. Chem. 275 (10), 6945-6955 (2000)
PUBMED
10702256
REFERENCE
Fioletta,V.C. and Young,W.S.
Direct Submission
Submitted (09-JUN-1999) SNGE, NIMH, 36 Convent Dr, MSC 4068,
Bethesda, MD 20892-4068, USA
JOURNAL
FEATURES
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## ORIGIN

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QY 217 ThrLysMetProThrThrgluArgGluThrGluPheAlaValLeuGlnGlnArgVal 236  
DB 714 GCCAGAAACCGACGAGTGAAACAGATTGCCAGAAATC----- 749  
QY 237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256  
DB 750 -----AGTATCCACCTTTTGGGGAAGCAGTACAGAGAAACTCAGGATTCCTCAGC 803  
QY 257 ProTyTrpArgGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLys 276  
DB 804 TTTCACCAACGACACCTTGAAAGAAATTTATTTCAAGGTGAAATGCAATTACTGGG 863  
QY 277 LeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysGlyLysAspGly 296  
DB 864 TTACCAAGCTACAGAGAAATTCGTACTGATTTAGTGTCCCAAGAAATATGAC--- 920  
QY 297 SerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlnAlaLys 316  
DB 921 ---AGTGCAGTAAAGTTTACTATGACACTTACCTTC-----AATGCTAGGCCATTC 968  
QY 317 SerProAlaSer---AspLeuLeuSerPheAspSerLeuLysIleGluSerGlnIleVal 335  
DB 969 AGCAATACACCTGGAGCTCAATTAGCCTTCACTCCACCAAGGTGAAAC----- 1019  
QY 336 TyHisGlyThrMetGlnGluLysAspLysInProGlnIleTyLysThrAlaThrAspLeu 355  
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QY 356 LysArgLeuIleSerLysAlaLeuGlnIle----- 365  
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QY 366 -----GluGlnSerLeu 369  
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QY 378 -----AspGlnIleAlaGlySerLeuPro--- 385  
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QY 386 -----AlaPheGlyProAspThrGlnSerGlnLeuPro 396  
DB 1317 CTGATTTTCAGCTGTGTTCTCTCCACGACCTGCAAGGAACTGTGTGAGAAAGTCT 1376  
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Qy      443 ---SerleuSerGluAlaPro-----ProPhePheMetAlaSerSer 455
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Qy      456 IlePheSerleuThrsAspIlnGlyThrThrAspThrMetAlaThrsAspIlnThrMet--- 474
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RESULT 10

CO870600 4165 bp DNA linear PAT 13-SEP-2004

LOCUS CO870600

DEFINITION Sequence 9 from Patent WO2004073657.

ACCESSION CO870600

VERSION CO870600.1 GI:52000111

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

Aziz,N., Gish,K.C., Wilson,K.B. and Zlotnick,A. Methods of diagnosis of cancer, composition and methods of screening for modulators of cancer

Patent: WO 2004073657-A 9 02-SEP-2004;

PROTEIN DESIGN LABS, INC. (US)

location/Qualifiers

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Best Local Similarity: 22.524 Indels: 405  
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US-10-007-270-2 (1-797) x CQ870600 (1-4165)

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QY 22 ---LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro-- 39  
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QY 40 -----ProArgAsnGluThr-----ThrGluSer 47  
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Db 666 GTGGAACATGAAAGCTTATCATGAAGAACTGACTTAT-----GGAAG 710  
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QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
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QY 427 ---HisGlyLeuProAspThrSerThrSerProProAlaMetAlaSerThr----- 442  
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QY 471 AspGlnThrMet----- 474  
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AF173155
LOCUS
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ACCESSION AF173155
VERSION AF173155.1 GI:6318679
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Kuehn, M.H. and Hageman, G.S.
TITLE Molecular characterization and genomic mapping of human IPM 200, a
second member of a novel family of proteoglycans
Mol. Cell Biol. Res. Commun. 2 (2), 103-110 (1999)
JOURNAL
PUBMED 10542133
REFERENCE
AUTHORS Kuehn, M.H. and Hageman, G.S.
TITLE Direct Submission
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Crosspark Rd., Coralville, IA 52241, USA
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US-10-007-270-2 (1-797) x AF173155 (1-4165)

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 QY 67 -----ArgThrLysArgSerAlaPhePheProThrGlyValLysValCys 81  
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1 (bases 1 to 816)
Felbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.F.
Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IPM1) gene: a candidate
for 6q-linked retinopathies
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
9691169
JOURNAL
PUBMED
2 (bases 1 to 816)
Gehrig,A., Felbor,U., Kessel,R., Hunt,D.M., Maumenee-Huesels,I.E.
and Weber,B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bilateral chorioretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDR1)
Unpublished
JOURNAL
REFERENCE
3 (bases 1 to 816)
Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
Direct Submission
Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
JOURNAL
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LOCUS  
DEFINITION  
Human DNA sequence from clone RP11-758J17 on chromosome 6 Contains the 3' end of the IMPG1 gene for Interphotoreceptor matrix proteoglycan 1, complete sequence.  
ACCESSION  
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VERSION  
AL392166.19 GI:13396652  
KEYWORDS  
HTG; IMPG1.  
SOURCE  
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ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 90766)  
REFERENCE  
Clark, S.  
Direct Submision  
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk  
Clone requests: clonerequest@sanger.ac.uk  
On Mar 20, 2001 this sequence version replaced gi:13234983.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr6  
RP11-758J17 is from the library RPEC1-11.3 constructed by the group of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACe3.6  
-----Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: vegas@sanger.ac.uk  
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
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complement(AL356962.8:1833..1891),  
complement(88813..complement(86620..86667),  
complement(85207..85283),complement(84251..84329),  
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RSFPRKDEISAEKTLGEGEIVISTVANVSLGPFPLTDDTLNLTINDTKD
MPTRETERPAVEREORVSLVSNOKFKLADPSPYOELAGKSLQOMOTFKK
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FMASIFSLTQGTDTMATDQMLVPLATITPSDYSAISQALGISHPPASDDRS
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CDS

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Score: 899.00 Matches: 178
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.44% Mismatch: 0
Query Match: 21.84% Indels: 0
Gaps: 0
DB: 8
US-10-007-270-2 (1-797) x AL392166 (1-90766)

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QY 431 AepThrSerTyrProAlaMetAlaSerThrSerLeuSerGluAlaProPhe 450
DB 32428 GACACTTCTGCTCCACCTGCTATGCTTACCTCCCTCTCGAAGAGCTCCACTTTC 32369
QY 451 PheMetAlaSerSerIlePheSerLeuThrAaPginglyThrThrAaPThrMetAlaThr 470
DB 32368 TTTATGGCATCAGCATCTTCTCTGACTGATCAAGGACACACAGATACATGCGCACT 32309
QY 471 AaPgingThrMetLeuValProGlyLeuThrIleProThrSerAaPtySerAlaIleSer 490
DB 32308 GACGACACATGCTGTGATCAGAGGCTCACACATCCACAGATTAATTCGCAATCAGC 32249
QY 491 GluLeuAlaLeuGlyIleSerIleProProAlaSerSerAaPAspSerAaPtySerAla 510
DB 32248 CAATCGGCTCTGGAAATTCACATTCACCTGATCTTCGATGACAGCCGATCAAGTGCA 32189
QY 511 GlyGlyGluAaPMetValArgHisLeuAaPgiuMetAaPLeuSerAaPThrProAlaPro 530
DB 32188 GGTGGCAAGATATGATGATGACACCTAGTAAATGATCTGTGACACCTCTGCCCCA 32129
QY 531 SerGluValProGluLeuSerGlyTyrValSerValProAaPHisPheLeuGluAaPThr 550
DB 32128 TCTGAGGATACAGAGCTCAGCAATATGTTCTGTCCCGATCATTTCTTGAGAGATAC 32069

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QY 551 ThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProtyGly 570
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QY 571 ArgGluLeuValIlePhePheSerLeuArgValIleAaMetAlaPheSerAaPLeu 590
DB 32008 CGAAGCTGCTGATGCTTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 31949
QY 591 PheAaPtySerSerLeuGlyTyrArgAlaLeuGlnGlnIlePheThrGlnLeuLeu 609
DB 31948 TTCAACAGAGCTCTGAGATACAGAGCTCTGAGAGCAATTCACAGAGCTG 31892
RESULT 15
LOCUS AL359817 132145 bp DNA linear HTG 10-JUL-2001
DEFINITION Homo sapiens chromosome 1 clone RP11-505B21, 26 unordered pieces.
ACCESSION AL359817
VERSION AL359817.6 GI:12225447
KEYWORDS HTG; HTGS; PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1
REFERENCE
McLay, K.
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 14, 2001 this sequence version replaced gi:12214326.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA505B21
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 117761 bases at least Q40
Consensus quality: 123343 bases at least Q30
Consensus quality: 126505 bases at least Q20
Insert size: 128645; sum-of-contigs
Insert size: 161195; 8.3% error; agarose-fp
Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality
coverage: 2.65x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
8913 8912: contig of 8912 bp in length
9013 9012: gap of 100 bp
12665 12665: contig of 3653 bp in length
12766 12765: gap of 100 bp
16825 16825: contig of 4660 bp in length
16826 16825: gap of 100 bp
16925 16925: gap of 100 bp
16926 16925: contig of 6033 bp in length
16927 16925: gap of 100 bp
22958 22958: gap of 100 bp
23058 23058: gap of 100 bp
23059 23058: contig of 2022 bp in length
25180 25180: gap of 100 bp
25181 25180: contig of 2992 bp in length
27272 27272: gap of 100 bp
27273 27272: gap of 100 bp
27372 27372: contig of 1382 bp in length
40754 40754: gap of 100 bp
40854 40854: gap of 100 bp
40855 40855: contig of 4293 bp in length

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*	455.8	45247:	gap of 100 bp
*	45248	48499:	contig of 3246 bp in length
*	48494	48593:	gap of 100 bp
*	48594	52881:	contig of 4288 bp in length
*	52882	52981:	gap of 100 bp
*	52982	57112:	contig of 4131 bp in length
*	57113	57212:	gap of 100 bp
*	57213	60637:	contig of 3425 bp in length
*	60638	60733:	gap of 100 bp
*	60738	62745:	contig of 2008 bp in length
*	62746	62845:	gap of 100 bp
*	62846	70684:	contig of 7839 bp in length
*	70685	70784:	gap of 100 bp
*	70785	74560:	contig of 3776 bp in length
*	74561	74660:	gap of 100 bp
*	74661	77242:	contig of 2582 bp in length
*	77243	77342:	gap of 100 bp
*	77343	81104:	contig of 3782 bp in length
*	81105	81204:	gap of 100 bp
*	81205	83750:	contig of 256 bp in length
*	83751	83850:	gap of 100 bp
*	83851	92962:	contig of 9112 bp in length
*	92963	93062:	gap of 100 bp
*	93063	106092:	contig of 13030 bp in length
*	106093	106193:	gap of 100 bp
*	106193	110995:	contig of 4803 bp in length
*	110996	111095:	gap of 100 bp
*	111096	114862:	contig of 3767 bp in length
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*	114963	118827:	contig of 3865 bp in length
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*	124185	128603:	contig of 4419 bp in length
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vector_side:left"
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12766..16825
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Percent Similarity:	99.44%	Mismatches:	0
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Query Match:		Gaps:	0
DB:	14		

  

US-10-007-270-2 (1-797) x AL359817 (1-132145)	
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Db 14959 GACACITCTTGTCCTCCACCTGCTAGGCTCTCACTCCCTGCAAACTCCACCTTTC	15018
QY 451 PhenelAlaSerSerIlePheSerIleuThrAspGlnGlyThrThrAspThreAlaThr	470
Db 15019 TTTATGACATCAAGCATTCTCTCTGACGTGATCAAGGACCAACGATATCATGGCCACT	15078
QY 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer	490
Db 15079 GACCAAGACATGCTAGTACAGGAGGCTCACCATCCACCAAGATATTATCTCAATCAGC	15138
QY 491 GlnLeuAlaIleuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSerAla	510
Db 15139 CAACTGGCTCTGGGAATTTCATCATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGA	15198
QY 511 GlyValGluAlaMetValArgHisLeuAlaAspGluMetAspLeuSerAspThrProAlaPro	530

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Qy      591    PheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeu 609
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Job time : 10577 secs